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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68, C12N 1/21, 5/12, G01N 33/569; 33/68, A61K 39/09	A2	(11) International Publication Number: WO 98/50554 (43) International Publication Date: 12 November 1998 (12.11.98)
(21) International Application Number: PCT/US98/08959 (22) International Filing Date: 4 May 1998 (04.05.98) (30) Priority Data: 60/044,031 6 May 1997 (06.05.97) US 60/046,655 16 May 1997 (16.05.97) US 60/066,009 14 November 1997 (14.11.97) US (71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): KUNSCH, Charles, A. [US/US]; 4083 Spalding Hollow, Norcross, GA 30092 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). BAILEY, Camella [US/US]; 32 Hickory Avenue, Takoma Park, MD 20912 (US). HROMOCKYJ, Alex [US/US]; 14909 Joshua Tree Road, N. Potomac, MD 20878 (US). (74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: <i>ENTEROCOCCUS FAECALIS</i> POLYNUCLEOTIDES AND POLYPEPTIDES (57) Abstract <p>The present invention relates to novel genes from <i>Enterococcus faecalis</i> and the polypeptides they encode. Also provided are vectors, host cells, antibodies and methods for producing the same. The invention additionally relates to diagnostic methods for detecting <i>Enterococcus</i> nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by <i>Enterococcus</i>.</p>		

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***Enterococcus faecalis* polynucleotides and polypeptides**

Field of the Invention

The present invention relates to novel *Enterococcus faecalis* genes (*E. faecalis*)
5 nucleic acids and polypeptides. Also provided are vectors, host cells and recombinant
methods for producing the same. Further provided are diagnostic methods for
detecting *Enterococcus faecalis* using probes, primers, and antibodies to the *E. faecalis*
nucleic acids and polypeptides of the present invention. The invention further relates
to screening methods for identifying agonists and antagonists of *E. faecalis*
10 polypeptide activity and to vaccines using *E. faecalis* nucleic acids and polypeptides.

Background of the Invention

Enterococci have been recognized as being pathogenic for humans since the
turn of the century when they were first described by Thiercelin in 1988 as
15 microscopic organisms. The genus *Enterococcus* includes the species *Enterococcus*
faecalis or *E. faecalis* which is the most common pathogen in the group, accounting for
80 - 90 percent of all enterococcal infections. See Lewis et al. (1990) Eur J. Clin
Microbiol Infect Dis.9:111-117.

The incidence of enterococcal infections has increased in recent years and
20 enterococci are now the second most frequently reported nosocomial pathogens.
Enterococcal infection is of particular concern because of its resistance to antibiotics.
Recent attention has focused on enterococci not only because of their increasing role in
nosocomial infections, but also because of their remarkable and increasing resistance to
antimicrobial agents. These factors are mutually reinforcing since resistance allows
25 enterococci to survive in an environment in which antimicrobial agents are heavily
used; the hospital setting provides the antibiotics which eliminate or suppress
susceptible bacteria, thereby providing a selective advantage for resistant organisms,
and the hospital also provides the potential for dissemination of resistant enterococci
via the usual routes of hand and environmental contamination.

Antimicrobial resistance can be divided into two general types, inherent or intrinsic property and that which is acquired. The genes for intrinsic resistance, like other species characteristics, appear to reside on the chromosome. Acquired resistance results from either a mutation in the existing DNA or acquisition of new DNA. The various inherent traits expressed by enterococci include resistance to semisynthetic penicillinase-resistant penicillins, cephalosporins, low levels of aminoglycosides, and low levels of clindamycin. Examples of acquired resistance include resistance to chloramphenicol, erythromycin, high levels of clindamycin, tetracycline, high levels of aminoglycosides, penicillin by means of penicillinase, fluoroquinolones, and vancomycin. Resistance to high levels of penicillin without penicillinase and resistance to fluoroquinolones are not known to be plasmid or transposon mediated and presumably are due to mutation(s).

Although the main reservoir for enterococci in humans is the gastrointestinal tract, the bacteria can also reside in the gallbladder, urethra and vagina.

E. faecalis has emerged as an important pathogen in endocarditis, bacteremia, urinary tract infections (UTIs), intraabdominal infections, soft tissue infections, and neonatal sepsis. See Lewis et al. (1990) *supra*.. In the 1970s and 1980s enterococci became firmly established as major nosocomial pathogens. They are now the fourth leading cause of hospital-acquired infection and the third leading cause of bacteremia in the United States. Fatality ratios for enterococcal bacteremia range from 12% to 68%, with death due to enterococcal sepsis in 4 to 50% of these cases. See T.G. Emori (1993) Clin. Microbiol. Rev. 6:428-442.

The ability of enterococci to colonize the gastrointestinal tract, plus the many intrinsic and acquired resistance traits, means that these organisms, which usually seem to have relatively low intrinsic virulence, are given an excellent opportunity to become secondary invaders. Since nosocomial isolates of enterococci have displayed resistance to essentially every useful antimicrobial agent, it will likely become increasingly difficult to successfully treat and control enterococcal infections.

Particularly when the various resistance genes come together in a single strain, an event almost certain to occur at some time in the future.

The etiology of diseases mediated or exacerbated by *Enterococcus faecalis*, involves the programmed expression of *E. faecalis* genes, and that characterizing these
5 genes and their patterns of expression would dramatically add to our understanding of the organism and its host interactions. Knowledge of the *E. faecalis* gene and genomic organization would improve our understanding of disease etiology and lead to improved and new ways of preventing, treating and diagnosing diseases. Thus, there is a need to characterize the genome of *E. faecalis* and for polynucleotides of this
10 organism.

Summary of the Invention

The present invention provides for isolated *E. faecalis* polynucleotides and polypeptides shown in Table 1 and SEQ ID NO:1 through SEQ ID NO:496
15 (polynucleotide sequences having odd SEQ ID NOs and polypeptide sequences having even SEQ ID NOs). One aspect of the invention provides isolated nucleic acid molecules comprising polynucleotides having a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence shown in Table 1; (b) a nucleotide sequence encoding any of the amino acid sequences of the polypeptides shown in
20 Table 1; and (c) a nucleotide sequence complementary to any of the nucleotide sequences in (a) or (b). The invention further provides for fragments of the nucleic acid molecules of (a), (b) & (c) above.

Further embodiments of the invention include isolated nucleic acid molecules that comprise a polynucleotide having a nucleotide sequence at least 90% identical,
25 and more preferably at least 95%, 96%, 97%, 98% or 99% identical, to any of the nucleotide sequences in (a), (b) or (c) above, or a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide in (a), (b) or (c) above. Additional nucleic acid embodiments of the invention relate to isolated nucleic acid molecules comprising polynucleotides which encode the amino acid sequences of

epitope-bearing portions of a *E. faecalis* polypeptide having an amino acid sequence in (a) above.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing
5 the recombinant vectors, as well as to methods of making such vectors and host cells. The present invention further relates to the use of these vectors in the production of *E. faecalis* polypeptides or peptides by recombinant techniques.

The invention further provides isolated *E. faecalis* polypeptides having an amino acid sequence selected from the group consisting of an amino acid sequence of
10 any of the polypeptides described in Table 1 or fragments thereof.

The polypeptides of the present invention also include polypeptides having an amino acid sequence with at least 70% similarity, and more preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% similarity to those described in Table 1, as well as polypeptides having an amino acid sequence at least 70% identical, more
15 preferably at least 75% identical, and still more preferably 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to those above; as well as isolated nucleic acid molecules encoding such polypeptides.

The present invention further provides a single or multi-component vaccine comprising one or more of the *E. faecalis* polynucleotides or polypeptides described
20 in Table 1, or fragments thereof, together with a pharmaceutically acceptable diluent, carrier, or excipient, wherein the *E. faecalis* polypeptide(s) are present in an amount effective to elicit an immune response to members of the *Enterococcus* genus, or at least *E. faecalis*, in an animal. The *E. faecalis* polypeptides of the present invention may further be combined with one or more immunogens of one or more other
25 Enterococcal or non-Enterococcal organisms to produce a multi-component vaccine intended to elicit an immunological response against members of the *Enterococcus* genus and, optionally, one or more non-Enterococcal organisms.

The vaccines of the present invention can be administered in a DNA form, e.g., "naked" DNA, wherein the DNA encodes one or more Enterococcal polypeptides

and, optionally, one or more polypeptides of a non-Enterococcal organism. The DNA encoding one or more polypeptides may be constructed such that these polypeptides are expressed as fusion proteins.

The vaccines of the present invention may also be administered as a
5 component of a genetically engineered organism or host cell. Thus, a genetically engineered organism or host cell which expresses one or more *E. faecalis* polypeptides may be administered to an animal. For example, such a genetically engineered organism or host cell may contain one or more *E. faecalis* polypeptides of the present invention intracellularly, on its cell surface, or in its periplasmic space. Further, such
10 a genetically engineered organism or host cell may secrete one or more *E. faecalis* polypeptides. The vaccines of the present invention may also be co-administered to an animal with an immune system modulator (*e.g.*, CD86 and GM-CSF).

The invention also provides a method of inducing an immunological response in an animal to one or more members of the *Enterococcus* genus, preferably one or
15 more isolates of the *E. faecalis* species, comprising administering to the animal a vaccine as described above.

The invention further provides a method of inducing a protective immune response in an animal, sufficient to prevent, attenuate, or control an infection by members of the *Enterococcus* genus, preferably at least *E. faecalis* species,
20 comprising administering to the animal a composition comprising one or more of the polynucleotides or polypeptides described in Table 1, or fragments thereof. Further, these polypeptides, or fragments thereof, may be conjugated to another immunogen and/or administered in admixture with an adjuvant.

The invention further relates to antibodies elicited in an animal by the
25 administration of one or more *E. faecalis* polypeptides of the present invention and to methods for producing such antibodies and fragments thereof. The invention further relates to recombinant antibodies and fragments thereof and to methods for producing such antibodies and fragments thereof.

The invention also provides diagnostic methods for detecting the expression of

the polynucleotides of Table 1 by members of the *Enterococcus* genus in an animal. One such method involves assaying for the expression of a polynucleotide encoding *E. faecalis* polypeptides in a sample from an animal. This expression may be assayed either directly (*e.g.*, by assaying polypeptide levels using antibodies elicited in
5 response to amino acid sequences described in Table 1) or indirectly (*e.g.*, by assaying for antibodies having specificity for amino acid sequences described in Table 1). The expression of polynucleotides can also be assayed by detecting the nucleic acids of Table 1. An example of such a method involves the use of the polymerase chain reaction (PCR) to amplify and detect *Enterococcus* nucleic acid sequences.

10 The present invention also relates to nucleic acid probes having all or part of a nucleotide sequence described in Table 1 (odd SEQ ID NOs) which are capable of hybridizing under stringent conditions to *Enterococcus* nucleic acids. The invention further relates to a method of detecting one or more *Enterococcus* nucleic acids in a biological sample obtained from an animal, said one or more nucleic acids encoding
15 *Enterococcus* polypeptides, comprising: (a) contacting the sample with one or more of the above-described nucleic acid probes, under conditions such that hybridization occurs, and (b) detecting hybridization of said one or more probes to the *Enterococcus* nucleic acid present in the biological sample.

Other uses of the polypeptides of the present invention include: *inter alia*, to
20 detect *E. faecalis* in immunoassays, as epitope tags, as molecular weight markers on SDS-PAGE gels, as molecular weight markers for molecular sieve gel filtration columns, to generate antibodies that specifically bind *E. faecalis* polypeptides of the present invention for the detection *E. faecalis* in immunoassays, to generate an immune response against *E. faecalis* and other *Enterococcus* species, and as vaccines
25 against *E. faecalis*, other *Enterococcus* species and other bacteria genres.

Isolated nucleic acid molecules of the present invention, particularly DNA molecules, are useful as probes for gene mapping and for identifying *E. faecalis* in a biological samples, for instance, by Southern and Northern blot analysis.

Polynucleotides of the present invention are also useful in detecting *E. faecalis* by

PCR using primers for a particular *E. faecalis* polynucleotide. Isolated polynucleotides of the present invention are also useful in making the polypeptides of the present invention.

5 Detailed Description

The present invention relates to recombinant *E. faecalis* nucleic acids and fragments thereof. The present invention further relates to recombinant *E. faecalis* polypeptides and fragments thereof. The invention also relates to methods for using these polypeptides to produce immunological responses and to confer immunological
10 protection to disease caused by members of the genus *Enterococcus*, at least isolates of the *E. faecalis* genus. The invention further relates to nucleic acid sequences which encode antigenic *E. faecalis* polypeptides and to methods for detecting *E. faecalis* nucleic acids and polypeptides in biological samples. The invention also relates to antibodies specific for the polypeptides and peptides of the present invention and
15 methods for detecting such antibodies produced in a host animal.

Definitions

The following definitions are provided to clarify the subject matter which the inventors consider to be the present invention.

20 As used herein, the phrase "pathogenic agent" means an agent which causes a disease state or affliction in an animal. Included within this definition, for examples, are bacteria, protozoans, fungi, viruses and metazoan parasites which either produce a disease state or render an animal infected with such an organism susceptible to a disease state (*e.g.*, a secondary infection). Further included are species and strains of
25 the genus *Enterococcus* which produce disease states in animals.

As used herein, the term "organism" means any living biological system, including viruses, regardless of whether it is a pathogenic agent.

As used herein, the term "*Enterococcus*" means any species or strain of bacteria which is members of the genus *Enterococcus*. Such species and strains are

known to those of skill in the art, and include those that are pathogenic and those that are not.

As used herein, the phrase "one or more *E. faecalis* polypeptides of the present invention" means polypeptides comprising the amino acid sequence of one or more of the *E. faecalis* polypeptides described in Table 1 (even SEQ ID NOs). These polypeptides may be expressed as fusion proteins wherein the *E. faecalis* polypeptides of the present invention are linked to additional amino acid sequences which may be of Enterococcal or non-Enterococcal origin. This phrase further includes polypeptide comprising fragments of the *E. faecalis* polypeptides of the present invention. Additional definitions are provided throughout the specification.

Explanation of Table 1

Table 1, below, provides information describing genes which encode polypeptides of *E. faecalis*. The table lists the gene identifier which consists of the letters EF, which denote *E. faecalis*, followed immediately by a three digit numeric code, which arbitrarily number the *E. faecalis* genes of the present invention. A number from 1 through 4 follows the three digit number. A number 1 represents the full length open reading frame of the gene specified by the preceeding three digit number. A number 2 represents the full length polypeptide encoded by the gene specified the preceeding three digit number. A number 3 represents a polynucleotide fragment, of the gene represented by the preceeding three digit number, used to produce an antigenic polypeptide. A number 4 represents an antigenic polypeptide fragment, of the gene represented by the preceeding three digit number, used to stimulate an immune response or as a vaccine. The nucleotide and amino acid sequences of each gene and fragment are also shown in the Sequence Listing under the SEQ ID NO listed in Table 1.

Explanation of Table 2

Table 2 lists accession numbers for the closest matching sequences between

the polypeptides of the present invention and those available through GenBank and Derwent databases. These reference numbers are the database entry numbers commonly used by those of skill in the art, who will be familiar with their denominations. The descriptions of the nomenclature for GenBank are available from the National Center for Biotechnology Information. Column 1 lists the gene or ORF of the present invention. Column 2 lists the accession number of a "match" gene sequence in GenBank or Derwent databases. Column 3 lists the description of the "match" gene sequence. Columns 4 and 5 are the high score and smallest sum probability, respectively, calculated by BLAST. Polypeptides of the present invention that do not share significant identity/similarity with any polypeptide sequences of GenBank and Derwent are not represented in Table 2. Polypeptides of the present invention that share significant identity/similarity with more than one of the polypeptides of GenBank and Derwent are represented more than once.

15 ***Explanation of Table 3.***

The *E. faecalis* polypeptides of the present invention may include one or more conservative amino acid substitutions from natural mutations or human manipulation as indicated in Table 3. Changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein. Residues from the following groups, as indicated in Table 3, may be substituted for one another: Aromatic, Hydrophobic, Polar, Basic, Acidic, and Small,

Explanation of Table 4

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in each of the full length *E. faecalis* polypeptides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). *E. faecalis*

polypeptide shown in Table 1 may one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown described in Table 4 correspond to the amino acid sequences for each full length gene sequence shown in Table 1 and in the Sequence Listing. Polypeptides of the present invention that do not have antigenic epitopes recognized by the Jameson-Wolf algorithm are not represented in Table 2.

10 *Selection of Nucleic Acid Sequences Encoding Antigenic E. faecalis Polypeptides*

Sequenced *E. faecalis* genomic DNA was obtained from the *E. faecalis* strain V586. The *E. faecalis* strain V586 was deposited 2 May 1997 at the ATCC, 10801 University Blvd. Manassas, VA 20110-2209, and given accession number 55969.

Some ORFs contained in the subset of fragments of the *E. faecalis* genome disclosed herein were derived through the use of a number of screening criteria detailed below. The ORFs are bounded at the amino terminus by a methionine or valine residue and usually at the carboxy terminus by a stop codon.

Most of the selected sequences consist of complete ORFs. The polypeptides that do not comprise a complete ORF can be determined by determining whether the corresponding polynucleotide sequence comprises a stop codon after the codon for the last amino acid residue in the polypeptide sequence. It is not always preferred to express a complete ORF in a heterologous system. It may be challenging to express and purify a highly hydrophobic protein by common laboratory methods. Some of the polypeptide vaccine candidates described herein have been modified slightly to simplify the production of recombinant protein. For example, nucleotide sequences which encode highly hydrophobic domains, such as those found at the amino terminal signal sequence, have been excluded from some constructs used for expression of the polypeptides. Furthermore, any highly hydrophobic amino acid sequences occurring at the carboxy terminus have also been excluded from the recombinant expression

constructs. Thus, in one embodiment, a polypeptide which represents a truncated or modified ORF may be used as an antigen.

While numerous methods are known in the art for selecting potentially immunogenic polypeptides, many of the ORFs disclosed herein were selected on the basis of screening *Enterococcus faecalis* ORFs for several aspects of potential immunogenicity. One set of selection criteria are as follows:

1. *Type I signal sequence*: An amino terminal type I signal sequence generally directs a nascent protein across the plasma and outer membranes to the exterior of the bacterial cell. Experimental evidence obtained from studies with *Escherichia coli* suggests that the typical type I signal sequence consists of the following biochemical and physical attributes (Izard, J. W. and Kendall, D. A. *Mol. Microbiol.* 13:765-773 (1994)). The length of the type I signal sequence is approximately 15 to 25 primarily hydrophobic amino acid residues with a net positive charge in the extreme amino terminus. In addition, the central region of the signal sequence adopts an alpha-helical conformation in a hydrophobic environment. Finally, the region surrounding the actual site of cleavage is ideally six residues long, with small side-chain amino acids in the -1 and -3 positions.

2. *Type IV signal sequence*: The type IV signal sequence is an example of the several types of functional signal sequences which exist in addition to the type I signal sequence detailed above. Although functionally related, the type IV signal sequence possesses a unique set of biochemical and physical attributes (Strom, M. S. and Lory, S., *J. Bacteriol.* 174:7345-7351 (1992)). These are typically six to eight amino acids with a net basic charge followed by an additional sixteen to thirty primarily hydrophobic residues. The cleavage site of a type IV signal sequence is typically after the initial six to eight amino acids at the extreme amino terminus. In addition, type IV signal sequences generally contain a phenylalanine residue at the +1 site relative to the cleavage site.

3. *Lipoprotein*: Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence

for lipoprotein cleavage. Nearly three-fourths of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C at positions -3 to +1, relative to the point of cleavage (Hayashi, S. and Wu, H. C., *J. Bioenerg. Biomembr.* 22:451-471 (1990)).

- 5 4. *LPXTG motif*: It has been experimentally determined that most anchored proteins found on the surface of gram-positive bacteria possess a highly conserved carboxy terminal sequence. More than fifty such proteins from organisms such as *S. pyogenes*, *S. mutans*, *E. faecalis*, *S. pneumoniae*, and others, have been identified based on their extracellular location and carboxy terminal amino acid sequence (Fischetti, V. A., *ASM News* 62:405-410 (1996)). The conserved region consists of six charged amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain. Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins examined. The amino acid sequence of this region is L-P-X-T-G-X, where X is any amino acid.
- 10
- 15

An algorithm for selecting antigenic and immunogenic *Enterococcus faecalis* polypeptides including the foregoing criteria was developed. The algorithm is similar to that described in U.S. patent application 08/781,986, filed January 3, 1997, which is fully incorporated by reference herein. Use of the algorithm by the inventors to select immunologically useful *Enterococcus faecalis* polypeptides resulted in the selection of a number of the disclosed ORFs. Polypeptides comprising the polypeptides identified in this group may be produced by techniques standard in the art and as further described herein.

20

25 ***Nucleic Acid Molecules***

Sequenced *E. faecalis* genomic DNA was obtained from the *E. faecalis* strain V586. As discussed elsewhere hererin, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining libraries and for sequencing are

provided below, for instance. A wide variety of *Enterococcus faecalis* strains that can be used to prepare *E. faecalis* genomic DNA for cloning and for obtaining polynucleotides and polypeptides of the present invention. A wide variety of *Enterococcus faecalis* strains are available to the public from recognized depository
5 institutions, such as the American Type Culture Collection (ATCC). It is recognized that minor variation in the nucleic acid and amino acid sequence may be expected from *E. faecalis* strain to strain. The present invention provides for genes, including both polynucleotides and polypeptides, of the of the present invention from all the *Enterococcus faecalis* strains.

10 Unless otherwise indicated, all nucleotide sequences determined by sequencing a DNA molecule herein were determined using an automated DNA sequencer (such as the Model 373 from Applied Biosystems, Inc., Foster City, CA), and all amino acid sequences of polypeptides encoded by DNA molecules determined herein were predicted by translation of a DNA sequence determined as above. Therefore, as is
15 known in the art for any DNA sequence determined by this automated approach, any nucleotide sequence determined herein may contain some errors. Nucleotide sequences determined by automation are typically at least about 90% identical, more typically at least about 95% to at least about 99.9% identical to the actual nucleotide sequence of the sequenced DNA molecule. The actual sequence can be more
20 precisely determined by other approaches including manual DNA sequencing methods well known in the art. As is also known in the art, a single insertion or deletion in a determined nucleotide sequence compared to the actual sequence will cause a frame shift in translation of the nucleotide sequence such that the predicted amino acid sequence encoded by a determined nucleotide sequence will be completely different
25 from the amino acid sequence actually encoded by the sequenced DNA molecule, beginning at the point of such an insertion or deletion. In case of conflict between Table 1 and either the nucleic acid sequence of the clones listed in Table 1 or the amino acid sequence of the protein expressed by the clones listed in Table 1, the clones listed in Table 1 are controlling. By "nucleotide sequence" of a nucleic acid molecule or

polynucleotide is intended to mean either a DNA or RNA sequence. Using the information provided herein, such as the nucleotide sequence in Table 1, a nucleic acid molecule of the present invention encoding a *E. faecalis* polypeptide may be obtained using standard cloning and screening procedures, such as those for cloning DNAs using genomic DNA as starting material. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). Illustrative of the invention, the nucleic acid molecule described in Table 1 was discovered in a DNA library derived from a *E. faecalis* genomic DNA.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA, or in the form of DNA, including, for instance, DNA and genomic DNA obtained by cloning or produced synthetically. The DNA may be double-stranded or single-stranded. Single-stranded DNA or RNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

By "isolated" nucleic acid molecule(s) is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. This includes segments of DNA comprising the *E. faecalis* polynucleotides of the present invention isolated from the native chromosome. These fragments include both isolated fragments consisting only of *E. faecalis* DNA and fragments comprising heterologous sequences such as vector sequences or other foreign DNA. For example, recombinant DNA molecules contained in a vector are considered isolated for the purposes of the present invention. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include such molecules produced synthetically.

In addition, isolated nucleic acid molecules of the invention include DNA molecules which comprise a sequence substantially different from those described above but which, due to the degeneracy of the genetic code, still encode a *E. faecalis* polypeptides and peptides of the present invention (e.g. polypeptides of Table 1).
5 That is, all possible DNA sequences that encode the *E. faecalis* polypeptides of the present invention. This includes the genetic code and species-specific codon preferences known in the art. Thus, it would be routine for one skilled in the art to generate the degenerate variants described above, for instance, to optimize codon expression for a particular host (e.g., change codons in the bacteria mRNA to those
10 preferred by a mammalian or other bacterial host such as *E. coli*).

The invention further provides isolated nucleic acid molecules having the nucleotide sequence shown in Table 1 or a nucleic acid molecule having a sequence complementary to one of the above sequences. Such isolated molecules, particularly DNA molecules, are useful as probes for gene mapping and for identifying *E. faecalis*
15 in a biological sample, for instance, by PCR, Southern blot, Northern blot, or other form of hybridization analysis.

The present invention is further directed to nucleic acid molecules encoding portions or fragments of the nucleotide sequences described herein. Fragments include portions of the nucleotide sequences of Table 1, or the *E. faecalis* nucleotide
20 sequences contained in the plasmid clones listed in Table 1, at least 10 contiguous nucleotides in length selected from any two integers, one of which representing a 5' nucleotide position and a second of which representing a 3' nucleotide position, where the first nucleotide for each nucleotide sequence in Table 1 is position 1. That is, every combination of a 5' and 3' nucleotide position that a fragment at least 10
25 contiguous nucleotides in length could occupy is included in the invention. At least means a fragment may be 10 contiguous nucleotide bases in length or any integer between 10 and the length of an entire nucleotide sequence of Table 1 minus 1. Therefore, included in the invention are contiguous fragments specified by any 5' and 3' nucleotide base positions of a nucleotide sequences of Table 1 wherein the

contiguous fragment is any integer between 10 and the length of an entire nucleotide sequence minus 1.

Further, the invention includes polynucleotides comprising fragments specified by size, in nucleotides, rather than by nucleotide positions. The invention includes
5 any fragment size, in contiguous nucleotides, selected from integers between 10 and the length of an entire nucleotide sequence minus 1. Preferred sizes of contiguous nucleotide fragments include 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides. Other preferred sizes of contiguous nucleotide fragments, which may be useful as diagnostic probes and primers, include fragments 50-300 nucleotides in
10 length which include, as discussed above, fragment sizes representing each integer between 50-300. Larger fragments are also useful according to the present invention corresponding to most, if not all, of the nucleotide sequences shown in Table 1 or of the *E. faecalis* nucleotide sequences of the plasmid clones listed in Table 1. The preferred sizes are, of course, meant to exemplify not limit the present invention as all
15 size fragments, representing any integer between 10 and the length of an entire nucleotide sequence minus 1, are included in the invention. Additional preferred nucleic acid fragments of the present invention include nucleic acid molecules encoding epitope-bearing portions of *E. faecalis* polypeptides identified in Table 4.

The present invention also provides for the exclusion of any fragment,
20 specified by 5' and 3' base positions or by size in nucleotide bases as described above for any nucleotide sequence of Table 1 or the plasmid clones listed in Table 1. Any number of fragments of nucleotide sequences in Table 1 or the plasmid clones listed in Table 1, specified by 5' and 3' base positions or by size in nucleotides, as described above, may be excluded from the present invention.

25 In another aspect, the invention provides an isolated nucleic acid molecule comprising a polynucleotide which hybridizes under stringent hybridization conditions to a portion of a polynucleotide in a nucleic acid molecules of the invention described above, for instance, nucleotide sequences of Table 1 or the *E. faecalis* sequences of the plasmid clones listed in Table 1. By "stringent hybridization

conditions" is intended overnight incubation at 42°C in a solution comprising: 50% formamide, 5x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at
5 about 65°C.

By a polynucleotide which hybridizes to a "portion" of a polynucleotide is intended a polynucleotide (either DNA or RNA) hybridizing to at least about 15 nucleotides bases, and more preferably at least about 20 nucleotides bases, still more preferably at least about 30 nucleotides bases, and even more preferably about 30-70
10 (e.g., 50) nucleotides bases of the reference polynucleotide. These are useful as diagnostic probes and primers as discussed above. By a portion of a polynucleotide of "at least 20 nucleotides bases in length," for example, is intended 20 or more contiguous nucleotides bases nucleotides from the nucleotide sequence of the reference polynucleotide (e.g., the nucleotide sequence as shown in Table 1). Portions of a
15 polynucleotide which hybridizes to a nucleotide sequence in Table 1, which can be used as probes and primers, may also be precisely specified by 5' and 3' base positions or by size in nucleotide bases as described above or precisely excluded in the same manner.

The nucleic acid molecules of the present invention include those encoding the
20 full length *E. faecalis* polypeptides of Table 1 and portions of the *E. faecalis* polypeptides of Table 1. Also included in the present invention are nucleic acids encoding the above full length sequences and further comprise additional sequences, such as those encoding an added secretory leader sequence, such as a pre-, or pro- or prepro- protein sequence. Further included in the present invention are nucleic acids
25 encoding the above full length sequences and portions thereof and further comprise additional heterologous amino acid sequences encoded by nucleic acid sequences from a different source.

Also included in the present invention are nucleic acids encoding the above protein sequences together with additional, non-coding sequences, including for

example, but not limited to non-coding 5' and 3' sequences. These sequences include transcribed, non-translated sequences that may play a role in transcription, and mRNA processing, for example, ribosome binding and stability of mRNA. Also included in the present invention are additional coding sequences which provide
5 additional functionalities.

Thus, a nucleotide sequence encoding a polypeptide may be fused to a marker sequence, such as a sequence encoding a peptide which facilitates purification of the fused polypeptide. In certain preferred embodiments of this aspect of the invention, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in
10 a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. For instance, hexa-histidine provides for convenient purification of the fusion protein. See Gentz et al. (1989) Proc. Natl. Acad. Sci. 86:821-24. The "HA" tag is another peptide useful for purification which corresponds to an epitope derived from the influenza hemagglutinin
15 protein. See Wilson et al. (1984) Cell 37:767. As discussed below, other such fusion proteins include the *E. faecalis* polypeptides of the present invention fused to Fc at the N- or C-terminus.

Variant and Mutant Polynucleotides

20 The present invention further relates to variants of the nucleic acid molecules which encode portions, analogs or derivatives of a *E. faecalis* polypeptides of Table 1 and variant polypeptides thereof including portions, analogs, and derivatives of the *E. faecalis* polypeptides. Variants may occur naturally, such as a natural allelic variant. By an "allelic variant" is intended one of several alternate forms of a gene occupying a
25 given locus on a chromosome of an organism. See, e.g., B. Lewin, Genes IV (1990). Non-naturally occurring variants may be produced using art-known mutagenesis techniques.

Such nucleic acid variants include those produced by nucleotide substitutions, deletions, or additions. The substitutions, deletions, or additions may involve one or

more nucleotides. The variants may be altered in coding regions, non-coding regions, or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of a *E. faecalis* protein of the present invention or portions thereof. Also especially preferred in this regard are conservative substitutions.

Such polypeptide variants include those produced by amino acid substitutions, deletions or additions. The substitutions, deletions, or additions may involve one or more residues. Alterations may produce conservative or non-conservative amino acid substitutions, deletions, or additions. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of a *E. faecalis* protein of the present invention or portions thereof. Also especially preferred in this regard are conservative substitutions.

The present invention also relates to recombinant vectors, which include the isolated nucleic acid molecules of the present invention, and to host cells containing the recombinant vectors, as well as to methods of making such vectors and host cells and for using them for production of *E. faecalis* polypeptides or peptides by recombinant techniques.

The present application is directed to nucleic acid molecules at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleic acid sequence shown in Table 1. The above nucleic acid sequences are included irrespective of whether they encode a polypeptide having *E. faecalis* activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having *E. faecalis* activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having *E. faecalis* activity include, *inter alia*, isolating an *E. faecalis* gene or allelic variants thereof from a DNA library, and detecting *E. faecalis*

mRNA expression samples, environmental samples, suspected of containing *E. faecalis* by Northern Blot analysis.

Preferred, are nucleic acid molecules having sequences at least 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequence shown in Table 1, which do, in fact, encode a polypeptide having *E. faecalis* protein activity. By "a polypeptide having *E. faecalis* activity" is intended polypeptides exhibiting activity similar, but not necessarily identical, to an activity of the *E. faecalis* protein of the invention, as measured in a particular biological assay suitable for measuring activity of the specified protein.

Due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 90%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequences shown in Table 1 will encode a polypeptide having *E. faecalis* protein activity. In fact, since degenerate variants of these nucleotide sequences all encode the same polypeptide, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having *E. faecalis* protein activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

The biological activity or function of the polypeptides of the present invention are expected to be similar or identical to polypeptides from other bacteria that share a high degree of structural identity/similarity. Tables 2 lists accession numbers and descriptions for the closest matching sequences of polypeptides available through Genbank and Derwent databases. It is therefore expected that the biological activity or function of the polypeptides of the present invention will be similar or identical to those polypeptides from other bacterial genuses, species, or strains listed in Table 2.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the *E. faecalis* polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted, inserted, or substituted with another nucleotide. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. See Brutlag et al. (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by first converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3'

truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only nucleotides outside the 5' and 3' nucleotides of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 nucleotide subject sequence is aligned to a 100 nucleotide query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 nucleotides at 5' end. The 10 unpaired nucleotides represent 10% of the sequence (number of nucleotides at the 5' and 3' ends not matched/total number of nucleotides in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 nucleotides were perfectly matched the final percent identity would be 90%. In another example, a 90 nucleotide subject sequence is compared with a 100 nucleotide query sequence. This time the deletions are internal deletions so that there are no nucleotides on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only nucleotides 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

Vectors and Host Cell

The present invention also relates to vectors which include the isolated DNA molecules of the present invention, host cells comprising the recombinant vectors, and the production of *E. faecalis* polypeptides and peptides of the present invention expressed by the host cells.

5 Recombinant constructs may be introduced into host cells using well known techniques such as infection, transduction, transfection, transvection, electroporation and transformation. The vector may be, for example, a phage, plasmid, viral or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in
10 complementing host cells.

 The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged *in vitro* using an appropriate packaging cell line
15 and then transduced into host cells.

 Preferred are vectors comprising *cis*-acting control regions to the polynucleotide of interest. Appropriate *trans*-acting factors may be supplied by the host, supplied by a complementing vector or supplied by the vector itself upon introduction into the host.

20 In certain preferred embodiments in this regard, the vectors provide for specific expression, which may be inducible and/or cell type-specific. Particularly preferred among such vectors are those inducible by environmental factors that are easy to manipulate, such as temperature and nutrient additives.

 Expression vectors useful in the present invention include chromosomal-,
25 episomal- and virus-derived vectors, *e.g.*, vectors derived from bacterial plasmids, bacteriophage, yeast episomes, yeast chromosomal elements, viruses such as baculoviruses, papova viruses, vaccinia viruses, adenoviruses, fowl pox viruses, pseudorabies viruses and retroviruses, and vectors derived from combinations thereof, such as cosmids and phagemids.

The DNA insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the *E. coli lac*, *trp* and *tac* promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few.

Other suitable promoters will be known to the skilled artisan. The expression

5 constructs will further contain sites for transcription initiation, termination and, in the transcribed region, a ribosome binding site for translation. The coding portion of the mature transcripts expressed by the constructs will preferably include a translation initiating site at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

10 As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin, or ampicillin resistance genes for culturing in *E. coli* and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as *E. coli*,
15 *Streptomyces* and *Salmonella typhimurium* cells; fungal cells, such as yeast cells; insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells; animal cells such as CHO, COS and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE9,
20 pQE10 available from Qiagen; pBS vectors, Phagescript vectors, Bluescript vectors, pNH8A, pNH16a, pNH18A, pNH46A available from Stratagene; pET series of vectors available from Novagen; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV,
25 pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Among known bacterial promoters suitable for use in the present invention include the *E. coli lacI* and *lacZ* promoters, the T3, T5 and T7 promoters, the *gpt* promoter, the lambda PR and PL promoters and the *trp* promoter. Suitable eukaryotic

promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, the early and late SV40 promoters, the promoters of retroviral LTRs, such as those of the Rous sarcoma virus (RSV), and metallothionein promoters, such as the mouse metallothionein-I promoter.

5 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection or other methods. Such methods are described in many standard laboratory manuals (for example, Davis, *et al.*, *Basic Methods In Molecular Biology* (1986)).

10 Transcription of DNA encoding the polypeptides of the present invention by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are *cis*-acting elements of DNA, usually about from 10 to 300 nucleotides that act to increase transcriptional activity of a promoter in a given host cell-type. Examples of enhancers include the SV40 enhancer, which is located on the late side of
15 the replication origin at nucleotides 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

For secretion of the translated polypeptide into the lumen of the endoplasmic reticulum, into the periplasmic space or into the extracellular environment,
20 appropriate secretion signals may be incorporated into the expressed polypeptide, for example, the amino acid sequence KDEL. The signals may be endogenous to the polypeptide or they may be heterologous signals.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals, but also additional heterologous
25 functional regions. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence in the host cell, during purification, or during subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the

polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability and to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize proteins. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is thoroughly advantageous for use in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified in the advantageous manner described. This is the case when Fc portion proves to be a hindrance to use in therapy and diagnosis, for example when the fusion protein is to be used as antigen for immunizations. In drug discovery, for example, human proteins, such as, hIL5-receptor has been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. See Bennett, D. et al. (1995) J. Molec. Recogn. 8:52-58 and Johanson, K. et al. (1995) J. Biol. Chem. 270 (16):9459-9471.

The *E. faecalis* polypeptides can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography and high performance liquid chromatography ("HPLC") is employed for purification. Polypeptides of the present invention include naturally purified products, products of chemical synthetic procedures, and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect and mammalian cells.

Polypeptides and Fragments

The invention further provides an isolated *E. faecalis* polypeptide having an amino acid sequence in Table 1, or a peptide or polypeptide comprising a portion of the above polypeptides.

5

Variant and Mutant Polypeptides

To improve or alter the characteristics of *E. faecalis* polypeptides of the present invention, protein engineering may be employed. Recombinant DNA technology known to those skilled in the art can be used to create novel mutant
10 proteins or muteins including single or multiple amino acid substitutions, deletions, additions, or fusion proteins. Such modified polypeptides can show, e.g., enhanced activity or increased stability. In addition, they may be purified in higher yields and show better solubility than the corresponding natural polypeptide, at least under certain purification and storage conditions.

15

N-Terminal and C-Terminal Deletion Mutants

It is known in the art that one or more amino acids may be deleted from the N-terminus or C-terminus without substantial loss of biological function. For instance, Ron et al. J. Biol. Chem., 268:2984-2988 (1993), reported modified KGF
20 proteins that had heparin binding activity even if 3, 8, or 27 N-terminal amino acid residues were missing. Accordingly, the present invention provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of the *E. faecalis* polypeptides shown in Table 1, and polynucleotides encoding such polypeptides.

25

Similarly, many examples of biologically functional C-terminal deletion muteins are known. For instance, Interferon gamma shows up to ten times higher activities by deleting 8-10 amino acid residues from the carboxy terminus of the protein See, e.g., Dobeli, et al. (1988) J. Biotechnology 7:199-216. Accordingly, the present invention provides polypeptides having one or more residues from the

carboxy terminus of the amino acid sequence of the *E. faecalis* polypeptides shown in Table 1. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini as described below.

The present invention is further directed to polynucleotide encoding portions
5 or fragments of the amino acid sequences described herein as well as to portions or
fragments of the isolated amino acid sequences described herein. Fragments include
portions of the amino acid sequences of Table 1, are at least 5 contiguous amino acid
in length, are selected from any two integers, one of which representing a N-terminal
position. The initiation codon of the polypeptides of the present inventions position
10 1. Every combination of a N-terminal and C-terminal position that a fragment at least
5 contiguous amino acid residues in length could occupy, on any given amino acid
sequence of Table 1 is included in the invention. At least means a fragment may be 5
contiguous amino acid residues in length or any integer between 5 and the number of
residues in a full length amino acid sequence minus 1. Therefore, included in the
15 invention are contiguous fragments specified by any N-terminal and C-terminal
positions of amino acid sequence set forth in Table 1 wherein the contiguous fragment
is any integer between 5 and the number of residues in a full length sequence minus 1.

Further, the invention includes polypeptides comprising fragments specified
by size, in amino acid residues, rather than by N-terminal and C-terminal positions.
20 The invention includes any fragment size, in contiguous amino acid residues, selected
from integers between 5 and the number of residues in a full length sequence minus 1.
Preferred sizes of contiguous polypeptide fragments include about 5 amino acid
residues, about 10 amino acid residues, about 20 amino acid residues, about 30 amino
acid residues, about 40 amino acid residues, about 50 amino acid residues, about 100
25 amino acid residues, about 200 amino acid residues, about 300 amino acid residues,
and about 400 amino acid residues. The preferred sizes are, of course, meant to
exemplify, not limit, the present invention as all size fragments representing any
integer between 5 and the number of residues in a full length sequence minus 1 are
included in the invention. The present invention also provides for the exclusion of any

fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above. Any number of fragments specified by N-terminal and C-terminal positions or by size in amino acid residues as described above may be excluded.

5 The above fragments need not be active since they would be useful, for example, in immunoassays, in epitope mapping, epitope tagging, to generate antibodies to a particular portion of the protein, as vaccines, and as molecular weight markers.

10 *Other Mutants*

 In addition to N- and C-terminal deletion forms of the protein discussed above, it also will be recognized by one of ordinary skill in the art that some amino acid sequences of the *E. faecalis* polypeptide can be varied without significant effect of the structure or function of the protein. If such differences in sequence are contemplated,
15 it should be remembered that there will be critical areas on the protein which determine activity.

 Thus, the invention further includes variations of the *E. faecalis* polypeptides which show substantial *E. faecalis* polypeptide activity or which include regions of *E. faecalis* protein such as the protein portions discussed below. Such mutants include
20 deletions, insertions, inversions, repeats, and type substitutions selected according to general rules known in the art so as to have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided. There are two main approaches for studying the tolerance of an amino acid sequence to change. See, Bowie, J. U. *et al.* (1990), Science 247:1306-1310. The first
25 method relies on the process of evolution, in which mutations are either accepted or rejected by natural selection. The second approach uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene and selections or screens to identify sequences that maintain functionality.

 These studies have revealed that proteins are surprisingly tolerant of amino

acid substitutions. The studies indicate which amino acid changes are likely to be permissive at a certain position of the protein. For example, most buried amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Other such phenotypically silent substitutions are described by

5 Bowie et al. (*supra*) and the references cited therein. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic

10 residues Phe, Tyr.

Thus, the fragment, derivative, analog, or homolog of the polypeptide of Table 1, or that encoded by the plasmids listed in Table 1, may be: (i) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted

15 amino acid residue may or may not be one encoded by the genetic code; or (ii) one in which one or more of the amino acid residues includes a substituent group; or (iii) one in which the *E. faecalis* polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol); or (iv) one in which the additional amino acids are fused to the above form of

20 the polypeptide, such as an IgG Fc fusion region peptide or leader or secretory sequence or a sequence which is employed for purification of the above form of the polypeptide or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Thus, the *E. faecalis* polypeptides of the present invention may include one or

25 more amino acid substitutions, deletions, or additions, either from natural mutations or human manipulation. As indicated, changes are preferably of a minor nature, such as conservative amino acid substitutions that do not significantly affect the folding or activity of the protein (see Table 3).

Amino acids in the *E. faecalis* proteins of the present invention that are

essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis. *See, e.g.,* Cunningham et al. (1989) Science 244:1081-1085. The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then
5 tested for biological activity using assays appropriate for measuring the function of the particular protein.

Of special interest are substitutions of charged amino acids with other charged or neutral amino acids which may produce proteins with highly desirable improved characteristics, such as less aggregation. Aggregation may not only reduce activity but
10 also be problematic when preparing pharmaceutical formulations, because aggregates can be immunogenic. *See, e.g.,* Pinckard et al., (1967) Clin. Exp. Immunol. 2:331-340; Robbins, et al., (1987) Diabetes 36:838-845; Cleland, et al., (1993) Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377.

The polypeptides of the present invention are preferably provided in an
15 isolated form, and preferably are substantially purified. A recombinantly produced version of the *E. faecalis* polypeptide can be substantially purified by the one-step method described by Smith et al. (1988) Gene 67:31-40. Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies directed against the polypeptides of the invention in methods which are well known in
20 the art of protein purification.

The invention further provides for isolated *E. faecalis* polypeptides comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequence of a full-length *E. faecalis* polypeptide having the complete amino acid sequence shown in Table 1; (b) the amino acid sequence of a full-length *E.*
25 *faecalis* polypeptide having the complete amino acid sequence shown in Table 1 excepting the N-terminal methionine; (c) the complete amino acid sequence encoded by the plasmids listed in Table 1; and (d) the complete amino acid sequence excepting the N-terminal methionine encoded by the plasmids listed in Table 1. The polypeptides of the present invention also include polypeptides having an amino acid

sequence at least 80% identical, more preferably at least 90% identical, and still more preferably 95%, 96%, 97%, 98% or 99% identical to those described in (a), (b), (c), and (d) above.

Further polypeptides of the present invention include polypeptides which
5 have at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98% or 99% similarity to those described above.

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a *E. faecalis* polypeptide having an amino acid sequence which contains at least one conservative amino acid substitution, but not
10 more than 50 conservative amino acid substitutions, not more than 40 conservative amino acid substitutions, not more than 30 conservative amino acid substitutions, and not more than 20 conservative amino acid substitutions. Also provided are polypeptides which comprise the amino acid sequence of a *E. faecalis* polypeptide, having at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 conservative amino
15 acid substitutions.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid
20 alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy
25 terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences

shown in Table 1 or to the amino acid sequence encoded by the plaimds listed in Table 1 can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al., (1990) Comp. App. Biosci. 6:237-245. In a sequence alignment the query and subject sequences are both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, the results, in percent identity, must be manually corrected. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query amino acid residues outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not match/align with the first 10 residues at the N-terminus. The 10 unpaired residues
5 represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query
10 sequence. This time the deletions are internal so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned
15 with the query sequence are manually corrected. No other manual corrections are to be made for the purposes of the present invention.

The above polypeptide sequences are included irrespective of whether they have their normal biological activity. This is because even where a particular polypeptide molecule does not have biological activity, one of skill in the art would
20 still know how to use the polypeptide, for instance, as a vaccine or to generate antibodies. Other uses of the polypeptides of the present invention that do not have *E. faecalis* activity include, *inter alia*, as epitope tags, in epitope mapping, and as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods known to those of skill in the art.

25 As described below, the polypeptides of the present invention can also be used to raise polyclonal and monoclonal antibodies, which are useful in assays for detecting *E. faecalis* protein expression or as agonists and antagonists capable of enhancing or inhibiting *E. faecalis* protein function. Further, such polypeptides can be used in the yeast two-hybrid system to "capture" *E. faecalis* protein binding proteins

which are also candidate agonists and antagonists according to the present invention. See, e.g., Fields et al. (1989) Nature 340:245-246.

Epitope-Bearing Portions

5 In another aspect, the invention provides peptides and polypeptides comprising epitope-bearing portions of the *E. faecalis* polypeptides of the present invention. These epitopes are immunogenic or antigenic epitopes of the polypeptides of the present invention. An "immunogenic epitope" is defined as a part of a protein that elicits an antibody response when the whole protein or polypeptide is the
10 immunogen. These immunogenic epitopes are believed to be confined to a few loci on the molecule. On the other hand, a region of a protein molecule to which an antibody can bind is defined as an "antigenic determinant" or "antigenic epitope." The number of immunogenic epitopes of a protein generally is less than the number of antigenic epitopes. See, e.g., Geysen, et al. (1983) Proc. Natl. Acad. Sci. USA 81:3998- 4002.
15 Predicted antigenic epitopes are shown in Table 4, below. It is pointed out that Table 4 only lists amino acid residues comprising epitopes predicted to have the highest degree of antigenicity. The polypeptides not listed in Table 4 and portions of polypeptides not listed in Table 4 are not considered non-antigenic. This is because they may still be antigenic *in vivo* but merely not recognized as such by the particular
20 algorithm used. Thus, Table 4 lists the amino acid residues comprising preferred antigenic epitopes but not a complete list. Amino acid residues comprising other antigenic epitopes may be determined by algorithms similar to the Jameson-Wolf analysis or by *in vivo* testing for an antigenic response using the methods described herein or those known in the art.

25 As to the selection of peptides or polypeptides bearing an antigenic epitope (*i.e.*, that contain a region of a protein molecule to which an antibody can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. See, e.g., Sutcliffe, et al., (1983) Science 219:660-666.

Peptides capable of eliciting protein-reactive sera are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins (*i.e.*, immunogenic epitopes) nor to the amino or carboxyl terminals. Peptides that are
5 extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer, peptides, especially those containing proline residues, usually are effective. *See*, Sutcliffe, et al., *supra*, p. 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the influenza virus hemagglutinin HA1
10 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Antigenic epitope-bearing peptides and polypeptides of the invention are therefore useful to raise antibodies, including monoclonal antibodies, that bind
15 specifically to a polypeptide of the invention. Thus, a high proportion of hybridomas obtained by fusion of spleen cells from donors immunized with an antigen epitope-bearing peptide generally secrete antibody reactive with the native protein. *See* Sutcliffe, et al., *supra*, p. 663. The antibodies raised by antigenic epitope-bearing peptides or polypeptides are useful to detect the mimicked protein, and antibodies to
20 different peptides may be used for tracking the fate of various regions of a protein precursor which undergoes post-translational processing. The peptides and anti-peptide antibodies may be used in a variety of qualitative or quantitative assays for the mimicked protein, for instance in competition assays since it has been shown that even short peptides (*e.g.*, about 9 amino acids) can bind and displace the larger
25 peptides in immunoprecipitation assays. *See, e.g.*, Wilson, et al., (1984) *Cell* 37:767-778. The anti-peptide antibodies of the invention also are useful for purification of the mimicked protein, for instance, by adsorption chromatography using methods known in the art.

Antigenic epitope-bearing peptides and polypeptides of the invention

designed according to the above guidelines preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) contained within the amino acid sequence of a polypeptide of the invention. However, peptides or polypeptides
5 comprising a larger portion of an amino acid sequence of a polypeptide of the invention, containing about 50 to about 100 amino acids, or any length up to and including the entire amino acid sequence of a polypeptide of the invention, also are considered epitope-bearing peptides or polypeptides of the invention and also are useful for inducing antibodies that react with the mimicked protein. Preferably, the
10 amino acid sequence of the epitope-bearing peptide is selected to provide substantial solubility in aqueous solvents (*i.e.*, the sequence includes relatively hydrophilic residues and highly hydrophobic sequences are preferably avoided); and sequences containing proline residues are particularly preferred.

Non-limiting examples of antigenic polypeptides or peptides that can be used
15 to generate an enterococcal-specific immune response or antibodies include portions of the amino acid sequences identified in Table 1. More specifically, Table 4 discloses a list of non-limiting residues that are involved in the antigenicity of the epitope-bearing fragments of the present invention. Therefore, the present invention provides for isolated and purified antigenic epitope-bearing fragments of the polypeptides of the
20 present invention comprising a peptide sequences of Table 4. The antigenic epitope-bearing fragments comprising a peptide sequence of Table 4 preferably contain a sequence of at least seven, more preferably at least nine and most preferably between about 10 to about 50 amino acids (i.e. any integer between 7 and 50) of a polypeptide of the present invention. That is, included in the present invention are antigenic
25 polypeptides between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4. Therefore, in most cases, the polypeptides of Table 4 make up only a portion of the antigenic polypeptide. All combinations of sequences between the integers of 7 and 50 amino acid in length comprising one or more of the sequences of Table 4 are included. The antigenic epitope-bearing

fragments may be specified by either the number of contiguous amino acid residues or by specific N-terminal and C-terminal positions as described above for the polypeptide fragments of the present invention, wherein the initiation codon is residue 1. Any number of the described antigenic epitope-bearing fragments of the present invention may also be excluded from the present invention in the same manner.

The epitope-bearing peptides and polypeptides of the invention may be produced by any conventional means for making peptides or polypeptides including recombinant means using nucleic acid molecules of the invention. For instance, an epitope-bearing amino acid sequence of the present invention may be fused to a larger polypeptide which acts as a carrier during recombinant production and purification, as well as during immunization to produce anti-peptide antibodies. Epitope-bearing peptides also may be synthesized using known methods of chemical synthesis. For instance, Houghten has described a simple method for synthesis of large numbers of peptides, such as 10-20 mg of 248 different 13 residue peptides representing single amino acid variants of a segment of the HA1 polypeptide which were prepared and characterized (by ELISA-type binding studies) in less than four weeks (Houghten, R. A. Proc. Natl. Acad. Sci. USA **82**:5131-5135 (1985)). This "Simultaneous Multiple Peptide Synthesis (SMPS)" process is further described in U.S. Patent No. 4,631,211 to Houghten and coworkers (1986). In this procedure the individual resins for the solid-phase synthesis of various peptides are contained in separate solvent-permeable packets, enabling the optimal use of the many identical repetitive steps involved in solid-phase methods. A completely manual procedure allows 500-1000 or more syntheses to be conducted simultaneously (Houghten et al. (1985) Proc. Natl. Acad. Sci. **82**:5131-5135 at 5134.

Epitope-bearing peptides and polypeptides of the invention are used to induce antibodies according to methods well known in the art. *See, e.g.,* Sutcliffe, et al., *supra*; Wilson, et al., *supra*; and Bittle, et al. (1985) J. Gen. Virol. **66**:2347-2354. Generally, animals may be immunized with free peptide; however, anti-peptide

antibody titer may be boosted by coupling of the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine may be coupled to carrier using a linker such as m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may
5 be coupled to carrier using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier-coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 µg peptide or carrier protein and Freund's adjuvant. Several booster injections may be needed, for instance, at intervals of about two
10 weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known
15 in the art.

Immunogenic epitope-bearing peptides of the invention, *i.e.*, those parts of a protein that elicit an antibody response when the whole protein is the immunogen, are identified according to methods known in the art. For instance, Geysen, *et al.*, *supra*, discloses a procedure for rapid concurrent synthesis on solid supports of hundreds of
20 peptides of sufficient purity to react in an ELISA. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner a peptide bearing an immunogenic epitope of a desired protein may be identified routinely by one of ordinary skill in the art. For instance, the immunologically important epitope in the coat protein of foot-and-mouth disease
25 virus was located by Geysen *et al. supra* with a resolution of seven amino acids by synthesis of an overlapping set of all 208 possible hexapeptides covering the entire 213 amino acid sequence of the protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope were synthesized, and the particular amino acids conferring specificity for the

reaction with antibody were determined. Thus, peptide analogs of the epitope-bearing peptides of the invention can be made routinely by this method. U.S. Patent No. 4,708,781 to Geysen (1987) further describes this method of identifying a peptide bearing an immunogenic epitope of a desired protein.

5 Further still, U.S. Patent No. 5,194,392, to Geysen (1990), describes a general method of detecting or determining the sequence of monomers (amino acids or other compounds) which is a topological equivalent of the epitope (*i.e.*, a "mimotope") which is complementary to a particular paratope (antigen binding site) of an antibody of interest. More generally, U.S. Patent No. 4,433,092, also to Geysen (1989),
10 describes a method of detecting or determining a sequence of monomers which is a topographical equivalent of a ligand which is complementary to the ligand binding site of a particular receptor of interest. Similarly, U.S. Patent No. 5,480,971 to Houghten, R. A. *et al.* (1996) discloses linear C₁-C₇-alkyl peralkylated oligopeptides and sets and libraries of such peptides, as well as methods for using such oligopeptide sets and
15 libraries for determining the sequence of a peralkylated oligopeptide that preferentially binds to an acceptor molecule of interest. Thus, non-peptide analogs of the epitope-bearing peptides of the invention also can be made routinely by these methods. The entire disclosure of each document cited in this section on "Polypeptides and Fragments" is hereby incorporated herein by reference.

20 As one of skill in the art will appreciate, the polypeptides of the present invention and the epitope-bearing fragments thereof described above can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life *in vivo*. This has been shown, *e.g.*, for chimeric proteins consisting of the
25 first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EPA 0,394,827; Traunecker *et al.* (1988) *Nature* 331:84-86. Fusion proteins that have a disulfide-linked dimeric structure due to the IgG part can also be more efficient in binding and neutralizing other molecules than a monomeric *E. faecalis* polypeptide or

fragment thereof alone. *See* Fountoulakis et al. (1995) J. Biochem. 270:3958-3964. Nucleic acids encoding the above epitopes of *E. faecalis* polypeptides can also be recombined with a gene of interest as an epitope tag to aid in detection and purification of the expressed polypeptide.

5

Antibodies

E. faecalis protein-specific antibodies for use in the present invention can be raised against the intact *E. faecalis* protein or an antigenic polypeptide fragment thereof, which may be presented together with a carrier protein, such as an albumin, to
10 an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier.

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules, single chain whole antibodies, and antibody fragments. Antibody fragments of the present invention include Fab and F(ab')₂ and
15 other fragments including single-chain Fvs (scFv) and disulfide-linked Fvs (sdFv). Also included in the present invention are chimeric and humanized monoclonal antibodies and polyclonal antibodies specific for the polypeptides of the present invention. The antibodies of the present invention may be prepared by any of a variety of methods. For example, cells expressing a polypeptide of the present
20 invention or an antigenic fragment thereof can be administered to an animal in order to induce the production of sera containing polyclonal antibodies. For example, a preparation of *E. faecalis* polypeptide or fragment thereof is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific
25 activity.

In a preferred method, the antibodies of the present invention are monoclonal antibodies or binding fragments thereof. Such monoclonal antibodies can be prepared using hybridoma technology. *See, e.g.,* Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988);

Hammerling, et al., in: MONOCLONAL ANTIBODIES AND T-CELL
HYBRIDOMAS 563-681 (Elsevier, N.Y., 1981). Fab and F(ab')₂ fragments may be
produced by proteolytic cleavage, using enzymes such as papain (to produce Fab
fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, *E. faecalis*
5 polypeptide-binding fragments, chimeric, and humanized antibodies can be produced
through the application of recombinant DNA technology or through synthetic
chemistry using methods known in the art.

Alternatively, additional antibodies capable of binding to the polypeptide
antigen of the present invention may be produced in a two-step procedure through the
10 use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies
are themselves antigens, and that, therefore, it is possible to obtain an antibody which
binds to a second antibody. In accordance with this method, *E. faecalis*
polypeptide-specific antibodies are used to immunize an animal, preferably a mouse.
The splenocytes of such an animal are then used to produce hybridoma cells, and the
15 hybridoma cells are screened to identify clones which produce an antibody whose
ability to bind to the *E. faecalis* polypeptide-specific antibody can be blocked by the
E. faecalis polypeptide antigen. Such antibodies comprise anti-idiotypic antibodies to
the *E. faecalis* polypeptide-specific antibody and can be used to immunize an animal
to induce formation of further *E. faecalis* polypeptide-specific antibodies.

20 Antibodies and fragments thereof of the present invention may be described
by the portion of a polypeptide of the present invention recognized or specifically
bound by the antibody. Antibody binding fragments of a polypeptide of the present
invention may be described or specified in the same manner as for polypeptide
fragments discussed above., i.e., by N-terminal and C-terminal positions or by size in
25 contiguous amino acid residues. Any number of antibody binding fragments, of a
polypeptide of the present invention, specified by N-terminal and C-terminal
positions or by size in amino acid residues, as described above, may also be excluded
from the present invention. Therefore, the present invention includes antibodies the
specifically bind a particularly described fragment of a polypeptide of the present

invention and allows for the exclusion of the same.

Antibodies and fragments thereof of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies and fragments that do not bind polypeptides of any other species of *Enterococcus* other than *E.*

5 *faecalis* are included in the present invention. Likewise, antibodies and fragments that bind only species of *Enterococcus*, i.e. antibodies and fragments that do not bind bacteria from any genus other than *Enterococcus*, are included in the present invention.

10 ***Diagnostic Assays***

The present invention further relates to methods for assaying *staphylococcal* infection in an animal by detecting the expression of genes encoding *staphylococcal* polypeptides of the present invention. The methods comprise analyzing tissue or body fluid from the animal for *Enterococcus*-specific antibodies, nucleic acids, or
15 proteins. Analysis of nucleic acid specific to *Enterococcus* is assayed by PCR or hybridization techniques using nucleic acid sequences of the present invention as either hybridization probes or primers. See, e.g., Sambrook et al. Molecular cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 2nd ed., 1989, page 54 reference); Ereemeeva et al. (1994) J. Clin. Microbiol. 32:803-810 (describing
20 differentiation among spotted fever group *Rickettsiae* species by analysis of restriction fragment length polymorphism of PCR-amplified DNA) and Chen et al. 1994 J. Clin. Microbiol. 32:589-595 (detecting *B. burgdorferi* nucleic acids via PCR).

Where diagnosis of a disease state related to infection with *Enterococcus* has already been made, the present invention is useful for monitoring progression or
25 regression of the disease state whereby patients exhibiting enhanced *Enterococcus* gene expression will experience a worse clinical outcome relative to patients expressing these gene(s) at a lower level.

By "biological sample" is intended any biological sample obtained from an animal, cell line, tissue culture, or other source which contains *Enterococcus*

polypeptide, mRNA, or DNA. Biological samples include body fluids (such as saliva, blood, plasma, urine, mucus, synovial fluid, etc.) tissues (such as muscle, skin, and cartilage) and any other biological source suspected of containing *Enterococcus* polypeptides or nucleic acids. Methods for obtaining biological samples such as
5 tissue are well known in the art.

The present invention is useful for detecting diseases related to *Enterococcus* infections in animals. Preferred animals include monkeys, apes, cats, dogs, birds, cows, pigs, mice, horses, rabbits and humans. Particularly preferred are humans.

Total RNA can be isolated from a biological sample using any suitable
10 technique such as the single-step guanidinium-thiocyanate-phenol-chloroform method described in Chomczynski et al. (1987) Anal. Biochem. 162:156-159. mRNA encoding *Enterococcus* polypeptides having sufficient homology to the nucleic acid sequences identified in Table 1 to allow for hybridization between complementary sequences are then assayed using any appropriate method. These include Northern blot analysis, S1
15 nuclease mapping, the polymerase chain reaction (PCR), reverse transcription in combination with the polymerase chain reaction (RT-PCR), and reverse transcription in combination with the ligase chain reaction (RT-LCR).

Northern blot analysis can be performed as described in Harada et al. (1990) Cell 63:303-312. Briefly, total RNA is prepared from a biological sample as described
20 above. For the Northern blot, the RNA is denatured in an appropriate buffer (such as glyoxal/dimethyl sulfoxide/sodium phosphate buffer), subjected to agarose gel electrophoresis, and transferred onto a nitrocellulose filter. After the RNAs have been linked to the filter by a UV linker, the filter is prehybridized in a solution containing formamide, SSC, Denhardt's solution, denatured salmon sperm, SDS, and sodium
25 phosphate buffer. A *E. faecalis* polynucleotide sequence shown in Table 1 labeled according to any appropriate method (such as the ³²P-multiprimered DNA labeling system (Amersham)) is used as probe. After hybridization overnight, the filter is washed and exposed to x-ray film. DNA for use as probe according to the present invention is described in the sections above and will preferably at least 15 nucleotides

in length.

S1 mapping can be performed as described in Fujita et al. (1987) Cell 49:357-367. To prepare probe DNA for use in S1 mapping, the sense strand of an above-described *E. faecalis* DNA sequence of the present invention is used as a
5 template to synthesize labeled antisense DNA. The antisense DNA can then be digested using an appropriate restriction endonuclease to generate further DNA probes of a desired length. Such antisense probes are useful for visualizing protected bands corresponding to the target mRNA (*i.e.*, mRNA encoding *Enterococcus* polypeptides).

10 Levels of mRNA encoding *Enterococcus* polypeptides are assayed, for *e.g.*, using the RT-PCR method described in Makino et al. (1990) Technique 2:295-301. By this method, the radioactivities of the "amplicons" in the polyacrylamide gel bands are linearly related to the initial concentration of the target mRNA. Briefly, this method involves adding total RNA isolated from a biological sample in a reaction
15 mixture containing a RT primer and appropriate buffer. After incubating for primer annealing, the mixture can be supplemented with a RT buffer, dNTPs, DTT, RNase inhibitor and reverse transcriptase. After incubation to achieve reverse transcription of the RNA, the RT products are then subject to PCR using labeled primers.

Alternatively, rather than labeling the primers, a labeled dNTP can be included in the
20 PCR reaction mixture. PCR amplification can be performed in a DNA thermal cycler according to conventional techniques. After a suitable number of rounds to achieve amplification, the PCR reaction mixture is electrophoresed on a polyacrylamide gel. After drying the gel, the radioactivity of the appropriate bands (corresponding to the mRNA encoding the *Enterococcus* polypeptides of the present invention) are

25 quantified using an imaging analyzer. RT and PCR reaction ingredients and conditions, reagent and gel concentrations, and labeling methods are well known in the art. Variations on the RT-PCR method will be apparent to the skilled artisan. Other PCR methods that can detect the nucleic acid of the present invention can be found in PCR PRIMER: A LABORATORY MANUAL (C.W. Dieffenbach et al. eds., Cold

Spring Harbor Lab Press, 1995).

The polynucleotides of the present invention, including both DNA and RNA, may be used to detect polynucleotides of the present invention or Enterococcal species including *E. faecalis* using bio chip technology. The present invention

5 includes both high density chip arrays (>1000 oligonucleotides per cm^2) and low density chip arrays (<1000 oligonucleotides per cm^2). Bio chips comprising arrays of polynucleotides of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. The bio

10 chips of the present invention may comprise polynucleotide sequences of other pathogens including bacteria, viral, parasitic, and fungal polynucleotide sequences, in addition to the polynucleotide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips can also be used to monitor an *E. faecalis* or other Enterococcal infections and to monitor the genetic

15 changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. The bio chip technology comprising arrays of polynucleotides of the present invention may also be used to simultaneously monitor the expression of a multiplicity of genes, including those of the present invention. The polynucleotides used to comprise a selected array may be specified in

20 the same manner as for the fragments, i.e. by their 5' and 3' positions or length in contiguous base pairs and include from. Methods and particular uses of the polynucleotides of the present invention to detect Enterococcal species, including *E. faecalis*, using bio chip technology include those known in the art and those of: U.S. Patent Nos. 5510270, 5545531, 5445934, 5677195, 5532128, 5556752, 5527681,

25 5451683, 5424186, 5607646, 5658732 and World Patent Nos. WO/9710365, WO/9511995, WO/9743447, WO/9535505, each incorporated herein in their entireties.

Biosensors using the polynucleotides of the present invention may also be used to detect, diagnose, and monitor *E. faecalis* or other Enterococcal species and

infections thereof. Biosensors using the polynucleotides of the present invention may also be used to detect particular polynucleotides of the present invention. Biosensors using the polynucleotides of the present invention may also be used to monitor the genetic changes (deletions, insertions, mismatches, etc.) in response to drug therapy in the clinic and drug development in the laboratory. Methods and particular uses of the polynucleotides of the present invention to detect *Enterococcal* species, including *E. faecalis*, using biosensors include those known in the art and those of: U.S. Patent Nos 5721102, 5658732, 5631170, and World Patent Nos. WO97/35011, WO/9720203, each incorporated herein in their entireties.

Thus, the present invention includes both bio chips and biosensors comprising polynucleotides of the present invention and methods of their use.

Assaying *Enterococcus* polypeptide levels in a biological sample can occur using any art-known method, such as antibody-based techniques. For example, *Enterococcus* polypeptide expression in tissues can be studied with classical immunohistological methods. In these, the specific recognition is provided by the primary antibody (polyclonal or monoclonal) but the secondary detection system can utilize fluorescent, enzyme, or other conjugated secondary antibodies. As a result, an immunohistological staining of tissue section for pathological examination is obtained. Tissues can also be extracted, *e.g.*, with urea and neutral detergent, for the liberation of *Enterococcus* polypeptides for Western-blot or dot/slot assay. *See, e.g.*, Jalkanen, M. et al. (1985) J. Cell. Biol. 101:976-985; Jalkanen, M. et al. (1987) J. Cell. Biol. 105:3087-3096. In this technique, which is based on the use of cationic solid phases, quantitation of a *Enterococcus* polypeptide can be accomplished using an isolated *Enterococcus* polypeptide as a standard. This technique can also be applied to body fluids.

Other antibody-based methods useful for detecting *Enterococcus* polypeptide gene expression include immunoassays, such as the ELISA and the radioimmunoassay (RIA). For example, a *Enterococcus* polypeptide-specific monoclonal antibodies can be used both as an immunoabsorbent and as an enzyme-labeled probe to detect and

quantify a *Enterococcus* polypeptide. The amount of a *Enterococcus* polypeptide present in the sample can be calculated by reference to the amount present in a standard preparation using a linear regression computer algorithm. Such an ELISA is described in Iacobelli et al. (1988) Breast Cancer Research and Treatment 11:19-30. In
5 another ELISA assay, two distinct specific monoclonal antibodies can be used to detect *Enterococcus* polypeptides in a body fluid. In this assay, one of the antibodies is used as the immunoabsorbent and the other as the enzyme-labeled probe.

The above techniques may be conducted essentially as a "one-step" or "two-step" assay. The "one-step" assay involves contacting the *Enterococcus*
10 polypeptide with immobilized antibody and, without washing, contacting the mixture with the labeled antibody. The "two-step" assay involves washing before contacting the mixture with the labeled antibody. Other conventional methods may also be employed as suitable. It is usually desirable to immobilize one component of the assay system on a support, thereby allowing other components of the system to be
15 brought into contact with the component and readily removed from the sample. Variations of the above and other immunological methods included in the present invention can also be found in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

Suitable enzyme labels include, for example, those from the oxidase group,
20 which catalyze the production of hydrogen peroxide by reacting with substrate. Glucose oxidase is particularly preferred as it has good stability and its substrate (glucose) is readily available. Activity of an oxidase label may be assayed by measuring the concentration of hydrogen peroxide formed by the enzyme-labeled antibody/substrate reaction. Besides enzymes, other suitable labels include
25 radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulphur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Further suitable labels for the *Enterococcus* polypeptide-specific antibodies of the present invention are provided below. Examples of suitable enzyme labels include

malate dehydrogenase, Enterococcal nuclease, delta-5-steroid isomerase, yeast-alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, and
5 acetylcholine esterase.

Examples of suitable radioisotopic labels include ^3H , ^{111}In , ^{125}I , ^{131}I , ^{32}P , ^{35}S , ^{14}C , ^{51}Cr , ^{57}To , ^{58}Co , ^{59}Fe , ^{75}Se , ^{152}Eu , ^{90}Y , ^{67}Cu , ^{217}Ci , ^{211}At , ^{212}Pb , ^{47}Sc , ^{109}Pd , etc. ^{111}In is a preferred isotope where *in vivo* imaging is used since it avoids the problem of dehalogenation of the ^{125}I or ^{131}I -labeled monoclonal antibody by the liver. In
10 addition, this radionucleotide has a more favorable gamma emission energy for imaging. See, e.g., Perkins et al. (1985) Eur. J. Nucl. Med. 10:296-301; Carasquillo et al. (1987) J. Nucl. Med. 28:281-287. For example, ^{111}In coupled to monoclonal antibodies with 1-(P-isothiocyanatobenzyl)-DPTA has shown little uptake in non-tumors tissues, particularly the liver, and therefore enhances specificity of tumor
15 localization. See, Esteban et al. (1987) J. Nucl. Med. 28:861-870.

Examples of suitable non-radioactive isotopic labels include ^{157}Gd , ^{55}Mn , ^{162}Dy , ^{52}Tr , and ^{56}Fe .

Examples of suitable fluorescent labels include an ^{152}Eu label, a fluorescein label, an isothiocyanate label, a rhodamine label, a phycoerythrin label, a phycocyanin
20 label, an allophycocyanin label, an o-phthaldehyde label, and a fluorescamine label.

Examples of suitable toxin labels include, *Pseudomonas* toxin, diphtheria toxin, ricin, and cholera toxin.

Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an
25 oxalate ester label, a luciferin label, a luciferase label, and an aequorin label.

Examples of nuclear magnetic resonance contrasting agents include heavy metal nuclei such as Gd, Mn, and iron.

Typical techniques for binding the above-described labels to antibodies are provided by Kennedy et al. (1976) Clin. Chim. Acta 70:1-31, and Schurs et al. (1977)

Clin. Chim. Acta 81:1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method, all of which methods are incorporated by reference herein.

5 In a related aspect, the invention includes a diagnostic kit for use in screening serum containing antibodies specific against *E. faecalis* infection. Such a kit may include an isolated *E. faecalis* antigen comprising an epitope which is specifically immunoreactive with at least one anti-*E. faecalis* antibody. Such a kit also includes means for detecting the binding of said antibody to the antigen. In specific
10 embodiments, the kit may include a recombinantly produced or chemically synthesized peptide or polypeptide antigen. The peptide or polypeptide antigen may be attached to a solid support.

 In a more specific embodiment, the detecting means of the above-described kit includes a solid support to which said peptide or polypeptide antigen is attached.
15 Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the *E. faecalis* antigen can be detected by binding of the reporter labeled antibody to the anti-*E. faecalis* polypeptide antibody.

 In a related aspect, the invention includes a method of detecting *E. faecalis* infection in a subject. This detection method includes reacting a body fluid, preferably
20 serum, from the subject with an isolated *E. faecalis* antigen, and examining the antigen for the presence of bound antibody. In a specific embodiment, the method includes a polypeptide antigen attached to a solid support, and serum is reacted with the support. Subsequently, the support is reacted with a reporter-labeled anti-human antibody. The support is then examined for the presence of reporter-labeled
25 antibody.

 The solid surface reagent employed in the above assays and kits is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plates or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or

covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

5 The polypeptides and antibodies of the present invention, including fragments thereof, may be used to detect Enterococcal species including *E. faecalis* using bio chip and biosensor technology. Bio chip and biosensors of the present invention may comprise the polypeptides of the present invention to detect antibodies, which specifically recognize Enterococcal species, including *E. faecalis*. Bio chip and
10 biosensors of the present invention may also comprise antibodies which specifically recognize the polypeptides of the present invention to detect Enterococcal species, including *E. faecalis* or specific polypeptides of the present invention. Bio chips or biosensors comprising polypeptides or antibodies of the present invention may be used to detect Enterococcal species, including *E. faecalis*, in biological and
15 environmental samples and to diagnose an animal, including humans, with an *E. faecalis* or other Enterococcal infection. Thus, the present invention includes both bio chips and biosensors comprising polypeptides or antibodies of the present invention and methods of their use.

 The bio chips of the present invention may further comprise polypeptide
20 sequences of other pathogens including bacteria, viral, parasitic, and fungal polypeptide sequences, in addition to the polypeptide sequences of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips of the present invention may further comprise antibodies or fragments thereof specific for other pathogens including bacteria, viral, parasitic, and fungal polypeptide
25 sequences, in addition to the antibodies or fragments thereof of the present invention, for use in rapid differential pathogenic detection and diagnosis. The bio chips and biosensors of the present invention may also be used to monitor an *E. faecalis* or other Enterococcal infection and to monitor the genetic changes (amino acid deletions, insertions, substitutions, etc.) in response to drug therapy in the clinic and drug

development in the laboratory. The bio chip and biosensors comprising polypeptides or antibodies of the present invention may also be used to simultaneously monitor the expression of a multiplicity of polypeptides, including those of the present invention. The polypeptides used to comprise a bio chip or biosensor of the present invention
5 may be specified in the same manner as for the fragments, i.e, by their N-terminal and C-terminal positions or length in contiguous amino acid residue. Methods and particular uses of the polypeptides and antibodies of the present invention to detect Enterococcal species, including *E. faecalis*, or specific polypeptides using bio chip and biosensor technology include those known in the art, those of the U.S. Patent Nos.
10 and World Patent Nos. listed above for bio chips and biosensors using polynucleotides of the present invention, and those of: U.S. Patent Nos. 5658732, 5135852, 5567301, 5677196, 5690894 and World Patent Nos. WO9729366, WO9612957, each incorporated herein in their entireties.

15 ***Treatment:***

Agonists and Antagonists - Assays and Molecules

The invention also provides a method of screening compounds to identify those which enhance or block the biological activity of the *E. faecalis* polypeptides of the present invention. The present invention further provides where the compounds
20 kill or slow the growth of *E. faecalis*. The ability of *E. faecalis* antagonists, including *E. faecalis* ligands, to prophylactically or therapeutically block antibiotic resistance may be easily tested by the skilled artisan. See, e.g., Straden et al. (1997) J Bacteriol. 179(1):9-16.

An agonist is a compound which increases the natural biological function or
25 which functions in a manner similar to the polypeptides of the present invention, while antagonists decrease or eliminate such functions. Potential antagonists include small organic molecules, peptides, polypeptides, and antibodies that bind to a polypeptide of the invention and thereby inhibit or extinguish its activity.

The antagonists may be employed for instance to inhibit peptidoglycan cross

bridge formation. Antibodies against *E. faecalis* may be employed to bind to and inhibit *E. faecalis* activity to treat antibiotic resistance. Any of the above antagonists may be employed in a composition with a pharmaceutically acceptable carrier.

5 *Vaccines*

The present invention also provides vaccines comprising one or more polypeptides of the present invention. Heterogeneity in the composition of a vaccine may be provided by combining *E. faecalis* polypeptides of the present invention. Multi-component vaccines of this type are desirable because they are likely to be
10 more effective in eliciting protective immune responses against multiple species and strains of the *Enterococcus* genus than single polypeptide vaccines.

Multi-component vaccines are known in the art to elicit antibody production to numerous immunogenic components. *See, e.g.,* Decker et al. (1996) J. Infect. Dis. 174:S270-275. In addition, a hepatitis B, diphtheria, tetanus, pertussis tetravalent
15 vaccine has recently been demonstrated to elicit protective levels of antibodies in human infants against all four pathogenic agents. *See, e.g.,* Aristegui, J. et al. (1997) Vaccine 15:7-9.

The present invention in addition to single-component vaccines includes multi-component vaccines. These vaccines comprise more than one polypeptide,
20 immunogen or antigen. Thus, a multi-component vaccine would be a vaccine comprising more than one of the *E. faecalis* polypeptides of the present invention.

Further within the scope of the invention are whole cell and whole viral vaccines. Such vaccines may be produced recombinantly and involve the expression of one or more of the *E. faecalis* polypeptides described in Table 1. For example, the
25 *E. faecalis* polypeptides of the present invention may be either secreted or localized intracellular, on the cell surface, or in the periplasmic space. Further, when a recombinant virus is used, the *E. faecalis* polypeptides of the present invention may, for example, be localized in the viral envelope, on the surface of the capsid, or internally within the capsid. Whole cells vaccines which employ cells expressing

heterologous proteins are known in the art. *See, e.g.,* Robinson, K. et al. (1997) Nature Biotech. 15:653-657; Sirard, J. et al. (1997) Infect. Immun. 65:2029-2033; Chabalgoity, J. et al. (1997) Infect. Immun. 65:2402-2412. These cells may be administered live or may be killed prior to administration. Chabalgoity, J. et al., *supra*,
5 for example, report the successful use in mice of a live attenuated *Salmonella* vaccine strain which expresses a portion of a platyhelminth fatty acid-binding protein as a fusion protein on its cells surface.

A multi-component vaccine can also be prepared using techniques known in the art by combining one or more *E. faecalis* polypeptides of the present invention, or
10 fragments thereof, with additional non-Enterococcal components (*e.g.,* diphtheria toxin or tetanus toxin, and/or other compounds known to elicit an immune response). Such vaccines are useful for eliciting protective immune responses to both members of the *Enterococcus* genus and non-Enterococcal pathogenic agents.

The vaccines of the present invention also include DNA vaccines. DNA
15 vaccines are currently being developed for a number of infectious diseases. *See, et al.,* Boyer, et al. (1997) Nat. Med. 3:526-532; reviewed in Spier, R. (1996) Vaccine 14:1285-1288. Such DNA vaccines contain a nucleotide sequence encoding one or more *E. faecalis* polypeptides of the present invention oriented in a manner that allows for expression of the subject polypeptide. For example, the direct
20 administration of plasmid DNA encoding *B. burgdorferi* OspA has been shown to elicit protective immunity in mice against borrelial challenge. *See, Luke et al. (1997) J. Infect. Dis.* 175:91-97.

The present invention also relates to the administration of a vaccine which is co-administered with a molecule capable of modulating immune responses. Kim et al.
25 (1997) Nature Biotech. 15:641-646, for example, report the enhancement of immune responses produced by DNA immunizations when DNA sequences encoding molecules which stimulate the immune response are co-administered. In a similar fashion, the vaccines of the present invention may be co-administered with either nucleic acids encoding immune modulators or the immune modulators themselves.

These immune modulators include granulocyte macrophage colony stimulating factor (GM-CSF) and CD86.

The vaccines of the present invention may be used to confer resistance to Enterococcal infection by either passive or active immunization. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through
5 active immunization, a vaccine of the present invention is administered to an animal to elicit a protective immune response which either prevents or attenuates a Enterococcal infection. When the vaccines of the present invention are used to confer resistance to Enterococcal infection through passive immunization, the vaccine is provided to a host
10 animal (*e.g.*, human, dog, or mouse), and the antisera elicited by this antisera is recovered and directly provided to a recipient suspected of having an infection caused by a member of the *Enterococcus* genus.

The ability to label antibodies, or fragments of antibodies, with toxin molecules provides an additional method for treating Enterococcal infections when passive
15 immunization is conducted. In this embodiment, antibodies, or fragments of antibodies, capable of recognizing the *E. faecalis* polypeptides disclosed herein, or fragments thereof, as well as other *Enterococcus* proteins, are labeled with toxin molecules prior to their administration to the patient. When such toxin derivatized antibodies bind to *Enterococcus* cells, toxin moieties will be localized to these cells and
20 will cause their death.

The present invention thus concerns and provides a means for preventing or attenuating a Enterococcal infection resulting from organisms which have antigens that are recognized and bound by antisera produced in response to the polypeptides of the present invention. As used herein, a vaccine is said to prevent or attenuate a disease if
25 its administration to an animal results either in the total or partial attenuation (*i.e.*, suppression) of a symptom or condition of the disease, or in the total or partial immunity of the animal to the disease.

The administration of the vaccine (or the antisera which it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically,

the compound(s) are provided in advance of any symptoms of Enterococcal infection. The prophylactic administration of the compound(s) serves to prevent or attenuate any subsequent infection. When provided therapeutically, the compound(s) is provided upon or after the detection of symptoms which indicate that an animal may be infected with a member of the *Enterococcus* genus. The therapeutic administration of the compound(s) serves to attenuate any actual infection. Thus, the *E. faecalis* polypeptides, and fragments thereof, of the present invention may be provided either prior to the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection.

The polypeptides of the invention, whether encoding a portion of a native protein or a functional derivative thereof, may be administered in pure form or may be coupled to a macromolecular carrier. Example of such carriers are proteins and carbohydrates. Suitable proteins which may act as macromolecular carrier for enhancing the immunogenicity of the polypeptides of the present invention include keyhole limpet hemacyanin (KLH) tetanus toxoid, pertussis toxin, bovine serum albumin, and ovalbumin. Methods for coupling the polypeptides of the present invention to such macromolecular carriers are disclosed in Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988).

A composition is said to be "pharmacologically or physiologically acceptable" if its administration can be tolerated by a recipient animal and is otherwise suitable for administration to that animal. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

While in all instances the vaccine of the present invention is administered as a pharmacologically acceptable compound, one skilled in the art would recognize that the composition of a pharmacologically acceptable compound varies with the animal to which it is administered. For example, a vaccine intended for human use will

generally not be co-administered with Freund's adjuvant. Further, the level of purity of the *E. faecalis* polypeptides of the present invention will normally be higher when administered to a human than when administered to a non-human animal.

As would be understood by one of ordinary skill in the art, when the vaccine
5 of the present invention is provided to an animal, it may be in a composition which may contain salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. Adjuvants are substances that can be used to specifically augment a specific immune response. These substances generally perform two functions: (1) they protect the antigen(s) from being rapidly catabolized
10 after administration and (2) they nonspecifically stimulate immune responses.

Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the animal being immunized. Adjuvants can be loosely divided into several groups based upon their composition. These groups include oil adjuvants (for example, Freund's complete and
15 incomplete), mineral salts (for example, $\text{AlK}(\text{SO}_4)_2$, $\text{AlNa}(\text{SO}_4)_2$, $\text{AlNH}_4(\text{SO}_4)$, silica, kaolin, and carbon), polynucleotides (for example, poly IC and poly AU acids), and certain natural substances (for example, wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, or *Bordetella pertussis*, and members of the genus *Brucella*. Other substances useful as adjuvants are the saponins
20 such as, for example, Quil A. (Superfos A/S, Denmark). Preferred adjuvants for use in the present invention include aluminum salts, such as $\text{AlK}(\text{SO}_4)_2$, $\text{AlNa}(\text{SO}_4)_2$, and $\text{AlNH}_4(\text{SO}_4)$. Examples of materials suitable for use in vaccine compositions are provided in REMINGTON'S PHARMACEUTICAL SCIENCES 1324-1341 (A. Osol, ed, Mack Publishing Co, Easton, PA, (1980) (incorporated herein by reference).

25 The therapeutic compositions of the present invention can be administered parenterally by injection, rapid infusion, nasopharyngeal absorption (intranasopharyngeally), dermoabsorption, or orally. The compositions may alternatively be administered intramuscularly, or intravenously. Compositions for parenteral administration include sterile aqueous or non-aqueous solutions,

suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral
5 administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening,
10 flavoring, or perfuming agents.

Therapeutic compositions of the present invention can also be administered in encapsulated form. For example, intranasal immunization using vaccines encapsulated in biodegradable microsphere composed of poly(DL-lactide-co-glycolide). *See*, Shahin, R. et al. (1995) *Infect. Immun.* 63:1195-1200. Similarly, orally administered
15 encapsulated *Salmonella typhimurium* antigens can also be used. Allaoui-Attarki, K. et al. (1997) *Infect. Immun.* 65:853-857. Encapsulated vaccines of the present invention can be administered by a variety of routes including those involving contacting the vaccine with mucous membranes (*e.g.*, intranasally, intracolonicly, intraduodenally).

20 Many different techniques exist for the timing of the immunizations when a multiple administration regimen is utilized. It is possible to use the compositions of the invention more than once to increase the levels and diversities of expression of the immunoglobulin repertoire expressed by the immunized animal. Typically, if multiple immunizations are given, they will be given one to two months apart.

25 According to the present invention, an "effective amount" of a therapeutic composition is one which is sufficient to achieve a desired biological effect. Generally, the dosage needed to provide an effective amount of the composition will vary depending upon such factors as the animal's or human's age, condition, sex, and extent of disease, if any, and other variables which can be adjusted by one of ordinary skill in

the art.

The antigenic preparations of the invention can be administered by either single or multiple dosages of an effective amount. Effective amounts of the compositions of the invention can vary from 0.01-1,000 $\mu\text{g/ml}$ per dose, more
5 preferably 0.1-500 $\mu\text{g/ml}$ per dose, and most preferably 10-300 $\mu\text{g/ml}$ per dose.

Examples

Example 1: Isolation of a Selected DNA Clone From the Deposited Sample of E. faecalis

10 Three approaches can be used to isolate a *E. faecalis* clone comprising a polynucleotide of the present invention from any *E. faecalis* genomic DNA library. The *E. faecalis* strain V586 has been deposited as a convenient source for obtaining a *E. faecalis* strain although a wide variety of strains *E. faecalis* strains can be used which are known in the art.

15 *E. faecalis* genomic DNA is prepared using the following method. A 20ml overnight bacterial culture grown in a rich medium (e.g., Trypticase Soy Broth, Brain Heart Infusion broth or Super broth), pelleted, washed two times with TES (30mM Tris-pH 8.0, 25mM EDTA, 50mM NaCl), and resuspended in 5ml high salt TES (2.5M NaCl). Lysostaphin is added to final concentration of approx 50ug/ml and the
20 mixture is rotated slowly 1 hour at 37C to make protoplast cells. The solution is then placed in incubator (or place in a shaking water bath) and warmed to 55C. Five hundred micro liter of 20% sarcosyl in TES (final concentration 2%) is then added to lyse the cells. Next, guanidine HCl is added to a final concentration of 7M (3.69g in 5.5 ml). The mixture is swirled slowly at 55C for 60-90 min (solution should clear).
25 A CsCl gradient is then set up in SW41 ultra clear tubes using 2.0ml 5.7M CsCl and overlaying with 2.85M CsCl. The gradient is carefully overlayed with the DNA-containing GuHCl solution. The gradient is spun at 30,000 rpm, 20C for 24 hr and the lower DNA band is collected. The volume is increased to 5 ml with TE buffer. The DNA is then treated with protease K (10 ug/ml) overnight at 37 C, and

precipitated with ethanol. The precipitated DNA is resuspended in a desired buffer.

In the first method, a plasmid is directly isolated by screening a plasmid *E. faecalis* genomic DNA library using a polynucleotide probe corresponding to a polynucleotide of the present invention. Particularly, a specific polynucleotide with
5 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (See, e.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The library is transformed into a suitable
10 host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley and Sons, N.Y. 1989). The transformants are plated on 1.5% agar plates (containing the
15 appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening. See, e.g., Sambrook et al. MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor, N.Y. 2nd ed. 1989); Ausubel et al., CURRENT PROTOCOLS IN MOLECULAR
20 BIOLOGY (John Wiley and Sons, N.Y. 1989) or other techniques known to those of skill in the art.

Alternatively, two primers of 15-25 nucleotides derived from the 5' and 3' ends of a polynucleotide of Table 1 are synthesized and used to amplify the desired DNA by PCR using a *E. faecalis* genomic DNA prep as a template. PCR is carried out
25 under routine conditions, for instance, in 25 μl of reaction mixture with 0.5 μg of the above DNA template. A convenient reaction mixture is 1.5-5 mM MgCl_2 , 0.01% (w/v) gelatin, 20 μM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a

Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

- 5 Finally, overlapping oligos of the DNA sequences of Table 1 can be chemically synthesized and used to generate a nucleotide sequence of desired length using PCR methods known in the art.

Example 2(a): Expression and Purification Enterococcal polypeptides in E. coli

- 10 The bacterial expression vector pQE60 was used for bacterial expression of some of the polypeptide fragments used in the soft tissue and systemic infection models discussed below. (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). pQE60 encodes ampicillin antibiotic resistance ("Ampr") and contains a bacterial origin of replication ("ori"), an IPTG inducible promoter, a ribosome binding
15 site ("RBS"), six codons encoding histidine residues that allow affinity purification using nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin (QIAGEN, Inc., *supra*) and suitable single restriction enzyme cleavage sites. These elements are arranged such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the carboxyl
20 terminus of that polypeptide.

- The DNA sequence encoding the desired portion of a *E. faecalis* protein of the present invention was amplified from *E. faecalis* genomic DNA using PCR oligonucleotide primers which anneal to the 5' and 3' sequences coding for the portions of the *E. faecalis* polynucleotide shown in Table 1. Additional nucleotides
25 containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' sequences, respectively.

 For cloning the mature protein, the 5' primer has a sequence containing an appropriate restriction site followed by nucleotides of the amino terminal coding sequence of the desired *E. faecalis* polynucleotide sequence in Table 1. One of

ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of the complete protein shorter or longer than the mature form.

The 3' primer has a sequence containing an appropriate restriction site followed by
5 nucleotides complementary to the 3' end of the polypeptide coding sequence of Table 1, excluding a stop codon, with the coding sequence aligned with the restriction site so as to maintain its reading frame with that of the six His codons in the pQE60 vector.

The amplified *E. faecalis* DNA fragment and the vector pQE60 were digested with restriction enzymes which recognize the sites in the primers and the digested
10 DNAs were then ligated together. The *E. faecalis* DNA was inserted into the restricted pQE60 vector in a manner which places the *E. faecalis* protein coding region downstream from the IPTG-inducible promoter and in-frame with an initiating AUG and the six histidine codons.

The ligation mixture was transformed into competent *E. coli* cells using
15 standard procedures such as those described by Sambrook et al., *supra*. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), was used in carrying out the illustrative example described herein. This strain, which was only one of many that are suitable for expressing a *E. faecalis* polypeptide, is available commercially
20 (QIAGEN, Inc., *supra*). Transformants were identified by their ability to grow on LB agar plates in the presence of ampicillin and kanamycin. Plasmid DNA was isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs were grown overnight ("O/N") in
25 liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture was used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells were grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. Isopropyl-β-D-thiogalactopyranoside ("IPTG") was then added to a final concentration of 1 mM to induce transcription

from the lac repressor sensitive promoter, by inactivating the lacI repressor. Cells subsequently were incubated further for 3 to 4 hours. Cells then were harvested by centrifugation.

The cells were then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8.

- 5 The cell debris was removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide was loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity were purified in a simple one-step procedure (for details see: The QIAexpressionist, 1995, QIAGEN, Inc., *supra*). Briefly the
- 10 supernatant was loaded onto the column in 6 M guanidine-HCl, pH 8, the column was first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the *E. faecalis* polypeptide was eluted with 6 M guanidine-HCl, pH 5.

- The purified protein was then renatured by dialyzing it against
- 15 phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein could be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of
- 20 1.5 hours or more. After renaturation the proteins can be eluted by the addition of 250 mM imidazole. Imidazole was removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein was stored at 4° C or frozen at -80° C.

- Some of the polypeptide of the present invention were prepared using a non-
- 25 denaturing protein purification method. For these polypeptides, the cell pellet from each liter of culture was resuspended in 25 mls of Lysis Buffer A at 4°C (Lysis Buffer A = 50 mM Na-phosphate, 300 mM NaCl, 10 mM 2-mercaptoethanol, 10% Glycerol, pH 7.5 with 1 tablet of Complete EDTA-free protease inhibitor cocktail (Boehringer Mannheim #1873580) per 50 ml of buffer). Absorbance at 550 nm was

approximately 10-20 O.D./ml. The suspension was then put through three freeze/thaw cycles from -70°C (using a ethanol-dry ice bath) up to room temperature. The cells were lysed via sonication in short 10 sec bursts over 3 minutes at approximately 80W while kept on ice. The sonicated sample was then centrifuged at
5 15,000 RPM for 30 minutes at 4°C. The supernatant was passed through a column containing 1.0 ml of CL-4B resin to pre-clear the sample of any proteins that may bind to agarose non-specifically, and the flow-through fraction was collected.

The pre-cleared flow-through was applied to a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (Quiagen, Inc., *supra*). Proteins with a 6 X His tag
10 bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure. Briefly, the supernatant was loaded onto the column in Lysis Buffer A at 4°C, the column was first washed with 10 volumes of Lysis Buffer A until the A280 of the eluate returns to the baseline. Then, the column was washed with 5 volumes of 40 mM Imidazole (92% Lysis Buffer A / 8% Buffer B) (Buffer B = 50 mM Na-
15 Phosphate, 300 mM NaCl, 10% Glycerol, 10 mM 2-mercaptoethanol, 500 mM Imidazole, pH of the final buffer should be 7.5). The protein was eluted off of the column with a series of increasing Imidazole solutions made by adjusting the ratios of Lysis Buffer A to Buffer B. Three different concentrations were used: 3 volumes of 75 mM Imidazole, 3 volumes of 150 mM Imidazole, 5 volumes of 500 mM
20 Imidazole. The fractions containing the purified protein were analyzed using 8 %, 10 % or 14% SDS-PAGE depending on the protein size. The purified protein was then dialyzed 2X against phosphate-buffered saline (PBS) in order to place it into an easily workable buffer. The purified protein was stored at 4°C or frozen at -80°.

The following alternative method may be used to purify *E. faecalis* expressed
25 in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per

unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

5 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

10 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

 Following high speed centrifugation (30,000 x g) to remove insoluble particles,
15 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

 To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared
20 tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same
25 buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

 Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive

Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A₂₈₀ monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 2(b): Alternative Expression and Purification Enterococcal polypeptides in E. coli

The vector pQE10 was alternatively used to clone and express some of the polypeptides of the present invention for use in the soft tissue and systemic infection models discussed below. The difference being such that an inserted DNA fragment encoding a polypeptide expresses that polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus of that polypeptide. The bacterial expression vector pQE10 (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311) was used in this example. The components of the pQE10 plasmid are arranged such that the inserted DNA sequence encoding a polypeptide of the present invention expresses the polypeptide with the six His residues (i.e., a "6 X His tag") covalently linked to the amino terminus.

The DNA sequences encoding the desired portions of a polypeptide of Table 1 were amplified using PCR oligonucleotide primers from genomic *E. faecalis* DNA. The PCR primers anneal to the nucleotide sequences encoding the desired amino acid

sequence of a polypeptide of the present invention. Additional nucleotides containing restriction sites to facilitate cloning in the pQE10 vector were added to the 5' and 3' primer sequences, respectively.

For cloning a polypeptide of the present invention, the 5' and 3' primers were
5 selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begins may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 5' primer was designed so the coding sequence of the 6 X His tag is aligned with the restriction site so as to maintain
10 its reading frame with that of *E. faecalis* polypeptide. The 3' was designed to include an stop codon. The amplified DNA fragment was then cloned, and the protein expressed, as described above for the pQE60 plasmid.

The DNA sequences encoding the amino acid sequences of Table 1 may also be cloned and expressed as fusion proteins by a protocol similar to that described
15 directly above, wherein the pET-32b(+) vector (Novagen, 601 Science Drive, Madison, WI 53711) is preferentially used in place of pQE10.

The above methods are not limited to the polypeptide fragments actually produced. The above method, like the methods below, can be used to produce either full length polypeptides or desired fragments thereof.

20

Example 2(c): Alternative Expression and Purification of Enterococcal polypeptides in E. coli

The bacterial expression vector pQE60 is used for bacterial expression in this example (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311). However, in
25 this example, the polypeptide coding sequence is inserted such that translation of the six His codons is prevented and, therefore, the polypeptide is produced with no 6 X His tag.

The DNA sequence encoding the desired portion of the *E. faecalis* amino acid sequence is amplified from an *E. faecalis* genomic DNA prep the deposited DNA

clones using PCR oligonucleotide primers which anneal to the 5' and 3' nucleotide sequences corresponding to the desired portion of the *E. faecalis* polypeptides. Additional nucleotides containing restriction sites to facilitate cloning in the pQE60 vector are added to the 5' and 3' primer sequences.

5 For cloning a *E. faecalis* polypeptides of the present invention, 5' and 3' primers are selected to amplify their respective nucleotide coding sequences. One of ordinary skill in the art would appreciate that the point in the protein coding sequence where the 5' and 3' primers begin may be varied to amplify a DNA segment encoding any desired portion of a polypeptide of the present invention. The 3' and 5' primers
10 contain appropriate restriction sites followed by nucleotides complementary to the 5' and 3' ends of the coding sequence respectively. The 3' primer is additionally designed to include an in-frame stop codon.

 The amplified *E. faecalis* DNA fragments and the vector pQE60 are digested with restriction enzymes recognizing the sites in the primers and the digested DNAs
15 are then ligated together. Insertion of the *E. faecalis* DNA into the restricted pQE60 vector places the *E. faecalis* protein coding region including its associated stop codon downstream from the IPTG-inducible promoter and in-frame with an initiating AUG. The associated stop codon prevents translation of the six histidine codons downstream of the insertion point.

20 The ligation mixture is transformed into competent *E. coli* cells using standard procedures such as those described by Sambrook et al. *E. coli* strain M15/rep4, containing multiple copies of the plasmid pREP4, which expresses the lac repressor and confers kanamycin resistance ("Kanr"), is used in carrying out the illustrative example described herein. This strain, which is only one of many that are suitable for
25 expressing *E. faecalis* polypeptide, is available commercially (QIAGEN, Inc., *supra*). Transformants are identified by their ability to grow on LB plates in the presence of ampicillin and kanamycin. Plasmid DNA is isolated from resistant colonies and the identity of the cloned DNA confirmed by restriction analysis, PCR and DNA sequencing.

Clones containing the desired constructs are grown overnight ("O/N") in liquid culture in LB media supplemented with both ampicillin (100 µg/ml) and kanamycin (25 µg/ml). The O/N culture is used to inoculate a large culture, at a dilution of approximately 1:25 to 1:250. The cells are grown to an optical density at 600 nm ("OD600") of between 0.4 and 0.6. isopropyl-b-D-thiogalactopyranoside ("IPTG") is then added to a final concentration of 1 mM to induce transcription from the *lac* repressor sensitive promoter, by inactivating the *lacI* repressor. Cells subsequently are incubated further for 3 to 4 hours. Cells then are harvested by centrifugation.

To purify the *E. faecalis* polypeptide, the cells are then stirred for 3-4 hours at 4°C in 6M guanidine-HCl, pH 8. The cell debris is removed by centrifugation, and the supernatant containing the *E. faecalis* polypeptide is dialyzed against 50 mM Na-acetate buffer pH 6, supplemented with 200 mM NaCl. Alternatively, the protein can be successfully refolded by dialyzing it against 500 mM NaCl, 20% glycerol, 25 mM Tris/HCl pH 7.4, containing protease inhibitors. After renaturation the protein can be purified by ion exchange, hydrophobic interaction and size exclusion chromatography. Alternatively, an affinity chromatography step such as an antibody column can be used to obtain pure *E. faecalis* polypeptide. The purified protein is stored at 4° C or frozen at -80° C.

The following alternative method may be used to purify *E. faecalis* polypeptides expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells are harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells were then lysed by passing the solution through a microfluidizer

(Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 x g for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

- 5 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 x g centrifugation for 15 min., the pellet is discarded and the *E. faecalis* polypeptide-containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

- Following high speed centrifugation (30,000 x g) to remove insoluble particles,
10 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

- To clarify the refolded *E. faecalis* polypeptide solution, a previously prepared
15 tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same
20 buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

- Fractions containing the *E. faecalis* polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive
25 Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5.

Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the *E. faecalis* polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant *E. faecalis* polypeptide exhibits greater than 95% purity after
5 the above refolding and purification steps. No major contaminant bands are observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein is also tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

10 *Example 2(d): Cloning and Expression of E. faecalis in Other Bacteria*

E. faecalis polypeptides can also be produced in: *E. faecalis* using the methods of S. Skinner et al., (1988) Mol. Microbiol. 2:289-297 or J. I. Moreno (1996) Protein Expr. Purif. 8(3):332-340; *Lactobacillus* using the methods of C. Rush et al., 1997 Appl. Microbiol. Biotechnol. 47(5):537-542; or in *Bacillus subtilis* using the methods
15 Chang et al., U.S. Patent No. 4,952,508.

Example 3: Cloning and Expression in COS Cells

A *E. faecalis* expression plasmid is made by cloning a portion of the DNA encoding a *E. faecalis* polypeptide into the expression vector pDNAI/Amp or
20 pDNAIII (which can be obtained from Invitrogen, Inc.). The expression vector pDNAI/amp contains: (1) an *E. coli* origin of replication effective for propagation in *E. coli* and other prokaryotic cells; (2) an ampicillin resistance gene for selection of plasmid-containing prokaryotic cells; (3) an SV40 origin of replication for propagation in eukaryotic cells; (4) a CMV promoter, a polylinker, an SV40 intron; (5) several
25 codons encoding a hemagglutinin fragment (i.e., an "HA" tag to facilitate purification) followed by a termination codon and polyadenylation signal arranged so that a DNA can be conveniently placed under expression control of the CMV promoter and operably linked to the SV40 intron and the polyadenylation signal by means of restriction sites in the polylinker. The HA tag corresponds to an epitope derived

from the influenza hemagglutinin protein described by Wilson et al. 1984 Cell 37:767. The fusion of the HA tag to the target protein allows easy detection and recovery of the recombinant protein with an antibody that recognizes the HA epitope. pDNAIII contains, in addition, the selectable neomycin marker.

5 A DNA fragment encoding a *E. faecalis* polypeptide is cloned into the polylinker region of the vector so that recombinant protein expression is directed by the CMV promoter. The plasmid construction strategy is as follows. The DNA from a *E. faecalis* genomic DNA prep is amplified using primers that contain convenient restriction sites, much as described above for construction of vectors for expression of
10 *E. faecalis* in *E. coli*. The 5' primer contains a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide. The 3' primer, contains nucleotides complementary to the 3' coding sequence of the *E. faecalis* DNA, a stop codon, and a convenient restriction site.

 The PCR amplified DNA fragment and the vector, pDNAI/Amp, are digested
15 with appropriate restriction enzymes and then ligated. The ligation mixture is transformed into an appropriate *E. coli* strain such as SURE™ (Stratagene Cloning Systems, La Jolla, CA 92037), and the transformed culture is plated on ampicillin media plates which then are incubated to allow growth of ampicillin resistant colonies. Plasmid DNA is isolated from resistant colonies and examined by restriction analysis
20 or other means for the presence of the fragment encoding the *E. faecalis* polypeptide

 For expression of a recombinant *E. faecalis* polypeptide, COS cells are transfected with an expression vector, as described above, using DEAE-dextran, as described, for instance, by Sambrook et al. (*supra*). Cells are incubated under conditions for expression of *E. faecalis* by the vector.

25 Expression of the *E. faecalis*-HA fusion protein is detected by radiolabeling and immunoprecipitation, using methods described in, for example Harlow et al., *supra*.. To this end, two days after transfection, the cells are labeled by incubation in media containing ³⁵S-cysteine for 8 hours. The cells and the media are collected, and the cells are washed and the lysed with detergent-containing RIPA buffer: 150 mM

NaCl, 1% NP-40, 0.1% SDS, 1% NP-40, 0.5% DOC, 50 mM TRIS, pH 7.5, as described by Wilson et al. (*supra*). Proteins are precipitated from the cell lysate and from the culture media using an HA-specific monoclonal antibody. The precipitated proteins then are analyzed by SDS-PAGE and autoradiography. An expression
5 product of the expected size is seen in the cell lysate, which is not seen in negative controls.

Example 4: Cloning and Expression in CHO Cells

The vector pC4 is used for the expression of *E. faecalis* polypeptide in this
10 example. Plasmid pC4 is a derivative of the plasmid pSV2-dhfr (ATCC Accession No. 37146). The plasmid contains the mouse DHFR gene under control of the SV40 early promoter. Chinese hamster ovary cells or other cells lacking dihydrofolate activity that are transfected with these plasmids can be selected by growing the cells in a selective medium (alpha minus MEM, Life Technologies) supplemented with the
15 chemotherapeutic agent methotrexate. The amplification of the DHFR genes in cells resistant to methotrexate (MTX) has been well documented. *See, e.g.,* Alt et al., 1978, J. Biol. Chem. 253:1357-1370; Hamlin et al., 1990, Biochem. et Biophys. Acta, 1097:107-143; Page et al., 1991, Biotechnology 9:64-68. Cells grown in increasing concentrations of MTX develop resistance to the drug by overproducing the target
20 enzyme, DHFR, as a result of amplification of the DHFR gene. If a second gene is linked to the DHFR gene, it is usually co-amplified and over-expressed. It is known in the art that this approach may be used to develop cell lines carrying more than 1,000 copies of the amplified gene(s). Subsequently, when the methotrexate is
25 withdrawn, cell lines are obtained which contain the amplified gene integrated into one or more chromosome(s) of the host cell.

Plasmid pC4 contains the strong promoter of the long terminal repeat (LTR) of the Rousc Sarcoma Virus, for expressing a polypeptide of interest, Cullen, et al. (1985) Mol. Cell. Biol. 5:438-447; plus a fragment isolated from the enhancer of the immediate early gene of human cytomegalovirus (CMV), Boshart, et al., 1985, Cell

41:521-530. Downstream of the promoter are the following single restriction enzyme cleavage sites that allow the integration of the genes: *Bam* HI, *Xba* I, and *Asp* 718.

Behind these cloning sites the plasmid contains the 3' intron and polyadenylation site of the rat preproinsulin gene. Other high efficiency promoters can also be used for the expression, e.g., the human β -actin promoter, the SV40 early or late promoters or the long terminal repeats from other retroviruses, e.g., HIV and HTLV. Clontech's Tet-Off and Tet-On gene expression systems and similar systems can be used to express the *E. faecalis* polypeptide in a regulated way in mammalian cells (Gossen et al., 1992, Proc. Natl. Acad. Sci. USA 89:5547-5551. For the polyadenylation of the mRNA other signals, e.g., from the human growth hormone or globin genes can be used as well. Stable cell lines carrying a gene of interest integrated into the chromosomes can also be selected upon co-transfection with a selectable marker such as gpt, G418 or hygromycin. It is advantageous to use more than one selectable marker in the beginning, e.g., G418 plus methotrexate.

The plasmid pC4 is digested with the restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel. The DNA sequence encoding the *E. faecalis* polypeptide is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' sequences of the desired portion of the gene. A 5' primer containing a restriction site, a Kozak sequence, an AUG start codon, and nucleotides of the 5' coding region of the *E. faecalis* polypeptide is synthesized and used. A 3' primer, containing a restriction site, stop codon, and nucleotides complementary to the 3' coding sequence of the *E. faecalis* polypeptides is synthesized and used. The amplified fragment is digested with the restriction endonucleases and then purified again on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC4 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene are used for

transfection. Five μg of the expression plasmid pC4 is cotransfected with 0.5 μg of the plasmid pSVneo using a lipid-mediated transfection agent such as Lipofectin™ or LipofectAMINE.™ (LifeTechnologies Gaithersburg, MD). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme
5 that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well
10 petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM , 2 μM , 5 μM , 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of
15 100-200 μM . Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 5: Quantitative Murine Soft Tissue Infection Model for E. faecalis

Compositions of the present invention, including polypeptides and peptides,
20 are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following quantitative murine soft tissue infection model. Mice (e.g., NIH Swiss female mice, approximately 7 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present
25 invention using methods known in the art, such as those discussed above. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5×10^8 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 with sterilized Cytodex 3 microcarrier beads preswollen in sterile PBS (3g/100ml). Mice are anesthetized briefly until docile, but still mobile and injected with 0.2 ml of the Cytodex 3 bead/bacterial mixture into each animal subcutaneously in the inguinal region. After four days, counting the day of injection as day one, mice are sacrificed and the contents of the abscess is excised and placed in a 15 ml conical tube containing 1.0ml of sterile PBS. The contents of the abscess is then enzymatically treated and plated as follows.

The abscess is first disrupted by vortexing with sterilized glass beads placed in the tubes. 3.0mls of prepared enzyme mixture (1.0ml Collagenase D (4.0 mg/ml), 1.0ml Trypsin (6.0 mg/ml) and 8.0 mls PBS) is then added to each tube followed by a 20 min. incubation at 37C. The solution is then centrifuged and the supernatant drawn off. 0.5 ml dH₂O is then added and the tubes are vortexed and then incubated for 10 min. at room temperature. 0.5 ml media is then added and samples are serially diluted and plated onto agar plates, and grown overnight at 37C. Plates with distinct and separate colonies are then counted, compared to positive and negative control samples, and quantified. The method can be used to identify composition and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

Example 6: Murine Systemic Neutropenic Model for E. faecalis Infection

Compositions of the present invention, including polypeptides and peptides, are assayed for their ability to function as vaccines or to enhance/stimulate an immune response to a bacterial species (e.g., *E. faecalis*) using the following qualitative murine systemic neutropenic model. Mice (e.g., NIH Swiss female mice, approximately 7
5 weeks old) are first treated with a biologically protective effective amount, or immune enhancing/stimulating effective amount of a composition of the present invention using methods known in the art, such as those discussed above. See, e.g., Harlow et al., ANTIBODIES: A LABORATORY MANUAL, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988). An example of an appropriate starting dose is 20ug per animal.
10 Mice are then injected with 250 - 300 mg/kg cyclophosphamide intraperitoneally. Counting the day of C.P. injection as day one, the mice are left untreated for 5 days to begin recovery of PMNL'S.

The desired bacterial species used to challenge the mice, such as *E. faecalis*, is grown as an overnight culture. The culture is diluted to a concentration of 5×10^8
15 cfu/ml, in an appropriate media, mixed well, serially diluted, and titered. The desired doses are further diluted 1:2 in 4% Brewer's yeast in media.

Mice are injected with the bacteria/brewer's yeast challenge intraperitoneally. The Brewer's yeast solution alone is used as a control. The mice are then monitored twice daily for the first week following challenge, and once a day for the next week to
20 ascertain morbidity and mortality. Mice remaining at the end of the experiment are sacrificed. The method can be used to identify compositions and determine appropriate and effective doses for humans and other animals by comparing the effective doses of compositions of the present invention with compositions known in the art to be effective in both mice and humans. Doses for the effective treatment of
25 humans and other animals, using compositions of the present invention, are extrapolated using the data from the above experiments of mice. It is appreciated that further studies in humans and other animals may be needed to determine the most effective doses using methods of clinical practice known in the art.

The disclosure of all publications (including patents, patent applications, journal articles, laboratory manuals, books, or other documents) cited herein are hereby incorporated by reference in their entireties.

The present invention is not to be limited in scope by the specific
5 embodiments described herein, which are intended as single illustrations of individual
aspects of the invention. Functionally equivalent methods and components are within
the scope of the invention, in addition to those shown and described herein and will
become apparant to those skilled in the art from the foregoing description and
accompanying drawings. Such modifications are intended to fall within the scope of
10 the appended claims.

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF001-1 (SEQ ID NO:1)

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TGAAAGAATA TTGCCAGAAC GTGGCGAGCA AATTGTTTTTA TAAATTTTTT TAAGGGAGAG
AAAAAATGA AGTTCAAAAC TCTAGCAACA ACAGTGTTAG CAACCGCAGC TATTTTCGCA
TTGGGGGCTT GTGGTAACGG TAATGGGGCC AAAGAATCAA ACGATATTGT GAAAGAAGTG
AAGGAAGATA CGACAATCAC TTTCTGGCAT GCAATGAATG GGGTTCAAGA AGAAGCGTTA
ACAAAATTAA CGAAAGACTT CATGAAAGAA AATCCAAAAA TTAAAGTGGA ATTACAAAAT
CAATCTGCTT ACCCTGATTT ACAAGCCAAA ATCAATTCTGA CTTTAACTTC ACCAAAAGAT
TTACCAACAA TTACGCAAGC GTACCCAGGC TGGTTATGGA ATGCTGCACA AGATGAAATG
TTAGTGGACT TAAAACCATA TATGGATGAT GACACAATCG GCTGGAAAGA TGCAGAGCCA
ATTCGTGAAG TATTGTTAGA CGGCGCCAAA ATCGACGGCA AACAAATACGG CATTCCATTT
AATAAATCGA CAGAAATGTT ATTCTATAAT GCTGATTGTG TGAAAGAATA TGGTGTTGAA
GTACCGAAAA CATTAGAGGA ATTAAAAGAA GCTTCTAAAA CAATTTACGA AAAATCCAAC
AAAGAAGTCG TTGGTGCTGG TTTTGACTCG TTAAATAACT ATTACGCAAT TGAATGAAA
AACAAAGGCG TTGATTTTAA TAAAGACTTA GATTTAACAA GCAAAGATTC ACAAGAAGTC
GTGGACTATT ACCGTGATGG TATCGAAGCA GGTACTTCC GCACAGCTGG TTCAGATAAA
TATTTATCTG GCCCATTTGC AAACAAAAAG GTAGCAATGT TTGTCGGTAG TATTGCTGGT
GCTGGTTTTG TTCAAAAAGA TGCTGAAGCT GGTGGCTATG AATACGGTGT TGCACCACGT
CCTGAAAAAA TCAACTTACA ACAAGGAACA GATATTTATA TGTTGATAG TGCTACGCCA
GAACAACGGA CAGCGGCATT TGAATTCATG AAATTCTTAG CTACTCCTGA TTCACAATTG
TACTGGGCAC AACAAACAGG TTATATGCCA ATTTTAGAAT CTGTTTACA CAGTGATGAG
TACAAAAATT CTAAGACAAC CAAAGTACCT GCACAACCTG AAAACGCAGT AAAAGATTTA
TTCGCTATCC CAGTAGAAGA AAATGCTGAT TCAGCCTATA ATGAAATGCG GACAATTATG
GAAAGTATTT TTGCTTCATC AAATAAAGAC ACGAGAAAAT TATTGAAAGA TGCAACATCA
CAATTTGAAC AAGCATGGAA CCAATAA

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EF001-2 (SEQ ID NO:2)

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MKFKTLATT VLATAAIFAL GACGNGNGAK ESNDIVKEVK
EDTTITFWHA MNGVQEEALT KLTKDFMKEN PKIKVELQNO SAYPDLQAKI NSTLTSPKDL
PTITQAYPGW LWNAAQDEML VDLKPYMDDD TIGWKDAEPI REVLLDGAKI DGKQYGIPFN
KSTEMLFYNA DLLKEYGVEV PKTLEELKEA SKTIYEKSNK EVVGAGFDSL NNNYAIGMKN
KGVDFNKDLD LTSKDSQEVV DYYRDGIEAG YFRTAGSDKY LSGPFANKKV AMFVGSIAGA
GFVQKDAEAG GYEYGVAPRP EKINLQQGTD IYMFD SATPE QRTAAFEFMK FLATPDSQLY
WAQQTGYMPI LESVLHSDEY KNSKTTKVPA QLENAVKDLF AIPVEENADS AYNEMRTIME
SIFASSNKDT RKLLKDATSQ FEQAWNQ

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EF001-3 (SEQ ID NO:3)

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TT GTGGTAACGG TAATGGGGCC AAAGAATCAA ACGATATTGT GAAAGAAGTG
AAGGAAGATA CGACAATCAC TTTCTGGCAT GCAATGAATG GGGTTCAAGA AGAAGCGTTA
ACAAAATTAA CGAAAGACTT CATGAAAGAA AATCCAAAAA TTAAAGTGGA ATTACAAAAT
CAATCTGCTT ACCCTGATTT ACAAGCCAAA ATCAATTCTGA CTTTAACTTC ACCAAAAGAT
TTACCAACAA TTACGCAAGC GTACCCAGGC TGGTTATGGA ATGCTGCACA AGATGAAATG
TTAGTGGACT TAAAACCATA TATGGATGAT GACACAATCG GCTGGAAAGA TGCAGAGCCA
ATTCGTGAAG TATTGTTAGA CGGCGCCAAA ATCGACGGCA AACAAATACGG CATTCCATTT
AATAAATCGA CAGAAATGTT ATTCTATAAT GCTGATTGTG TGAAAGAATA TGGTGTTGAA
GTACCGAAAA CATTAGAGGA ATTAAAAGAA GCTTCTAAAA CAATTTACGA AAAATCCAAC
AAAGAAGTCG TTGGTGCTGG TTTTGACTCG TTAAATAACT ATTACGCAAT TGAATGAAA
AACAAAGGCG TTGATTTTAA TAAAGACTTA GATTTAACAA GCAAAGATTC ACAAGAAGTC
GTGGACTATT ACCGTGATGG TATCGAAGCA GGTACTTCC GCACAGCTGG TTCAGATAAA
TATTTATCTG GCCCATTTGC AAACAAAAAG GTAGCAATGT TTGTCGGTAG TATTGCTGGT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCTGGTTTTG	TTCAAAAAGA	TGCTGAAGCT	GGTGGCTATG	AATACGGTGT	TGCACCACGT
CCTGAAAAAA	TCAACTTACA	ACAAGGAACA	GATATTTATA	TGTTTCGATAG	TGCTACGCCA
GAACAACGGA	CAGCGGCATT	TGAATTCATG	AAATTCTTAG	CTACTCCTGA	TTCACAATTG
TACTGGGCAC	AACAAACAGG	TTATATGCCA	ATTTTAGAAT	CTGTTTTACA	CAGTGATGAG
TACAAAAATT	CTAAGACAAC	CAAAGTACCT	GCACAAC'TTG	AAAACGCAGT	AAAAGATTTA
TTCGCTATCC	CAGTAGAAGA	AAATGCTGAT	TCAGCCTATA	ATGAAATGCG	GACAATTATG
GAAAGTATTT	TTGCTTCATC	AAATAAAGAC	ACGAGAAAAT	TATTGAAAAGA	TGCAACATCA
CAATTTGAAC	AAGCATGGAA	CCAA			

EF001-4 (SEQ ID NO:4)

CGNGNGAK ESNDIVKEVK

EDTTITFWHA	MNGVQEEALT	KLTKDFMKEN	PKIKVELQNO	SAYPDLQAKI	NSTLTSPKDL
PTITQAYPGW	LWNAAQDEML	VDLKPYMDDD	TIGWKDAEPI	REVLDDGAKI	DGKQYGIPFN
KSTEMLFYNA	DLLKEYGVEV	PKTLEELKEA	SKTIYEKSNK	EVVGAGFDSL	NNYYAIGMKN
KGVDNFNKDL	LTSKDSQEVV	DYVRDIEAG	YFRTAGSDKY	LSGPFANKKV	AMFVGSIAAG
GFVQKDAEAG	GYEYGVAPRP	EKINLQQGTD	IYMFDSATPE	QRTAAFEFMK	FLATPDSQLY
WAQQTGYMPI	LESVLHSDEY	KNSKTTKVPA	QLENVAVKDLF	AIPVEENADS	AYNEMRTIME
SIFASSNKDT	RKLLKDATSQ	FEQAWNQ			

EF002-1 (SEQ ID NO:5)

TAAATAGCGG	AGGTAGTACA	AATGAAATTT	TGGAAAAAAG	GCTTAACAGC	GGCAGCGCTG
TTAGCAGTGG	CGGCAGTAAC	TTTAACAGCA	TGTGGTGGTT	CAAGTGAAAA	GAAAGCAACT
GAAAAGAGTG	AAGATGGCAA	AACAAAATTA	ACAGTAACTA	CTTGGAATTA	TGACACGACC
CCAGAATTTG	AGAAATTATT	CAGAGCTTTT	GAAGCGGAAA	ATCCTGATAT	CACTATTGAA
CCGGTGGACA	TTGCTTCAGA	TGATTATGAC	ACAAAAGTAA	CAACGATGCT	TTTCATCAGGA
GATACGACGG	ATATTTTAAC	CATGAAAAAC	TTACTTTTCAT	ATTCTAATTA	CGCGCTACGC
AATCAATTGG	TGGATTTAAC	CGATCACGTT	AAAGATTTAG	ATATCGAACC	TGCCAAAAGCA
AGTTACGAGA	TGTATGAAAT	CGATGGTAAA	ACCTATGCTC	AGCCTTACCG	TACAGATTTT
TGGGTATTGT	ATTACAATAA	AAAAATGTTT	GATGAAGCCG	GAATTGCCTA	TCCCGATAAC
TTAACTTGGG	ATGAATATGA	AGCGTTAGCG	AAAAAATTAT	CTAAACCAGA	AGAACAAGTA
TATGGTGCCT	ATCAACATAC	TTGGCGCTCA	ACCGTTCAAG	CGATTGCTGC	TGCTCAAAAC
AATGCCAATT	TGATTGAACC	AAAATACAAT	TATATGGAAA	CTTATTATGA	TCGCGCATTG
AGAATGCAAA	AAGATCAATC	ACAAATGGAT	TTTGGAACAG	CAAAATCAAC	AAAAGTAACG
TATCAATCAC	AATTTGAAAA	TTCAAAAGCG	GCGATGATGT	ACATGGGTAG	CTGCTACATG
GGGACTTTAT	TAACAAACAT	TGATGATGGC	AAAACAAATG	TCGAATGGGG	GATTGCCGAA
ATACCACAAC	AAGAAAAAGG	CAAAGCAACT	ACCTTTGGCT	CACCGACAAG	TTTTGCAATT
AATAAAAAACA	GTAAAAAACA	AAAAGCTGCT	CAAAAATTCT	TAGACTTTGC	TTTCAAGTAAA
GAAGGTGCAA	AACTTTTAGC	AGAAGTAGGG	GTGGTTCCTT	CTTATAAAAC	AGATGAAATT
GATAAAATCT	ACTTTGCAAG	AAAAGGAATG	CCTTCAGACG	AGTCTCACAA	AAAGCCTTTA
ACCCAGATAC	AATTAATTTA	G			

EF002-2 (SEQ ID NO:6)

MKFW KKGLTAAALL AVAAVTLTAC GGSSEKKATE KSEDGKTKLT VTTWNYDTPP

EFEKLFRAFE	AENPDITIEP	VDIASDDYDT	KVTTMLSSGD	TTDILTMKNL	LSYSNYALRN
QLVDLTDHVK	DLIDIEPAKAS	YEMYEIDGKT	YAQPYRTDFW	VLYYNKKMFD	EAGIAYPDNL
TWDEYEALAK	KLSKPEEQVY	GAYQHTWRST	VQAIAAAQNN	ANLIEPKYNY	METYYDRALR
MQKDQSQMDF	GTAKSTKVTY	QSQFENSKAA	MMYMGSWYMG	TLLTNIDDGK	TNVEWGIAEI
PQQEKGKATT	FGSPTSFAIN	KNSKKQKAAQ	KFLDFASGKE	GAKLLAEVGV	VPSYKTDEID

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KIYFARKGMP SDESHKKPLT QIQLI

EF002-3 (SEQ ID NO:7)

A TGTGGTGGTT CAAGTGAAAA GAAAGCAACT
 GAAAAGAGTG AAGATGGCAA AACAAAATTA ACAGTAACTA CTTGGAATTA TGACACGACC
 CCAGAATTTG AGAAATTATT CAGAGCTTTT GAAGCGGAAA ATCCTGATAT CACTATTGAA
 CCGGTGGACA TTGCTTCAGA TGATTATGAC ACAAAGTAA CAACGATGCT TTCATCAGGA
 GATACGACGG ATATTTTAAC CATGAAAAAC TTACTTTCAT ATTCTAATTA CGCGCTACGC
 AATCAATTGG TGGATTTAAC CGATCACGTT AAAGATTTAG ATATCGAACC TGCCAAAGCA
 AGTTACGAGA TGTATGAAAT CGATGGTAAA ACCTATGCTC AGCCTTACCG TACAGATTTT
 TGGGTATTGT ATTACAATAA AAAAATGTTT GATGAAGCCG GAATTGCCCTA TCCCGATAAC
 TTAAGTTGGG ATGAATATGA AGCGTTAGCG AAAAAATTAT CTAAACCAGA AGAACAAGTA
 TATGGTGCCT ATCAACATAC TTGGCGCTCA ACCGTTCAAG CGATTGCTGC TGCTCAAAAC
 AATGCCAATT TGATTGAACC AAAATACAAT TATATGGAAT CTTATTATGA TCGCGCATTG
 AGAATGCAAA AAGATCAATC ACAAATGGAT TTTGGAACAG CAAAATCAAC AAAAGTAACG
 TATCAATCAC AATTTGAAAA TTCAAAAGCG GCGATGATGT ACATGGGTAG CTGGTACATG
 GGGACTTTAT TAACAAACAT TGATGATGGC AAAACAAATG TCGAATGGGG GATTGCCGAA
 ATACCACAAC AAGAAAAAGG CAAAGCAACT ACCTTTGGCT CACCGACAAG TTTTGCAATT
 AATAAAACA GTAAAAACA AAAAGCTGCT CAAAAATTCT TAGACTTTGC TTCAGGTAAA
 GAAGGTGCAA AACTTTTAGC AGAAGTAGGG GTGGTTCCTT CTTATAAAAC AGATGAAATT
 GATAAAATCT ACTTTGCAAG AAAAGGAATG CCTTCAGACG AGTCTCACAA AAAGCCTTTA
 ACCCAGATAC AATTAATT

EF002-4 (SEQ ID NO:8)

C GGSSEKKATE KSEDGKTKLT VTTWNYDTP
 EFELKFRAFE AENPDITIEP VDIASDDYDT KVTTMLSSGD TTDILTMKNL LSYSNYALRN
 QLVLDLTDHVK DLDIEPAKAS YEMYEIDGKT YAQPYRTDFW VLYYNKKMFD EAGIAYPDNL
 TWDEYEALAK KLSKPEEQVY GAYQHTWRST VQAIAAAQNN ANLIEPKYNY METYYDRALR
 MQKDQSQMDF GTAKSTKVTY QSOFENSKAA MMYMGSWYMG TLLTNIDDGK TNVEWGIAEI
 PQQEKGKATT FGSPTSFAIN KNSKKQKAAQ KFLDFASGKE GAKLLAEVGV VPSYKTDEID
 KIYFARKGMP SDESHKKPLT QIQLI

EF003-1 (SEQ ID NO:9)

TAGGAGGACA AAAGAATGAA GAAGTTTTAT TTAGCNACAT TCGCTGTTAT TGCAACAGTT
 ATTTTAGCTG CCTGTGGGGG AAATAAACAA GCAGACCAGA AAGAAGACAA GGAGATTACC
 GTTGCCGTC AATTGGAATC TTCAAAAGAT ATCTTGAGAGA TTGCCAAGAA AGAAGCTGAG
 AAAAAAGGGT ACAAATTAAC CATTATGGAA GTGAGCGACA ATGTTGCCTA CAACGATGCC
 GTGCAACATG ACGAAGCGGA TGCTAATTTT GCGCAACATC AACCCTTCAT GGAAATGTTT
 AACAAAGAGA AAAAAGCTGA TTTAGTGGCT GTGCAACCGA TTTATTATTT TGCTGGTGGT
 TTCTATTCAA AAGAATACCA AGATGCGAAA GATTTACCTG AAAATGCCAA AGTGGGGATT
 CCTAGCGATC CAACCAATGA AGGTCGTGCT TTAGCAATTT TAAATGCAAA CGGCGTGATT
 AAATTAAGAG AAGGTGTCGG CTTTAACGGC ACGGTGGCAG ATGTCGTGGA AAATCCTAAA
 AACATCACTT TTGAAAGCAT TGATTTACTG AATTTAGCTA AAGCCTATGA TGAAAAAGAC
 ATCGCTATGG TGTTCGCTA CCCAGCCTAC TTAGAACCTG CTGGTTTAAC AACGAAAGAT
 GCGATCTTGT TAGAAGATAA AGAAGCAAGT AAACATTACG CATTGCAAGT TGTGACACGC
 AAAGGCGAAA AAGATAGCGA AAAAAACAAG GTTTTAAAAG AAGCGATGAC AACAAAAGAA
 GTTGCTGAAT ACATCAAGAA AAATCTTAAA GGCGCCAATA TTCTGCGTT TTAA

EF003-2 (SEQ ID NO:10)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

MKKFYI ATFVIAITVI LAACGGNKQA DQKEDKEITV AVQLESSKDI LEIAKKEAEK
 KGYKINIMEV SDNVAYNDAV QHDEADANFA QHQPFFMEMFN KEKKADLVAV QPIYYFAGGF
 YSKEYQDAKD LPENAKVGIP SDPTNEGRAL AILNANGVIK LKEGVGFNGT VADVVENPKN
 ITFESIDLLN LAKAYDEKDI AMVFCYPAYL EPAGLTTKDA ILLEDKEASK HYALQVVTRK
 GEKDSEKIKV LKEAMTTKEV AEYIKKNSKG ANIPAF

EF003-3 (SEQ ID NO:11)

CTGTGGGGG AAATAAACAA GCAGACCAGA AAGAAGACAA GGAGATTACC
 GTTGCCGTGC AATTGGAATC TTCAAAAGAT ATCTTGGAGA TTGCCAAGAA AGAAGCTGAG
 AAAAAAGGGT ACAAATTAAT CATTATGGAA GTGAGCGACA ATGTTGCCTA CAACGATGCC
 GTGCAACATG ACGAAGCGGA TGCTAATTTT GCGCAACATC AACCTTTCAT GGAAATGTTT
 AACAAAGAGA AAAAAGCTGA TTTAGTGGCT GTGCAACCGA TTTATTATTT TGCTGGTGGT
 TTCTATTCAA AAGAATACCA AGATGCGAAA GATTACCTG AAAATGCCAA AGTGGGGATT
 CCTAGCGATC CAACCAATGA AGGTCGTGCT TTAGCAATTT TAAATGCAAA CGGCGTGATT
 AAATTAAAAG AAGGTGTCGG CTTTAACGGC ACGGTGGCAG ATGTCGTGGA AAATCCTAAA
 AACATCACTT TTGAAAGCAT TGATTTACTG AATTTAGCTA AAGCCTATGA TGAAAAAGAC
 ATCGCTATGG TGTCTGCTA CCCAGCCTAC TTAGAACCTG CTGGTTTAAAC AACGAAAGAT
 GCGATCTTGT TAGAAGATAA AGAAGCAAGT AAACATTACG CATTGCAAGT TGTGACACGC
 AAAGGCGAAA AAGATAGCGA AAAAATCAAG GTTTTAAAAG AAGCGATGAC AACAAAAGAA
 GTTGCTGAAT ACATCAAGAA AAATTCTAAA GGCGCCAATA TTCCTGCGTT T

EF003-4 (SEQ ID NO:12)

CGGNKQA DQKEDKEITV AVQLESSKDI LEIAKKEAEK
 KGYKINIMEV SDNVAYNDAV QHDEADANFA QHQPFFMEMFN KEKKADLVAV QPIYYFAGGF
 YSKEYQDAKD LPENAKVGIP SDPTNEGRAL AILNANGVIK LKEGVGFNGT VADVVENPKN
 ITFESIDLLN LAKAYDEKDI AMVFCYPAYL EPAGLTTKDA ILLEDKEASK HYALQVVTRK
 GEKDSEKIKV LKEAMTTKEV AEYIKKNSKG ANIPAF

EF004-1 (SEQ ID NO:13)

TAAATCGAAA GAAGGATGAT AGAAATGAAA AAAATGATTA AATTTGCAGG CATTGCTCTT
 ATTTTTCAG CTCTTCTCTC TGCCTGTAGC AACGCAAAAA ATAATACACA AAAGAAAGCC
 GAAACTGCTG CCCAGTCAAG CACTATTGAA GCTTCAGACA GTAACGAAAA CGAGCCTAAT
 ACAGAAAACA TAACCCAAGC AGTTAAACAG TTAGAAGAAA AATTTAACTC TGACGAGAAA
 TTAGTAAAAA TAGATGTTAA AAATAATGTT AAAGATGACA CATCAGATAA CCCTCACGCT
 GTCATTACGG TTAAGGTAAT TAATGATGAA GCAAAAAAAA ATATGGAAGA AATGCAGACT
 GCGATAGATT CCAACTCAGG TACAGAGGCA CAAAAGACTG CCATATACGG AATTCAATTA
 AATGTTGAAG AAGTAGCCAA AACATTAGAA AATGATAACG ATGTTATTTT TTTTCATCACA
 CCTTACACGA ATGGGAACGA CAGAACCATA GCAAAATCAA CTAAAAATGA AAATATTATT
 CCGTTAGTAA AATAA

EF004-2 (SEQ ID NO:14)

MKK MIKFAGIALI FAALLSACSN AKNNTQKKAE TAAQSSTIEA SDSNENEPNT
 ENITQAVKQL EEKFNSEKL VKIDVKNVVK DDTSDNPHAV ITVKVINDEA KKNMEEMQTA
 IDNSNGTEAQ KTAIYGIQLN VEEVAKTLEN DNDVISFITP YTNNGNDRTIA KSTKNENIIP
 LVK

EF004-3 (SEQ ID NO:15)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CTGTAGC AACGCAAAAA ATAATACACA AAAGAAAGCC
 GAAACTGCTG CCCAGTCAAG CACTATTGAA GCTTCAGACA GTAACGAAAA CGAGCCTAAT
 ACAGAAAAACA TAACCCAAGC AGTTAAACAG TTAGAAGAAA AATTTAACTC TGACGAGAAA
 TTAGTAAAAA TAGATGTTAA AAATAATGTT AAAGATGACA CATCAGATAA CCCTCACGCT
 GTCATTACGG TTAAGGTAAT TAATGATGAA GCAAAAAAAAA ATATGGAAGA AATGCAGACT
 GCGATAGATT CCAACTCAGG TACAGAGGCA CAAAAGACTG CCATATACGG AATTCAATTA
 AATGTTGAAG AAGTAGCCAA AACATTAGAA AATGATAACG ATGTTATTTT TTTTCATCACA
 CCTTACACGA ATGGGAACGA CAGAACCATA GCAAATCAA CTAAAAATGA AAATATTATT
 CCGTTAGTAA AA

EF004-4 (SEQ ID NO:16)

CSN AKNNTQKKAE TAAQSSTIEA SDSNENEPNT
 ENITQAVKQL EEKFNSEKLV VKIDVKNVVK DDTSDNPHAV ITVKVINDEA KKNMEEMQTA
 IDNSNGTEAQ KTAIYGIQLN VEEVAKTLEN DNDVISFITP YTNGNDRTIA KSTKNENIIP
 LVK

EF005-1 (SEQ ID NO:17)

TAAAAAATGA AAAAACGATT GACGATTGTG GGGATGCTTT TTCTGGCCAT TTTAGTAATG
 GTTGCTGTG GTAAAAATCA GCAAGCAACG ACAAAGAAA AAGAGACAAA ACCTGAAGAA
 CTAACCTCTT ACATTGTGCG CCACGGAAAA ACCATGTTAA ATACGACGGA CCGCGTACAA
 GGATGGTCAG ATGCGGTCCT AACACCAGAA GGTGAAAAAG TTGTGACAGC AACTGGGATT
 GGACTGAAAG ATGTTGCCTT TCAAAATGCA TATAGTAGTG ATAGTGGCCG CGCCTTGCAA
 ACTGCTCAAC TTATTTTAGA TCAAAATAAA GCAGGCAAAG ACCTTGAAGT CGTGCGTGAC
 CCAGATTTAC GTGAATTTAA TTTTGGTAGC TATGAAGGGG ATTTAAATAA GACAATGTGG
 CAGGATATTG CTGATGATCA AGGTGTTTCC TTAGAAGAAT TTATGAAAAA CATGACTCCT
 GAATCCTTTG CCAATAGTGT AGCTAAACTG GATCAACAGC GCGAGGAAAAG CAAGAATAAC
 TGGCCTGCAG AAGACTATGC TACAATTACT AAACGTTTGA AAAAAAGGCTT AGATAAAATT
 GTTGCCACAG AATCAGCCAA TTCTGGGAAT GGCAATGTTT TAGTGGTCTC TCATGGCTTG
 AGTATTTTAC CGTTGTTAGC AACTTTATTT GATGATTTTA AAGTCCCAGA AGGCGGTTTG
 AAGAATGCTA GTGTCACAAC AATTCATTAC AAAAATGGCG AATATACTTT GGATAAAGTC
 AATGATGTCA GCTACTTAGA AGCAGGCGAA AAAGAATCAA AATAA

EF005-2 (SEQ ID NO:18)

MKKRLTIVG MLFLAILVMV GCGKNQQATT KEKETKPEEL TLYIVRHGKT MLNTTDRVQG
 WSDAVLTPEG EKVVTATGIG LKDVAFQNAV SSDSGRALQT AQLILDQNK A GKDLEVVRDP
 DLREFNFGSY EGDNLKTMWQ DIADDQGVSL EEFMKNMTPE SFANSVAKLD QQREESKNNW
 PAEDYATITK RLKKGLDKIV ATEANSNGNG NVLVVSHGLS ISALLATLFD DFKVPEGGLK
 NASVTTIHYK NGEYTLDKVN DVSYLEAGEK ESK

EF005-3 (SEQ ID NO:19)

TTGTG GTAAAAATCA GCAAGCAACG ACAAAGAAA AAGAGACAAA ACCTGAAGAA
 CTAACCTCTT ACATTGTGCG CCACGGAAAA ACCATGTTAA ATACGACGGA CCGCGTACAA
 GGATGGTCAG ATGCGGTCCT AACACCAGAA GGTGAAAAAG TTGTGACAGC AACTGGGATT
 GGACTGAAAG ATGTTGCCTT TCAAAATGCA TATAGTAGTG ATAGTGGCCG CGCCTTGCAA
 ACTGCTCAAC TTATTTTAGA TCAAAATAAA GCAGGCAAAG ACCTTGAAGT CGTGCGTGAC
 CCAGATTTAC GTGAATTTAA TTTTGGTAGC TATGAAGGGG ATTTAAATAA GACAATGTGG
 CAGGATATTG CTGATGATCA AGGTGTTTCC TTAGAAGAAT TTATGAAAAA CATGACTCCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAATCCTTTG CCAATAGTGT AGCTAAACTG GATCAACAGC GCGAGGAAAG CAAGAATAAC
 TGGCCTGCAG AAGACTATGC TACAATTACT AAACGTTTGA AAAAAGGCTT AGATAAAATT
 GTTGCCACAG AATCAGCCAA TTCTGGGAAT GGCAATGTTT TAGTGGTCTC TCATGGCTTG
 AGTATTTTCTAG CGTTGTAGC AACTTTATTT GATGATTTTA AAGTCCCAGA AGGCGGTTTG
 AAGAATGCTA GTGTCACAAC AATTCATTAC AAAAATGGCG AATATACTTT GGATAAAGTC
 AATGATGTCA GCTACTTAGA AGCAGGCGAA AAAGAATCAA AA

EF005-4 (SEQ ID NO:20)

CGKNQQATT KEKETKPEEL TLYIVRHGKT MLNTTDRVQG
 WSDAVLTPEG EKVVTATGIG LKDVAFQNAV SSDSGRALQT AQLILDQNK A GKDLEVVRDP
 DLREFNFGSY EGDNLKTMWQ DIADDQGVSL EEFMKNMTPE SFANSVAKLD QQREESKNNW
 PAEDYATITK RLKKGLDKIV ATESANSNG NVLVVSHGLS ISALLATLFD DFKVPEGGLK
 NASVTTIHYK NGEYTLDKVN DVSYLEAGEK ESK

EF006-1 (SEQ ID NO:21)

TAAACGATAA ATGGAGGGAA TAAGATGAAA AAACGTACAT TATGGTCAGT AATTACTGTA
 GCAGTAGCTG TCTTAGTTTT AGGGGCTTGC GGCAATAAAA AGAGTGATGA CTCGGTCTTG
 AAAGTTGGAG CTTCACCACT TCCACATGCA GAGATTTTAG AACATGTAAA ACCTTTATTA
 GAAAAAGAAG GCGTAAAATT AGAAGTGACG ACTTATACAG ATTACGTGCT ACCTAACAAG
 GCGTTGAAA GTGGCGATAT CGATGCCAAC TATTTCCAAC ATGTGCCGTT CTTAATGAA
 GCGGTTAAAG AAAATGATTA TGACTTTGTG AATGCAGGTG CGATTCATTT AGAACCAGTT
 GGGCTTTACT CGAAAAAATA CAAATCGTTA CAAGAAATTC CTGATGGTTC AACGATTTAC
 GTTAGCTCTT CCGTTTCAGA TTGGCCACGC GTATTAACTA TCTTAGAAGA TGCTGGTTTA
 ATCAGCTGA AAGAAGGGGT AGACCGGACA ACTGCTACTT TCGATGATAT TGATAAAAAAT
 ACTAAAAAGT TGAAATTCAA TCATGAAAGT GATCCAGCAA TCATGACCAC TCTTTATGAC
 AATGAAGAAG GGGCTGCGGT TTTAATTAACT TCAAACCTTG CCGTGGATCA AGGATTAAAT
 CCCGAAAAAG ATGCGATTGC CTTAGAAAAA GAAAGTTTAC CTTATGCCAA TATTATTGCG
 GTTCGTAAAG AAGACGAAAA CAACGAAAAAT GTAAAAAAT TAGTCAAAGT GTTACGTAGC
 AAAGAAGTCC AAGATTGGAT TACGAAAAAA TGAACGGCG CTATTGTTCC AGTCAATGAA
 TAA

EF006-2 (SEQ ID NO:22)

MKK RTLWSVITVA VAVLVLGACG NKSDDSVLK VGASPVPHAE ILEHVKPLLE
 KEGVKLEVTT YTDYVLPNKA LESGDIDANY FQHVFFNEA VKENDYDFVN AGAIHLEPVG
 LYSKKYKSLQ EIPDGSTIYV SSSVSDWPRV LTILEDAGLI TLKEGVDRIT ATFDDIDKNT
 KKLKFNHESD PAIMTTLYDN EEGAAVLINS NFAVDQGLNP KKDAIALEKE SSPYANIIAV
 RKEDENNENV KKLKVLRSK EVQDWITKKW NGAIVPVNE

EF006-3 (SEQ ID NO:23)

TTGC GGCAATAAAA AGAGTGATGA CTCGGTCTTG
 AAAGTTGGAG CTTCACCACT TCCACATGCA GAGATTTTAG AACATGTAAA ACCTTTATTA
 GAAAAAGAAG GCGTAAAATT AGAAGTGACG ACTTATACAG ATTACGTGCT ACCTAACAAG
 GCGTTGAAA GTGGCGATAT CGATGCCAAC TATTTCCAAC ATGTGCCGTT CTTAATGAA
 GCGGTTAAAG AAAATGATTA TGACTTTGTG AATGCAGGTG CGATTCATTT AGAACCAGTT
 GGGCTTTACT CGAAAAAATA CAAATCGTTA CAAGAAATTC CTGATGGTTC AACGATTTAC
 GTTAGCTCTT CCGTTTCAGA TTGGCCACGC GTATTAACTA TCTTAGAAGA TGCTGGTTTA
 ATCAGCTGA AAGAAGGGGT AGACCGGACA ACTGCTACTT TCGATGATAT TGATAAAAAAT
 ACTAAAAAGT TGAAATTCAA TCATGAAAGT GATCCAGCAA TCATGACCAC TCTTTATGAC
 AATGAAGAAG GGGCTGCGGT TTTAATTAACT TCAAACCTTG CCGTGGATCA AGGATTAAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCGAAAAAAG ATGCGATTGC CTTAGAAAAA GAAAGTTCAC CTTATGCCAA TATTATTGCG
 GTTCGTAAAG AAGACGAAAA CAACGAAAAAT GTAAAAAAT TAGTCAAAGT GTTACGTAGC
 AAAGAAGTCC AAGATTGGAT TACGAAAAAA TGGAACGGCG CTATTGTTCC AGTCAATGAA

EF006-4 (SEQ ID NO:24)

CG NKKSDDSVLK VGASPVPHAE ILEHVKPLLE
 KEGVKLEVTT YTDYVLPNKA LESGDIDANY FQHVPPFNEA VKENDYDFVN AGAIHLEPVG
 LYSKKYKSLQ EIPDGSTIYV SSSVSDWPRV LTILEDAGLI TLKEGVDRIT ATFDIDKNT
 KKLKFNHESD PAIMTTLYDN EEGAALVINS NFAVDQGLNP KKDAIALEKE SSPYANIIAV
 RKEDENNENV KKLKVLRSK EVQDWITKKW NGAIVPVNE

EF008-1 (SEQ ID NO:25)

TAAACCGTGA GAAAGAAATG GAGGAATCAA CGAATGAAAA AATTTAGTTT ATTTTTTTTA
 ACACTTTTAG CAGGGTTAAC GTTAGCTGCT TCGGGAATC AAGCCGCTGA AAAGAAAGAA
 AAATTAGCAA TTGTGACAAC GAACTCGATC CTATCTGATT TAGTGAAAAA TGTTGGGCAA
 GACAAAATTG AGCTGCATAG TATTGTGCCA ATTTGGACAG ACCCTCACGA ATATGAACCG
 TTACCAGAAG ACATTGCGAA AGCTTCTGAA GCGGACATTT TATTCTTTAA CGGCTTGAAC
 TTAGAAACAG GCGGAAATGG CTGGTTTAAC AAATTAATGA AAACGGCCAA AAAAGTTGAG
 AATAAAGATT ACTTTTCTAC AAGCAAAAAT GTTACGCCAC AATATTTAAC AAGTGCCGGT
 CAAGAACAAA CAGAAGATCC ACATGCTTGG TTAGACATTG AAAATGGCAT TAAATATGTA
 GAAAACATTC GTGACGTGTT AGTAGAAAAA GATCCAAAAA ATAAAGATTT CTATACAGAA
 AACGCGAAAA ATTATACCGA AAAACTTAGC AAATACATG AGGAAGCCAA AGCTAAATTT
 GCTGATATTC CTGATGATAA AAAATTATTA GTTACAAGTG AAGGTGCCTT TAAATATTTT
 TCCAAAGCTT ATGATTTTAA TGCCGCTTAT ATTTGGGAAA TTAACACAGA AAGTCAAGGN
 ACACCTGAAC AAATGACCAC GATTATTGAT ACCATTAAGA AATCAAAAGC ACCTGTGTTA
 TTTGTTGAAA CCAGTGTGCGA TAAACGTAGT ATGGAACGGG TCTCAAAAGA AGTGAAACGA
 CCAATTTACG ATACACTTTT CACAGACTCT CTTGCCAAAG AAGGAACAGA AGGCGATACG
 TACTACAGCA TGATGAACTG GAATTTAACA AAAATCCATG ATGGCTTAAT GAGTAAATAA

EF008-2 (SEQ ID NO:26)

MKKFSLFFLT LLAGLTLAAC GNQAAEKKEK LAIVTTNSIL SDLVKNVGQD
 KIELHSIVPI GTDPHEYEP L PEDIAKASEA DILFFNGLNL ETGGNGWFNK LMKTAKKVEN
 KDYFSTSKNV TPQYLTSAGQ EQTEDPHAWL DIENGIKYVE NIRDVLVEKD PKNKDFYTEN
 AKNYTEKLSK LHEEAKAKFA DIPDDKKLLV TSEGAFKYFS KAYDLNAAYI WEINTESQGT
 PEQMTTIIDT IKKSKAPVLF VETSVDKRSR ERVSKEVKRP IYDTLFTDSL AKEGTEGDTY
 YSMNWNLT K IHGDLMSK

EF008-3 (SEQ ID NO:27)

T TCGGGAATC AAGCCGCTGA AAAGAAAGAA
 AAATTAGCAA TTGTGACAAC GAACTCGATC CTATCTGATT TAGTGAAAAA TGTTGGGCAA
 GACAAAATTG AGCTGCATAG TATTGTGCCA ATTTGGACAG ACCCTCACGA ATATGAACCG
 TTACCAGAAG ACATTGCGAA AGCTTCTGAA GCGGACATTT TATTCTTTAA CGGCTTGAAC
 TTAGAAACAG GCGGAAATGG CTGGTTTAAC AAATTAATGA AAACGGCCAA AAAAGTTGAG
 AATAAAGATT ACTTTTCTAC AAGCAAAAAT GTTACGCCAC AATATTTAAC AAGTGCCGGT
 CAAGAACAAA CAGAAGATCC ACATGCTTGG TTAGACATTG AAAATGGCAT TAAATATGTA
 GAAAACATTC GTGACGTGTT AGTAGAAAAA GATCCAAAAA ATAAAGATTT CTATACAGAA
 AACGCGAAAA ATTATACCGA AAAACTTAGC AAATACATG AGGAAGCCAA AGCTAAATTT
 GCTGATATTC CTGATGATAA AAAATTATTA GTTACAAGTG AAGGTGCCTT TAAATATTTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCAAAGCTT ATGATTATAA TGCCGCTTAT ATTTGGGAAA TTAACACAGA AAGTCAAGGN
 ACACCTGAAC AAATGACCAC GATTATTGAT ACCATTAGA AATCAAAAAGC ACCTGTGTTA
 TTTGTTGAAA CCAGTGTCGA TAAACGTAGT ATGGAACGGG TCTCAAAAAGA AGTGAAACGA
 CCAATTTACG ATACACTTTT CACAGACTCT CTTGCCAAAG AAGGAACAGA AGGCGATACG
 TACTACAGCA TGATGAACTG GAATTTAACA AAAATCCATG ATGGCTTAAT GAGTAAA

EF008-4 (SEQ ID NO:28)

C GNQAAEKKEK LAIVTTNSIL SDLVKNVQD
 KIELHSIVPI GTDPHEYEP L PEDIAKASEA DILFFNGLNL ETGGNGWFNK LMK TAKKVEN
 KDYFSTSKNV TPQYLSAGQ EQTEDPHAWL DIENGIKYVE NIRDVLVEKD PKNKDFYTEN
 AKNYTEKLSK LHEEAKAKFA DIPDDKKLLV TSEGAFKYFS KAYDLNAAI WEINTESQGT
 PEQMTTIIDT IKKSKAPVLF VETSVDKRSM ERVSKEVKRP IYDTLFTDSL AKEGTEGDTY
 YSMNNWNLT K IHGGLMSK

EF009-1 (SEQ ID NO:29)

TGACAAATGA AAAAATTTAG TAAATTAATT GGAATTATTG GGGTATTAGC TTTTACGATT
 GCAGGTTGTG CATCGGGGTC TGTGAAGGAT ACTAAGACAG AAACCGTTAA ACTAGGGGTT
 GTAGGAACAA AAAATGATGA ATGGGAATCG GTCAAAGACC GTTTGAAAAA GAAAAATATT
 GATTTACAAT TGGTAGAATT TACAGACTAT ACGCAACCAA ACGCAGCATT AGCAGAAAAA
 GAAATTGATT TAAATGCCTT TCAGCATCAA ATCTTTTTAG ACAATTACAA TAAAGAGCAT
 GGAACGAAAT TAGTATCAAT TGGCAATACA GTCAATGCAC CATTGGGAAT TTACGCTAAT
 AAATTGAAAG ATATCACGAA AATTAAAGAC GGCGGAGAAA TTGCTATTCC TAATGACCCA
 ACGAATGGCG GGCGGGCGTT AATTTTATTA CAAACTGCAG GACTGATAAA AGTAGATCCT
 GCGAAACAGC AACTACCGAC TGTCAGTGAT ATTACTGAAA ATAAACGCCA ATTGAAAATA
 ACTGAATTAG ATGCTACGCA AACAGCGCGC GCTTTACAAG ATGTCGATGC TTCAGTGATT
 AATAGCGGCA TGGCTGTCGA TGCTGGGTAT ACACCAGATA AAGATGCTAT TTTCTTAGAA
 CCTGTAAACG AAAAAGCGAA ACCTTATGTG AACATTGTG TGGCCCGAGA AGAAGATCAA
 GAGAATAAAC TTTATCAAAA AGTTGTAGAA GAATATCAAC AAGAAGAAAC GAAAAAGGTC
 ATTGACAGAA CATCAAAAGG CGCCAATGTT CCAGCCTGGG AAACATTTGG TAAAAAATAA

EF009-2 (SEQ ID NO:30)

MKKFSKLIG LIGVLAFTIA GCASGSVKDT KTETVKLG VV GTKNDEWESV KDRLKKKNID
 LQLVEFTDYT QPNAALAEKE IDLNAFQHQI FLDNYNKEHG TKLVSIGNTV NAPLGIYANK
 LKDITKIKDG GEIAIPNDPT NGGRALILLQ TAGLIKVDPA KQQLPTVSDI TENKRQLKIT
 ELDATQTARA LQDVDAVIN SGMAVDAGYT PDKDAIFLEP VNEKAKPYVN IVVAREEDQE
 NKLYQKVVEE YQEEETKKVI AETSKGANVP AWETFGKK

EF009-3 (SEQ ID NO:31)

TTGTG CATCGGGGTC TGTGAAGGAT ACTAAGACAG AAACCGTTAA ACTAGGGGTT
 GTAGGAACAA AAAATGATGA ATGGGAATCG GTCAAAGACC GTTTGAAAAA GAAAAATATT
 GATTTACAAT TGGTAGAATT TACAGACTAT ACGCAACCAA ACGCAGCATT AGCAGAAAAA
 GAAATTGATT TAAATGCCTT TCAGCATCAA ATCTTTTTAG ACAATTACAA TAAAGAGCAT
 GGAACGAAAT TAGTATCAAT TGGCAATACA GTCAATGCAC CATTGGGAAT TTACGCTAAT
 AAATTGAAAG ATATCACGAA AATTAAAGAC GGCGGAGAAA TTGCTATTCC TAATGACCCA
 ACGAATGGCG GGCGGGCGTT AATTTTATTA CAAACTGCAG GACTGATAAA AGTAGATCCT
 GCGAAACAGC AACTACCGAC TGTCAGTGAT ATTACTGAAA ATAAACGCCA ATTGAAAATA
 ACTGAATTAG ATGCTACGCA AACAGCGCGC GCTTTACAAG ATGTCGATGC TTCAGTGATT
 AATAGCGGCA TGGCTGTCGA TGCTGGGTAT ACACCAGATA AAGATGCTAT TTTCTTAGAA
 CCTGTAAACG AAAAAGCGAA ACCTTATGTG AACATTGTG TGGCCCGAGA AGAAGATCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAGAATAAAC TTTATCAAAA AGTTGTAGAA GAATATCAAC AAGAAGAAAC GAAAAAGGTC
ATTGCAGAAA CATCAAAAAGG CGCCAATGTT CCAGCCTGGG AAACATTTGG TAAAAAA

EF009-4 (SEQ ID NO:32)

CASGSVKDT KTETVKLGTV GTKNDEWESV KDRLKKKNID
LQLVEFTDYT QPNAALAEKE IDLNAFQHQI FLDNYNKEHG TKLVSIGNTV NAPLGIYANK
LKDITKIKDG GEIAIPNDPT NGGRALILLQ TAGLIKVDPA KQQLPTVSDI TENKRQLKIT
ELDATQTARA LQDVDAVIN SGMAVDAGYT PDKDAIFLEP VNEKAKPYVN INVAREEDQE
NKLYQKVVEE YQQEETKKVI AETSKGANVP AWETFGKK

EF010-1 (SEQ ID NO:33)

TGAAAGAATA AAATTGTACA GGAGGAAATA AGGAATGAAA AAATGGCAAA AAGGATTAGC
CGTAGCTGGC GCACAGCTTT AGCTGTAGGA CTAAGCGCGT GCGGTAAATC TTCAAAGAT
GCAGCGTCAA AAGGTGATGA TAGTACACCA ACGTTATTAA TGTATCGTGT TGGGGACAAA
CCAGATAATT ATGACCAATT AATCGATAAT GCGAATAAAA TTATCGAGAA AAAAATTGGG
GCAAAATTAA AAATGGAATT TGTTGGTTGG GCGGATTGGG ACCAAAAAAT GTCAACAATC
GTTGCTTCTG GTGAAAGCTA TGATATTTCA TTAGCACAAA ATTATGCAAC GAATGCACAA
AAAGGCGCCT ATGCTGATTT AACTGATTTA GCACCTAAAT ATGCCAAAGA AGCCTATGAT
CAATTGCCAG ATAACATATAT TAAAGGAAAT ACGATTAAAT GAAAACTGTA TGCCTTCCCA
ATTTTAGGTA ACTCTTACGG TCAACAAGTT TTAACTTTTA ATAAAGAATA TGTCGATAAA
TACAATTTAG ATATTAGTAA AGTCGATGGT AGTTATGAAA GTGCAACGGA AGTTCTAAAA
GAATTCCNTA AAAANGANCC AAATATTGCT GCTTTTGCTA TCGGCCAAAC ATTCTTTGCA
ACAGGTAATT ATGACTTCCC TATTGGTAAC CAATATCCAT TTGCAGTAAA AACAACATGAT
ACTGGCTCAC CAAAAATTAT TAACCAATAT GCCGACAAAG ACATGATTAA TAACCTAAAA
GTCTTGCTATC AATGGTATAA AGATGGCTTG ATTCCAACAG ATGCTGCTAC AAGTACAACA
CCATATGACT TAAATACCAA TACTTGTTT ATGCGTCAAG AAACACAAGG ACCTATGGAT
TATGGTGATA CAATCTTAAC ACAAGCTGCT GGCAAACCAC TTGTTTCTCG TCCACTAACA
GAACCATTAA AAACAACAGC TCAAGCGCAA ATGGCTAACT ATGTTGTTGC AAACACGTCT
AAAAACAAAG AAAAATCTGT TGAATTGTTA GGTTTATTAA ACAGCAATCC AGAATTGTTA
AACGGACTTG TTTATGGTGA AGAAGGCAAA CAATATGAAA AAGTTGGCGA TGATCGTGTG
AAATTGTTGA AAGATTACAC ACCAACAACAT CATTTGAGTG CTTGGAACAC AGGAAACAAC
TTAATCATTT GGCCAGAAGA ATCTGTCAT GAAGAAATGG TTAAAGAACG TGATAAGAGC
ATCGAAGAAG CAAAAGATTC ACCAATTCTT GGTTTTACTT TTGTAAATGA TAAAGTGAAA
ACTGAAATCA CTAACGTTGC TACAGTTATG AACCGTTACG CAGCAAGCTT AAATACAGGA
ACTGTTGATC CAGAAGAAAC ACTTCCAAAA TTAATGGATG ACCTAAAAAC AGCTGGCTGG
GATAAAGTTC AAAAAGAAAT GCAAAACAAA TTAGACGAAT ATATCCAATC TCAAAAATAA

EF010-2 (SEQ ID NO:34)

MAKRISR SWRTALAVGL SACGKSSKDA ASKGDDSTPT LLMYRVGDKP
DNYDQLIDNA NKIEKKIGA KLKMEFVGWG DWDQKMSTIV ASGESYDISL AQNYATNAQK
GAYADLTDLA PKYAKEAYDQ LPDNYIKGNT INGKLYAFPI LGNSYQQQVL TFNKEYVDKY
NLDISKVDGS YESATEVLKE FXKXPNIAA FAIGQTFAT GNYDFPIGNQ YPFAVKTTDT
GSPKIINQYA DKDMINNLKV LHQWYKDGLI PTDAATSTTP YDLNNTWFM RQETQGPMDY
GDTILTQAAG KPLVSRPLTE PLKTTAQAM ANYVVANTSK NKEKSVLLG LLNSNPELLN
GLVYGEEGKQ YEKVGDDRVK LLKDYTPPTH LSAWNTGNL IIWPEESVTE EMVKERDKSI
EEAKDSPILG FTFVNDKVKI EITNVATVMN RYAASLNTGT VDPEETLPKL MDDLKTAGWD
KVQKEMQTQL DEYIQSQK

EF010-3 (SEQ ID NO:35)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GT GCGGTAAATC TTCAAAAGAT

GCAGCGTCAA	AAGGTGATGA	TAGTACACCA	ACGTTATTAA	TGTATCGTGT	TGGGGACAAA
CCAGATAATT	ATGACCAATT	AATCGATAAT	GCGAATAAAA	TTATCGAGAA	AAAAATTGGG
GCAAAATTAA	AAATGGAATT	TGTTGGTTGG	GGCGATTGGG	ACCAAAAAAT	GTCAACAATC
GTTGCTTCTG	GTGAAAGCTA	TGATATTTCA	TTAGCACAAA	ATTATGCAAC	GAATGCACAA
AAAGGCGCCT	ATGCTGATTT	AACTGATTTA	GCACCTAAAT	ATGCCAAAGA	AGCCTATGAT
CAATTGCCAG	ATAACTATAT	TAAAGGAAAT	ACGATTAATG	GAAAAC TGTA	TGCGTTCCCA
ATTTTAGGTA	ACTCTTACGG	TCAACAAGTT	TTAACTTTTA	ATAAAGAATA	TGTCGATAAA
TACAATTTAG	ATATTAGTAA	AGTCGATGGT	AGTTATGAAA	GTGCAACGGA	AGTTCTAAAA
GAATTCNTA	AAAANGANCC	AAATATTGCT	GCTTTTGCTA	TCGGCCAAAC	ATTCCTTGCA
ACAGGTAATT	ATGACTTCCC	TATTGGTAAC	CAATATCCAT	TTGCAGTAAA	AACAAC TGAT
ACTGGCTCAC	CAAAAATTAT	TAACCAATAT	GCCGACAAAG	ACATGATTAA	TAACCTAAAA
GTCTTGCATC	AATGGTATAA	AGATGGCTTG	ATTCCAACAG	ATGCTGCTAC	AAGTACAACA
CCATATGACT	TAAATACCAA	TACTTGGTTT	ATGCGTCAAG	AAACACAAGG	ACCTATGGAT
TATGGTGATA	CAATCTTAAC	ACAAGCTGCT	GGCAAACCAC	TTGTTTCTCG	TCCACTAACA
GAACCATTA	AAACAACAGC	TCAAGCGCAA	ATGGCTAACT	ATGTTGTTGC	AAACACGTCT
AAAAACAAAG	AAAAATCTGT	TGAATTGTTA	GGTTTATTAA	ACAGCAATCC	AGAATTGTTA
AACGGACTTG	TTTATGGTGA	AGAAGGCAAA	CAATATGAAA	AAGTTGGCGA	TGATCGTGTG
AAATTGTTGA	AAGATTACAC	ACCAACAAC	CATTTGAGTG	CTTGGAACAC	AGGAAACAAC
TTAATCATTT	GGCCAGAAGA	ATCTGTCACT	GAAGAAATGG	TTAAAGAACG	TGATAAGAGC
ATCGAAGAAG	CAAAAGATT	ACCAATTCTT	GGTTTACTTT	TTGTAAATGA	TAAAGTGAAA
ACTGAAATCA	CTAACGTTGC	TACAGTTATG	AACCGTTACG	CAGCAAGCTT	AAATACAGGA
ACTGTTGATC	CAGAAGAAAC	ACTTCCAAAA	TTAATGGATG	ACCTAAAAAC	AGCTGGCTGG
GATAAAGTTC	AAAAAGAAAT	GCAAACACAA	TTAGACGAAT	ATATCCAATC	TCAAAAA

EF010-4 (SEQ ID NO:36)

CGKSSKDA ASKGDDSTPT LLMYRVGDKP

DNYDQLIDNA	NKIIEKKIGA	KLKMEFVGWG	DWDQKMSTIV	ASGESYDISL	AQNYATNAQK
GAYADLTDLA	PKYAKEAYDQ	LPDNYIKGNT	INGKLYAFPI	LGNSYQQQVL	TFNKEYVDKY
NLDISKVDGS	YESATEVLKE	FXKXXPNIAA	FAIGQTFEAT	GNYDFPIGNQ	YPFVAVKTTDT
GSPKIINQYA	DKDMINNLKV	LHQWYKDGLI	PTDAATSTTP	YDLNNTNWF	RQETQGPMDY
GDTILTQAAG	KPLVSRPLTE	PLKTTAQAQM	ANYVVANTSK	NKEKSVELLG	LLNSNPELLN
GLVYGEEGKQ	YEKVGDDRVR	LLKDYTPPTH	LSAWNTGNL	IIWPEESVTE	EMVKERDKSI
EEAKDSPILG	FTFVNDKVKT	EITNVATVMN	RYAASLNTGT	VDPEETLPKL	MDDLKTAGWD
KVQKEMQTQL	DEYIQSQK				

EF011-1 (SEQ ID NO:37)

TAACGTTTTT	GGAGGAAAAG	AATGAAAAG	AAATTTTTAG	CAATGATGGC	AGTTTCAATG
ATGGGACTGT	TAATGTTAAG	TGCTTGTC	ACAAATAAAA	AAACAGCAGA	TTCTGCAACA
ACAGAAACAA	CAGCTAAAAC	GGAAGTCACA	GTCAAAGACA	CCAATGGTCA	ATTAACCGTT
CCCAAAAATC	CTAAGAAAAG	CGTTGTTTTT	GATAATGGTT	CCTTGATAC	AATGGATGCA
CTAGGTGTCG	GTGACCGCGT	GGTAGGTGCG	CCAACATAAA	ATATCCCTGC	GTATTTGAAA
AAATACCAAA	AAGTTGAATC	AGCAGGCGGC	ATTAAAGAAC	CAGATTTAGA	AAAAATCAAT
CAACTAAAAC	CAGACTTAAT	TATTATTTCT	GGTCGTCAAC	AAGATTATCA	AGAACAATTA
AAAGCCATTG	CGCCAACCAT	TTACTTAGCT	GTAGATGCCA	AAAATCCTTG	GGCATCAACG
AAACAAAATA	TCGAAACGTT	AGGCACTATT	TTTGATAAAG	AAGAGGTAGC	TAAAGAAAAA
ATAACTGGCT	TAGAAAAAGA	AATTGCTGAC	GTGAAAAAAC	AAGCAGAAGC	TAGCGCGAAT
AATGCGCTTG	TTGTGTTAGT	TAACGAAGGA	CAACTTTCCG	CTTACGGA	AGGCTCTCGT
TTCCGTTTAA	TTCATGATAC	ATTTGGCTTC	AAAGCAGCAG	ACGATAAGAT	TGAAGCTTCC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACTCATGGGC AAAGTGTTC TTACGAATAT GTTTTAGAAA AAAATCCTGG GATTCTCTTT
 GTGGTAGATC GCACCAAAGC AATTGGTGGC GACGATTCAA AAGATAACGT CGCTGCAAAC
 GAATTGATTC AAAAAACCGA TGCTGGTAAA AATGATAAAG TCATTATGCT TCAACCAGAT
 GTTTGGTATC TAAGCGGTGG TGGATTAGAA TCAATGCATT TGATGATAGA AGATGTTAAA
 AAAGGATTAG AGTAA

EF011-2 (SEQ ID NO:38)

MKKK FLAMMAVSM GLLMLSACQT NKKTADSATT ETTAKTEVTV KDTNGQLTVP
 KNPVKVVVFD NGS�DTMDAL GVGDRVVGAP TKNIPAYLKK YQKVESAGGI KEPDLEKINQ
 LKPDLLIISG RQQDYQEQLK AIAPTIYLAV DAKNPWASTK QNIETLGTIF DKEEVAKEKI
 TGLEKEIADV KKQAEASANN ALVVLVNEGQ LSAYGKGSRF GLIHDTFGFK AADDKIEAST
 HGQSVSYEVV LEKNPGILFV VDRTKAIGGD DSKDNVAANE LIQKTDAGKN DKVIMLQPDV
 WYLSGGGLES MHLMIEDVKK GLE

EF011-3 (SEQ ID NO:39)

TTGTCAA ACAAATAAAA AAACAGCAGA TTCTGCAACA
 ACAGAAACAA CAGCTAAAAC GGAAGTCACA GTCAAAGACA CCAATGGTCA ATTAACCGTT
 CCCAAAAATC CTAAGAAAGT CGTTGTTTTT GATAATGGTT CCTTGGATAC AATGGATGCA
 CTAGGTGTCG GTGACCGCGT GGTAGGTGCG CCAACTAAAA ATATCCCTGC GTATTTGAAA
 AAATACCAAA AAGTTGAATC AGCAGCGCGC ATTAAAGAAC CAGATTTAGA AAAATCAAT
 CAACTAAAAC CAGACTTAAT TATTATTTCT GGTCTGCAAC AAGATTATCA AGAACAAATTA
 AAAGCCATTG CGCCAACCAT TTACTTAGCT GTAGATGCCA AAAATCCTTG GGCATCAACG
 AAACAAAATA TCGAACCGTT AGGCACTATT TTTGATAAAG AAGAGGTAGC TAAAGAAAAA
 ATAAGCTGGCT TAGAAAAAGA AATTGCTGAC GTGAAAAAAC AAGCAGAAGC TAGCGCGAAT
 AATGCGCTTG TTGTGTTAGT TAACGAAGGA CAACTTTCCG CTTACGGAAA AGGCTCTCGT
 TTCGGTTTAA TTCATGATAC ATTTGGCTTC AAAGCAGCAG ACGATAAGAT TGAAGCTTCC
 ACTCATGGGC AAAGTGTTC TTACGAATAT GTTTTAGAAA AAAATCCTGG GATTCTCTTT
 GTGGTAGATC GCACCAAAGC AATTGGTGGC GACGATTCAA AAGATAACGT CGCTGCAAAC
 GAATTGATTC AAAAAACCGA TGCTGGTAAA AATGATAAAG TCATTATGCT TCAACCAGAT
 GTTTGGTATC TAAGCGGTGG TGGATTAGAA TCAATGCATT TGATGATAGA AGATGTTAAA
 AAAGGATTAG AG

EF011-4 (SEQ ID NO:40)

CQT NKKTADSATT ETTAKTEVTV KDTNGQLTVP
 KNPVKVVVFD NGS�DTMDAL GVGDRVVGAP TKNIPAYLKK YQKVESAGGI KEPDLEKINQ
 LKPDLLIISG RQQDYQEQLK AIAPTIYLAV DAKNPWASTK QNIETLGTIF DKEEVAKEKI
 TGLEKEIADV KKQAEASANN ALVVLVNEGQ LSAYGKGSRF GLIHDTFGFK AADDKIEAST
 HGQSVSYEVV LEKNPGILFV VDRTKAIGGD DSKDNVAANE LIQKTDAGKN DKVIMLQPDV
 WYLSGGGLES MHLMIEDVKK GLE

EF012-1 (SEQ ID NO:41)

TGAGGGGGCA ACAACATGAA ATTGGGGAAA AAAGTAGTAG GTTTGATTGC AACAGGGTTT
 CTTTTAGCCG CATGTGGCGG AACCAAAGAA GCGGCAGAGA AAGTAGATTC GGGAAATTTA
 GCAGCTGAAC AAAAAATCAG TATTAGTTCA CCTGCACCAA TCTCAACATT GGATACAACA
 CAAACAACAG ATAAAAATAC CTTTACAATG GCACAACATT TATTTGAAGG CCTTTATCGG
 TTTGATGATG ATAGTGCCAC GGTGCCAGCT CTAGCTAAAG ATGTCAAGAT TAGTGACGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GGGCGCAAGT ACCACTTTAC CTTGCGGGAG GGGATTAAGT GGAGCAACGG CGAGCCAATC
ACGGCCCAAG ATTTTGTTTA TTCTTGAAA AAACGGTGA CACCAGCGAC GATTGGACCG
AATGCCTATT TACTAGACAG TGTTAAAAAT AGTTTGTAAA TACGCAACGG TGAAAAGTCA
GTGCATGAAT TAGGGATTTC AGCCCCGAAT GACAAAGAAT TCATTGTTGA ATTAAAACAG
GCCCCAACCTT CCTTCTTAGC AGTCGTTTCG ATTGCTTGGT TAGCGCCACA AAATCAAAAA
TTTGTGCAAG CGCAAGGCAA AGATTACGCC TTGGATAGTG AACATTTACT TTATAGCGGG
CCATTTACGC TAGCCAATTG GGATGCGACT TCAGATACTT GGACATTGAA AAAAAATCCA
GAATACTATG ATGCGGATCA AGTGAAACTG GAAGAAGTTG CGGTTAGCAC AATCAAAGAA
GATAATACTG GGATTAACCT ATATCAAGTG AATGAACTAG ACTTAGTTTCG CATTAAACGGA
CAATATGTTT AACAATATCA AGATGATCCA GGCTATGTCA GTCATCCAGA TGTGGCCAAC
TACTTCTTAG ATTTCAACAA AAAAGAAGGA ACGCCATTAG CGAATGTTCA TTTACGAAAA
GCGATTGGCC AAGCAATTGA TAAAGAAGCC TTAACACAAA GTGTCTTAAA CGATGGGTCA
AAACCCCTTA ACGGATTGAT TCCAAGTAAA CTTTATGCGA ATCCAGAAAC GGATGAAGAT
TTCCGAGCTT ACAGTGCGCA ATATTTGAAA AATGACGTC AAAAAAGCTCA AGCTGAATGG
ACGAAAGCCC AAGCGGATGT CGGTAAAAAA GTGAAACTTT CATTGCTGGC GGCAGACACA
GATCAAGGAA AACGAATTGC TGAATATGTT CAAAGTCAGT TGCAAGAAAA TCTGCCAGGT
TTAGAAATTA CCATTTTCATC GCAACCAAGT AATAATGTGA ACCAATCGCG ACGTGAAAAA
AATTATGAGT TGTCTCTTTC AGGATGGATT GCCGGCAGTA GTGAATTAGA CTCTTACTTT
AACTTATATG CAGGAGAATC AAGTTACAAT TACGGCAATT ATCATAATGC CAAATACGAC
CAATTGGTAG AAGAGGCACG AACGATTAAT GCCAATAATC CAGAGAAACA GTTTGCAGAA
TACAAAGAAG CGGAAGACAT CTTGTTGAAC CAAGATGCTG CCCAAGTACC GCTGTATCAA
AGTGCCTCAA ATTATCTAAT CAATCCTAAA TTGAAAGGCA TTAGTTATCA CTTGTATGGG
GATTATTTCC ACTTGCGCAA TGCCTATTTA ACAGAATGA

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EF012-2 (SEQ ID NO:42)

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MKLGKK VVGLIATGFL LAACGGTKEA AEKVDSGNLA AEQKISSP APISTLDTTQ
TTDKNTFTMA QHLFEGLYRF DDSATVPAL AKDVKISDDG RKYHFTLREG IKWSNGEPIT
AQDFVYSWKK LVTPATIGPN AYLLDSVKNS FEIRNGEKSV DELGISAPND KEFIVELKQA
QPSFLAVVSI AWLAPQNQKF VEAQGKDIAL DSEHLLYSGP FTLANWDATS DTWTLKKNPE
YYDADQVKLE EVAVSTIKED NTGINLYQVN ELDLVRINGQ YVQQYQDDPG YVSHPDVANY
FLDFNKKEGT PLANVHLRKA IGQAIDKEAL TQSVLNDGSK PLNGLIPSKL YANPETDEDF
RAYSGEYLKN DVKKAQAEWT KAQADVGVKKV KLSLLAADTD QGKRIAIEYVQ SQLQENLPGL
EITISSQPSN NVNQSRREKN YELSLSGWIA GSSELDSEYFN LYAGESSYNY GNYHNAKYDQ
LVEEARTINA NNPEKQFAEY KEAEDILLNQ DAAQVPLYQS ASNYLINPKL KGISYHLYGD
YFHLRNAYLT E

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EF012-3 (SEQ ID NO:43)

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ATGTGGCGG AACCAAAGAA GCGGCAGAGA AAGTAGATTC GGGAAATTTA
GCAGCTGAAC AAAAAATCAG TATTAGTTCA CCTGCACCAA TCTCAACATT GGATACAACA
CAAACAACAG ATAAAAATAC CTTTACAATG GCACAACATT TATTTGAAGG CCTTTATCGG
TTTGATGATG ATAGTGCCAC GGTGCCAGCT CTAGCTAAAG ATGTCAAGAT TAGTGACGAT
GGGCGCAAGT ACCACTTTAC CTTGCGGGAG GGGATTAAGT GGAGCAACGG CGAGCCAATC
ACGGCCCAAG ATTTTGTTTA TTCTTGAAA AAACGGTGA CACCAGCGAC GATTGGACCG
AATGCCTATT TACTAGACAG TGTTAAAAAT AGTTTGTAAA TACGCAACGG TGAAAAGTCA
GTGCATGAAT TAGGGATTTC AGCCCCGAAT GACAAAGAAT TCATTGTTGA ATTAAAACAG
GCCCCAACCTT CCTTCTTAGC AGTCGTTTCG ATTGCTTGGT TAGCGCCACA AAATCAAAAA
TTTGTGCAAG CGCAAGGCAA AGATTACGCC TTGGATAGTG AACATTTACT TTATAGCGGG
CCATTTACGC TAGCCAATTG GGATGCGACT TCAGATACTT GGACATTGAA AAAAAATCCA
GAATACTATG ATGCGGATCA AGTGAAACTG GAAGAAGTTG CGGTTAGCAC AATCAAAGAA
GATAATACTG GGATTAACCT ATATCAAGTG AATGAACTAG ACTTAGTTTCG CATTAAACGGA
CAATATGTTT AACAATATCA AGATGATCCA GGCTATGTCA GTCATCCAGA TGTGGCCAAC

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TACTTCTTAG ATTTCAACAA AAAAGAAGGA ACGCCATTAG CGAATGTTCA TTTACGAAAA
 GCGATTGGCC AAGCAATTGA TAAAGAAGCC TTAACACAAA GTGTCTTAAA CGATGGGTCA
 AAACCCCTTA ACGGATTGAT TCCAAGTAAA CTTTATGCGA ATCCAGAAAC GGATGAAGAT
 TTCCGAGCTT ACAGTGGCGA ATATTTGAAA AATGACGTCA AAAAAGCTCA AGCTGAATGG
 ACGAAAAGCCC AAGCGGATGT CGGTAAAAAA GTGAAACTTT CATTGCTGGC GGCAGACACA
 GATCAAGGAA AACGAATTGC TGAATATGTT CAAAGTCAGT TGCAAGAAAA TCTGCCAGGT
 TTAGAAATTA CCATTTTCATC GCAACCAAGT AATAATGTGA ACCAATCGCG ACGTGA AAAA
 AATTATGAGT TGTCTCTTTC AGGATGGATT GCCGGCAGTA GTGAATTAGA CTCTTACTTT
 AACTTATATG CAGGAGAATC AAGTTACAAT TACGGCAATT ATCATAATGC CAAATACGAC
 CAATTGGTAG AAGAGGCACG AACGATTAAT GCCAATAATC CAGAGAAACA GTTTGCAGAA
 TACAAAGAAG CGGAAGACAT CTTGTTGAAC CAAGATGCTG CCCAAGTACC GCTGTATCAA
 AGTGCCCTCAA ATTATCTAAT CAATCCTAAA TTGAAAGGCA TTAGTTATCA CTTGTATGGG
 GATTATTTC ACTTGCGCAA TGCCATTTTA ACAGAA

EF012-4 (SEQ ID NO:44)

CGGTKEA AEKVDSGNLA AEQKISISSP APISTLDTTQ
 TTDKNTFTMA QHLFEGLYRF DDDSATVPAL AKDVKISDDG RKYHFTLREG IKWSNGEPIT
 AQDFVYSWKK LVTPATIGPN AYLLDSVKNS FEIRNGEKSV DELGISAPND KEFIVELKQA
 QPSFLAVVSI AWLAPQNQKF VEAQ GKDYAL DSEHLLYSGP FTLANWDATS DTWTLKKNPE
 YYDADQVKLE EVAVSTIKED NTGINLYQVN ELDLVRINGQ YVQQYQDDPG YVSHPDVANY
 FLDFNKKEGT PLANVHLRKA IGQAIDKEAL TQSVLNDGSK PLNGLIPSKL YANPETDEDF
 RAYSGEYLKN DVKKAQAEWT KAQADV GKKV KLSLLAADTD QGKRIA EYVQ SQLQENLPGL
 EITISSQPSN NVNQSRREKN YELSLSGWIA GSSELD SYFN LYAGESSYNY GNYHNAKYDQ
 LVEEARTINA NNPEKQFAEY KEAEDILLNQ DAAQVPLYQS ASNYLINPKL KGISYHLYGD
 YFHLRNAYLT E

EF013-1 (SEQ ID NO:45)

TAACGAAAAA TGAAAAAAT TGCTTTGTTC AGTATGTTAA CGTTCAGTGT ATTGTCTTTA
 AGTCTAGCAG GATGTGAAA CAAAAAACA GCAAGCACAA ATGATTCTAA GCCAAAGCAA
 GAAACAAAGA AAGCCACGCA GAAATCCTCT AGCCAACAAG AAATGAAAAG TAGTCATTCG
 TCTGTCACGG GTCAAAATTC TAATGTGACA GGGGAAAATC CGTCAGAAAA TGCCACGCAG
 CCTTCTGCAG GAACTGATGA AACGAATGAA GTCCCTCAAA ACCAAGCACC TGATACAAAC
 ATTACAATTA CCAATGTTGT TTTCAATCCT GAAAGAAATG AAATTAATGG TACTACATTA
 CCTAATGCAA CCATTACAGC AACGGTAGTC GGTGATGCTT CTGCACAAGC AGGTGTTTTT
 TATGCGGATG CCAATGGCAA TTTTACAGTA ATTAGTCCCA GAGCGGGAGC GACTACTCAA
 TTAATCGCAA CCGTTGATCA ACGGAATAGT GCACCTGTCC AAATTGATAT TCCAAGTTCA
 GGACAAGAAG CAGCGCTTTC TTTTAGCAAT ATTACGATTG ATCCGAAACA AGGGACAATT
 TCTGGTAAAA CAGCACCGAA TGCAACTATT TTAGTGTCAC GTGCAGATGA TGCGCGGGTG
 ATTTTAGCAA GTTTTACTGC GGATGCCCAA GGGAAATTTCA CAGCCAGTAA TTTAGTTCCC
 GGCACAAAAA ATCGCTTAGA TGTTACGTTA AATGGAGAAA TAGGGACACC TTACTTGT
 GATTTACCAA ATTAA

EF013-2 (SEQ ID NO:46)

MKKIALFS MLTFSVLSLS LAGCGNKKTA STNDSKPKQE TKKATQKSSS QQEMKSSHSS
 VTGQNSNVTG ENPSENATQP SAGTDETNV PQNQAPDTNI TITNVVFNPE RNEINGTTLP
 NATITATVVG DASAQAGVfy ADANGNFTVI SPRAGATTQL IATVDQRNSA PVQIDIPSSG
 QEAAALSFSNI TIDPKQGTIS GKTAPNATIL VSRADDARVI LASFTADAQG NFTASNLPVG
 TKNRLDVTLN GEIGTPYLFDP LPN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF013-3 (SEQ ID NO:47)

ATGTGGAAA CAAAAAACA GCAAGCACAA ATGATTCTAA GCCAAAGCAA
 GAAACAAAGA AAGCCACGCA GAAATCCTCT AGCCAACAAG AAATGAAAAG TAGTCATTCTG
 TCTGTACCGG GTCAAAATTC TAATGTGACA GGGGAAAATC CGTCAGAAAA TGCCACGCAG
 CCTTCTGCAG GAACTGATGA AACGAATGAA GTCCCTCAAA ACCAAGCACC TGATACAAAC
 ATTACAATTA CCAATGTTGT TTTCAATCCT GAAAGAAATG AAATTAATGG TACTACATTA
 CCTAATGCAA CCATTACAGC AACGGTAGTC GGTGATGCTT CTGCACAAGC AGGTGTTTTT
 TATGCGGATG CCAATGGCAA TTTTACAGTA ATTAGTCCCA GAGCGGGAGC GACTACTCAA
 TTAATCGCAA CCGTTGATCA ACGGAATAGT GCACCTGTCC AAATTGATAT TCCAAGTTCA
 GGACAAGAAG CAGCGCTTTC TTTTAGCAAT ATTACGATTG ATCCGAAACA AGGGACAATT
 TCTGGTAAAA CAGCACCGAA TGCAACTATT TTAGTGTCAC GTGCAGATGA TGCGCGGGTG
 ATTTTAGCAA GTTTTACTGC GGATGCCCAA GGGAAATTTCA CAGCCAGTAA TTTAGTTCCC
 GGCACAAAAA ATCGCTTAGA TGTTACGTTA AATGGAGAAA TAGGGACACC TTACTTGT
 GATTACCAA AT

EF013-4 (SEQ ID NO:48)

CGNKKA STNDSKPKQE TKKATQKSSS QQEMKSSHSS
 VTGQNSNVTG ENPSENATQP SAGTDETFNEV PQNQAPDTNI TITNVVFNP RNEINGTTLP
 NATITATVVG DASAQAGVFI ADANGNFTVI SPRAGATTQL IATVDQRNSA PVQIDIPSSG
 QEALSFNSI TIDPKQGTIS GKTAPNATIL VSRADDARVI LASFTADAQG NFTASNLVPG
 TKNRLDVTILN GEIGTPYLFDP LPN

EF014-1 (SEQ ID NO:49)

TGATGGTGGA GACTTTTTTAA GAGAGAGGAA GTACAGCCAA TGAGTAGGAA GCGAAAAATC
 AGCTTAATTA GTTTAGTCAT CATTTTGGTT TTTGTACAG TCGGCTCAGC ATACTTTGCT
 GTAGCGGGTA GCTATTTTAA GAAAACAATT GATAAAGGCT ATGTTCCCAT AAAAAATGAT
 TATAATGAAG CGCAAAATAA AGATAGTCAA TCGTTTTTGA TTATGGGGCT AGACAATACA
 ATTGAACGGA AATTAGGCAC AACTAGGACT GATGCTATGA TGGTGATTAC CGTGAATAAC
 AAGACGAAGA AAATAACCTA TTTAAGTTTG CCACGGGATA GTTTTGTTC AATTGATGCG
 AAAAATTACC AAGGGATGCA GCGAATTGAA GCCGCCTATA CCTACGATGG ACCAACAGCT
 TCTGTAAACA CAGTTGAGAA ATTATTGAAT ATTCCAATCA ATCATTACGT TGTGTTAAC
 TTTTATCTT TTATTAAGTT AATTGATGCG GTTGGCGGCA TAGATGTCAA TGTCAAGCAG
 GCGTTGATG GTGTCACCAA AGACGGGCA GGATCCATTC ATTTTGATGC AGGGAAACAG
 CATTTAGATG GTACGAAAGC TTTATCTTAT GCCCGTGAAA GACATAGCGA TAACGATATT
 ATGCGTGGAT TCCGACAACA AGAAATTATT CAAGCAGTTG AAGACAAGTT GAAATCTGGT
 CAATCAATCA TGAAAATAAT GGACATTATT GATTCGTAA ATGGAAACAT TCAAACATGAT
 GTGGATTCCA ATGAATTGAC TCATTTAGTC AAAGAAGGTT TGACTTGGAC CAATTATGAT
 AAACAACAGC TTTCTTTTGA CTGGCGCACT TTTAGTAATG AAGGGCGCAG TATGGTTGAA
 CTATACCCAG ATAGTATTGA AAATGTCCGT CATCAATTAC GTGTGTCTTT AAATTTAGAA
 AAGCCAGATG AACGAGATCA AGACGGCTAT GTCTTCCATA CGAACGGTGA ATTTTATAT
 CAAAGTGATT ATACCGTTCA AGATGAAGCA GCTGAGGAAA ACGAAATGAC TTCCATCAAC
 GGCAATACGT ATATTGGTGT TCCTGGTAAT ACACAGACCG GCCCGTTGCC ATCAGTTAAA
 ACGGAAAATG GCTTTATAAA ATAA

EF014-2 (SEQ ID NO:50)

MSRRKRKIS LISLVIILVF VTVGSAYFAV AGSYLKKTID KGYVPIKNDY
 NEAQNKDSQS FLIMGLDNTI ERKLGTTTRTD AMMVITVNNK TKKITYLSLP RDSFVQIDAK
 NYQMQRIEA AYTYDGPTAS VNTVEKLLNI PINHYVVFNF LSFIKLIDAV GGIDVNVKQA
 FDGVTKDGP SIHFDAGKQH LDGTKALSYA RERHSDNDIM RGFRQOEIIQ AVEDKLKSGQ
 SIMKIMDIID SLNGNIQTDV DSNEHLHLVK EGLTWTNYDK QQLSFDWRTF SNEGRSMVEL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YPDSIENVRH QLRVSLNLEK PDERDQDGYV FHTNGEFLYQ SDYTVQDEAA EENEMTSING
NTYIGVPGNT QTGPLPSVKT ENGFIK

EF014-3 (SEQ ID NO:51)

TGCT

GTAGCGGGTA GCTATTTTAAA GAAAACAATT GATAAAGGCT ATGTTCCCAT AAAAAATGAT
TATAATGAAG CGCAAAATAA AGATAGTCAA TCGTTTTTGA TTATGGGGCT AGACAATACA
ATTGAACGGA AATTAGGCAC AACTAGGACT GATGCTATGA TGGTGATTAC CGTGAATAAC
AAGACGAAGA AAATAACCTA TTTAAGTTTG CCACGGGATA GTTTTGTTCA AATTGATGCG
AAAAATTACC AAGGGATGCA GCGAATTGAA GCCGCCTATA CCTACGATGG ACCAACAGCT
TCTGTTAACA CAGTTGAGAA ATTATTGAAT ATTCCAATCA ATCATTACGT TGTGTTTAAAC
TTTTTATCTT TTATTAAGTT AATTGATGCG GTTGGCGGCA TAGATGTCAA TGTCAAGCAG
GCGTTTGATG GTGTCACCAA AGACGGGCCA GGATCCATTC ATTTTGATGC AGGGAAACAG
CATTTAGATG GTACGAAAGC TTTATCTTAT GCCCGTGAAA GACATAGCGA TAACGATATT
ATGCGTGGAT TCCGACAACA AGAAATTATT CAAGCAGTTG AAGACAAAGT GAAATCTGGT
CAATCAATCA TGAAAATAAT GGACATTATT GATTCGTTAA ATGGAAACAT TCAAACATGAT
GTGGATTCCA ATGAATTGAC TCATTTAGTC AAAGAAGGTT TGAAGTTGAC CAATTATGAT
AAACAACAGC TTTCCTTTTGA CTGGCGCACT TTTAGTAATG AAGGGCGCAG TATGGTTGAA
CTATACCCAG ATAGTATTGA AAATGTCCGT CATCAATTAC GTGTGTCTTT AAATTTAGAA
AAGCCAGATG AACGAGATCA AGACGGCTAT GTCTTCCATA CGAACGGTGA ATTTTATATAT
CAAAGTGATT ATACCGTTCA AGATGAAGCA GCTGAGGAAA ACGAAATGAC TTCCATCAAC
GGCAATACGT ATATTGGTGT TCCTGGTAAT ACACAGACCG GCCCGTTGCC ATCAGTTAAA
ACGGAAAATG GCTTTATAAA A

EF014-4 (SEQ ID NO:52)

AV AGSYLKKTID KGYVPIKNDY

NEAQNKDSQS FLIMGLDNTI ERKLGTTTRTD AMMVITVNNK TKKITYLSLP RDSFVQIDAK
NYQGMQRIEA AYTYDGPTAS VNTVEKLLNI PINHYVVFNF LSFYKLIDAV GGIDVNVKQA
FDGVTKDGP SIHFDAGKQH LDGKALSIA RERHSDNDIM RGFRQOEIIQ AVEDKLKSGQ
SIMKIMDIID SLNGNIQTDV DSNELTHLVK EGLTWTNYDK QQLSFDWRTF SNEGRSMVEL
YPDSIENVRH QLRVSLNLEK PDERDQDGYV FHTNGEFLYQ SDYTVQDEAA EENEMTSING
NTYIGVPGNT QTGPLPSVKT ENGFIK

EF015-1 (SEQ ID NO:53)

TAATTAAAAA TGTGTAAAAA GGGTCTGATG AAAAAAGGAG ACATAATAGT TATTATCTTT
TTAATAGCTA TCTCTTTTTC TCCATATTTT ATTTTTTTTC ACAATAATCC ATTTAACTCC
AAAAGTTTTG ACGACACTAA ATATGCTGTG GTCAAGATAG ATGGGAAAGA GATTGAGCGT
ATAAATTTAG ATGATTCAAA AGAATTTATC AAAACATATT ATCCATCAAA AGGGCAATAT
AATACTATAG AAGTTAAAAA TGGGCACGTT CGTGTAAGAA AAGATAATAG TCCAGATCAA
ATTGCGGTGA AAACAGGATG GATATCAGAA CCAGGGCNAA CTAGTATCTG TATTCCTCAC
AGATTCATTT TAGAAATTGT TCAACAATAT TCTAAGGATT ATTATATTTA CTA

EF015-2 (SEQ ID NO:54)

MK KGDIIIVIFL IAISFSPYFI FFHNNPFNSK SFDDTKYAVV KIDGKEIERI
NLDDSKFIK TYPSKGQYN TIEVKNGHVR VKKDNSPDQI AVKTGWISEP GXTSICIPHR
FILEIVQOYS KDYYIY

EF015-3 (SEQ ID NO:55)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAATAATCC ATTAACTCC

AAAAGTTTTG ACGACACTAA ATATGCTGTG GTCAAGATAG ATGGGAAAGA GATTGAGCGT
 ATAAATTTAG ATGATTCAAA AGAATTTATC AAAACATATT ATCCATCAAA AGGGCAATAT
 AATACTATAG AAGTTAAAAA TGGGCACGTT CGTGTAAAAA AAGATAATAG TCCAGATCAA
 ATTGCGGTGA AAACAGGATG GATATCAGAA CCAGGGCNAA CTAGTATCTG TATTCCTCAC
 AGATTCATTT TAGAAATTGT TCAACAATAT TCTAAGGATT ATTATATTTA C

EF015-4 (SEQ ID NO:56)

NNPFNSK SFDDTKYAVV KIDGKEIERI
 NLDDSKFIK TYPSKGQYN TIEVKNGHVR VKKDNSPDQI AVKTGWISEP GXTSICIPHR
 FILEIVQQYS KDYYIY

EF016-1 (SEQ ID NO:57)

TGACGGTTGC CCCCGTCCAA TAGAAAGGAG TTTATGATGA AAAAGAAATA TTCTTTAGCC
 TTGCTGGTTA TCTGTTGTAG TTTACTCCTA TTTGCAGGTT GTGGTAAAAG AAAAAGCAAC
 GAAGATCAAT GGACACGGAT TAACGAAGAA AAACGGATTA TTATTGGCTT AGATGACTCC
 TTTGTGCCCA TGGGTTTTCA AGATAAATCA GGCAAAATG TCGGCTTTGA TGTCGACTTA
 GCCAAAGCGG TTTTAAACT TTATGGCATT TCCGTTGACT TCCAACCGAT TGATTGGTCT
 ATGAAAGAAA CAGAATTACA AAATCAAACC ATTGATCTTA TTTGGAACGG CTACACTAAA
 ACGAGCGAGC GGGCCGAAAA AGTTCAATTC ACACAACCTT ACATGACGAA CGACCAAGTA
 CTTGTTTTCTT TAAAAGAAAA AAACATTGCA ACAGCGAGCG ACATGCAAGG CAAAATTTTA
 GGGGTTCAAA ACGGCTCTTC TGGCTATGAT GGCTTCGAAA GTCAGCCTGA CGTTTTGAAA
 AAATTTGTTA AAGACCAAAC ACCTATTTTA TATGACGGCT TTAATGAAGC TTTCTTAGAT
 TTAAATCTG GTCGAATTGA CGGACTCCTA ATCGATCGCG TTTACGCCAA CTACTATCTT
 TCCCACGAAG ATAATTAA AAACATACT ATTTCTCATG TAGGCTATGA CAATGAAGAT
 TTTGCTGTGG GCGTCCGCAA ATCAGACAAT CAATTAGTCC AAAAAATCAA TACTGCCTTT
 GAAACGTTAC GAAAAGATGG CACCCTTAGT AAAATTTCTC AAAAAATGGT TGGAGAGGAC
 GTTACAAATA ACACAAAAAT AAATAA

EF016-2 (SEQ ID NO:58)

MMKKKYSLL LVICCSLLLF AGCGKRKSNE DQWTRINEEK RIIIGLDDSF
 VPMGFQDKSG KIVGFDVDLA KAVFKLYGIS VDFQPIDWSM KETELQNQTI DLIWNGYTKT
 SERAEKVQFT QPYMTNDQVL VSLKEKNIAT ASDMQGKILG VQNGSSGYDG FESQPDVLKK
 FVKDQTPILY DGFNEAFLDL KSGRIDGLLI DRVYANYLS HEDNLKNYTI SHVGYDNEDF
 AVGVRSNDQ LVQKINTAFE TLRKDGTL SK ISQKWFGE DV TNNTKIN

EF016-3 (SEQ ID NO:59)

AAGCAAC

GAAGATCAAT GGACACGGAT TAACGAAGAA AAACGGATTA TTATTGGCTT AGATGACTCC
 TTTGTGCCCA TGGGTTTTCA AGATAAATCA GGCAAAATG TCGGCTTTGA TGTCGACTTA
 GCCAAAGCGG TTTTAAACT TTATGGCATT TCCGTTGACT TCCAACCGAT TGATTGGTCT
 ATGAAAGAAA CAGAATTACA AAATCAAACC ATTGATCTTA TTTGGAACGG CTACACTAAA
 ACGAGCGAGC GGGCCGAAAA AGTTCAATTC ACACAACCTT ACATGACGAA CGACCAAGTA
 CTTGTTTTCTT TAAAAGAAAA AAACATTGCA ACAGCGAGCG ACATGCAAGG CAAAATTTTA
 GGGGTTCAAA ACGGCTCTTC TGGCTATGAT GGCTTCGAAA GTCAGCCTGA CGTTTTGAAA
 AAATTTGTTA AAGACCAAAC ACCTATTTTA TATGACGGCT TTAATGAAGC TTTCTTAGAT
 TTAAATCTG GTCGAATTGA CGGACTCCTA ATCGATCGCG TTTACGCCAA CTACTATCTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCCACGAAG ATAATTTAAA AAACATATACT ATTTCTCATG TAGGCTATGA CAATGAAGAT
 TTTGCTGTGG GCGTCCGCAA ATCAGACAAT CAATTAGTCC AAAAAATCAA TACTGCCCTTT
 GAAACGTTAC GAAAAGATGG CACCCTTAGT AAAATTTCTC AAAAAATGGTT TGGAGAGGAC
 GTTACAAATA ACACAAAAAT AAAC

EF016-4 (SEQ ID NO:60)

SNE DQWTRINEEK RIIIGLDDSF
 VPMGFQDKSG KIVGFDVDLA KAVFKLYGIS VDFQPIDWSM KETELQNQTI DLIWNGYTKT
 SERAEKVQFT QPYMTNDQVL VSLKEKNIAT ASDMQGKILG VQNGSSGYDG FESQPDVLKK
 FVKDQTPILY DGFNEAFLDL KSGRIDGLLI DRVYANYYLS HEDNLKNYTI SHVGYDNEDF
 AVGVKRSNDQ LVQKINTAFE TLRKDGTLSK ISQKWFGEVD TNNTKIN

EF017-1 (SEQ ID NO:61)

TGAGGTGTTT TTATGAAAAG GGCAACAAAG CAAAGGCTGT CTTTGCCAGC AATCATGGTT
 CTACTTCTCT CGGGCTGTGG AAGTGTGGG AAAGAAACCA AAAAGCAAGA ACAACAGGTA
 TTACGGGTCG GGATTGATTC GGAATTATCA ACGGCAGACG TGTCGTTGGC AATGGATAAT
 ACCGCAGCAG ATGTAATGAG CCAAGTAGGG GAGGGACTTT TCTCCTTTGA CGAAAAAGGA
 GAAGCGAAAC CAGCATTGGC AACTGAAAAA GTACAGCCCT CCAATGATGG TTTAAGCTAT
 ACTTTTACGA TTCGAAAAGA TGCAAAATGG AGTAACGGCG AGCCAATCAC AGCAAATGAT
 TTTGAATACT CTTGGAAGCG CACAGTGGAC CCAAAAACAG CTTCCCCGCA AGCGTATTAC
 TTTGAAGGGT TAAAAAATTA TCGTGCTATT GTTGACGGTA GCAAATCTAA AGAAGAGTTA
 GGGGTAACAG CCATTGATGA CCATACCTTG GAAGTAGAGC TAAGCTATCC TATGAGTTAT
 TTTCAACAAT TATTGGCGGT ACCAGCTTTT TATCCTTTAA ATGAAGCATT TGTGCAAAAA
 ACGGGCAAAA ACTATGGTAC ATCAGCTGAG TCAACACTTT ACAATGGCGC CTTACATTA
 GAAGGTTGGG ATGGCACGAA TAATACTTGG TCCTATGTGA AGAATAAAAA TTATTGGGAT
 CAAGCGAATG TTTCCGCTAGA TAAGGTGGAT GTCCAAGTAG TTAAAGAAAGT CAATACTGGG
 AAAAATCTTT TCGAAGGGAA AGAATTAGAT GTTGTA AAAA TTTCTGGAGA AATTGTTGCA
 CAAGAACAAG GCAATGCAGC TTTGAAAATT CGTGAAATTC CTGGAACGTA TTATATCCAA
 TTAAATACGC AAAAAGATCT TTTGGCAAAT AAGAATGCAC GTCGAGCAAT AGCATTATCA
 TTGAATTCTG AGCGTTTAGC TAAAAATGTT TTAAATGATG GCTCAAAAAA AGCACTTGGC
 TTCGTGCCAA CAGGTTTCAC TAATCAAGAA ACGCAAAAAG ATTTTGCAGA GGAATTAGGA
 GATTTAAATC CTAGTGAACC AGAAAAAGCG AAAGAGTTAT GGCAAACGGC TAAAAAAGAA
 TTAGGAATTG AAAAAGCGGA GCTAACGATT TTAAGTTCGG ATACAGAAAA TGCTAAAAAA
 ATCAGTGAGT ATGTTCAAGG AGCTTTAGCA GATAATTTAG AAAATTTAAC AGTCAATGTT
 TCACCAAGTTC CTTTAAATAA TCGTTTAGAA AAAAGTCGCA GCGGAGATTT CGACATTGTG
 GTTGGTGGCT GGACGUCAGT ATATGCTGAT CCAATCGATT TCTTAAACTT ACTGCAATCA
 AAAAATTCCA ATAAATTTGG TAAATGGTCT AATAAGACCT TTGATCAGTT GCTTCAAGAA
 GCAAACGTAA CTTATGCAAA TAAATATGAA GAACGTTGGA AAACATTACA AAAAGCGGAT
 CAATTGGTTG CGGAAGAAGC CCCCCTAGTT CCTCTTTATC AATTAACAGA AGCACGCTTA
 GTGGCCGATT CTGTCCAAAA TTTAGTCTAT GGTCCATTAG GTTCAGGCTA TTACAAATCA
 GTCTCTATCG GCGACAAGTA A

EF017-2 (SEQ ID NO:62)

MKRATKQ RLSLAAIMVL LLSGCGSVGK ETKKQEQQVL RVGIDSELST ADVSLAMDNT
 AADVMSQVGE GLFSFDEKGE AKPALATEKV QPSNDGLSYT FTIRKDAKWS NGEPITANDF
 EYSWKRTVDP KTASPQAYYF EGLKNYRAIV DGSKSKEELG VTAIDDHTLE VELSYPMYSYF
 QQLLAVPAFY PLNEAFVEKT GKNYGTSAES TLYNGAFTLE GWDGTNNTWS YVKNKNYWDQ
 ANVSLDKVDV QVVKEVNTGK NLFEGKELDV VKISGEIVAQ EQGNAALKIR EIPGTYYIQI
 NTQKDLLANK NARRAIALSL NSERLAKNVL NDGSKKALGF VPTGFTNQET QKDFAEELGD

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LNPSEPEKAK ELWQTAKKEL GIEKAELTIL SSDTENAKKI SEYVQALAD NLENLTVNV
 PVPFNNRLEK SRSGDFDIVV GGWTPVYADP IDFLNLLQSK NSNFGKWSN KTFDQLLQEA
 NVTYANKYEE RWKTLQKADQ LVAEEAPLVP LYQLTEARLV ADSVQNLVYG PLGSGYYKSV
 SIGDK

EF017-3 (SEQ ID NO:63)

CTGTGG AAGTGTGGG AAAGAAACCA AAAAGCAAGA ACAACAGGTA
 TTACGGGTCG GGATTGATTC GGAATTATCA ACGGCAGACG TGTCGTTGGC AATGGATAAT
 ACCGCAGCAG ATGTAATGAG CCAAGTAGGG GAGGGACTTT TCTCCTTTGA CGAAAAAGGA
 GAAGCGAAAC CAGCATTGGC AACTGAAAAA GTACAGCCCT CCAATGATGG TTTAAGCTAT
 ACTTTTACGA TTCGAAAAGA TGCAAAATGG AGTAACGGCG AGCCAATCAC AGCAAATGAT
 TTTGAATACT CTTGGAAGCG CACAGTGGAC CCAAAAACAG CTTCCCCGCA AGCGTATTAC
 TTTGAAGGGT TAAAAAATTA TCGTGCTATT GTTGACGGTA GCAAATCTAA AGAAGAGTTA
 GGGGTAACAG CCATTGATGA CCATACCTTG GAAGTAGAGC TAAGCTATCC TATGAGTTAT
 TTTCAACAAT TATTGGCGGT ACCAGCTTTT TATCCTTTAA ATGAAGCATT TGTCGAAAAA
 ACGGGCAAAA ACTATGGTAC ATCAGCTGAG TCAACACTTT ACAATGGCGC CTTACATTA
 GAAGGTGGG ATGGCACGAA TAATACTTGG TCCTATGTGA AGAATAAAAA TTATTGGGAT
 CAAGCGAATG TTTGCTAGA TAAGGTGGAT GTCCAAGTAG TTAAAGAAGT CAATACTGGG
 AAAAATCTTT TCGAAGGGAA AGAATTAGAT GTTGTAAGAA TTTCTGGAGA AATTGTTGCA
 CAAGAACAAG GCAATGCAGC TTTGAAAATT CGTGAAATTC CTGGAACGTA TTATATCCAA
 TTAAATACGC AAAAAGATCT TTTGGCAAAT AAGAATGCAC GTCGAGCAAT AGCATTATCA
 TTGAATTCAG AGCGTTTAGC TAAAAATGTT TTAATGATG GCTCAAAAAA AGCACTTGGC
 TTCGTGCCAA CAGGTTTCAC TAATCAAGAA ACGCAAAAAG ATTTTGCAGA GGAATTAGGA
 GATTTAAATC CTAGTGAACC AGAAAAAGCG AAAGAGTTAT GGCAACGGC TAAAAAGAA
 TTAGGAATTG AAAAAGCGGA GCTAACGATT TTAAGTTCCG ATACAGAAAA TGCTAAAAAA
 ATCAGTGAGT ATGTTCAAGG AGCTTTAGCA GATAATTTAG AAAATTTAAC AGTCAATGTT
 TCACCAGTTC CTTTAAATAA TCGTTTAGAA AAAAGTCGCA GCGGAGATTT CGACATTGTG
 GTTGGTGGCT GGACGCCAGT ATATGCTGAT CCAATCGATT TCTTAACTT ACTGCAATCA
 AAAAATTTCA ATAATTTTGG TAAATGGTCT AATAAGACCT TTGATCAGTT GCTTCAAGAA
 GCAAACGTAA CTTATGCAAA TAAATATGAA GAACGTTGGA AAACATTACA AAAAGCGGAT
 CAATTGGTTG CGGAAGAAGC CCCCTAGTT CCTCTTTATC AATTAACAGA AGCACGCTTA
 GTGGCCGATT CTGTCCAAAA TTTAGTCTAT GGTCCATTAG GTTCAGGCTA TTACAAATCA
 GTCTCTATCG GCGACAAG

EF017-4 (SEQ ID NO:64)

CGSVGK ETKKQEQQVL RVGIDSELST ADVSLAMDNT
 AADVMSQVGE GLFSFDEKGE AKPALATEKV QPSNDGLSYT FTIRKDAKWS NGEPIITANDF
 EYSWKRTVDP KTASPQAYYF EGLKNYRAIV DGSKSKEELG VTAIDDHTLE VELSYPMYSYF
 QQLLAVPAFY PLNEAFVEKT GKNYGTSAES TLYNGAFTLE GWDGTNNTWS YVKNKNYWDQ
 ANVSLDKVDV QVVKEVNTGK NLFEGKELDV VKISGEIVAQ EQGNAALKIR EIPGTYIQL
 NTQKDLLANK NARRAIALSL NSERLAKNVL NDGSKKALGF VPTGFTNQET QKDFAEELGD
 LNPSEPEKAK ELWQTAKKEL GIEKAELTIL SSDTENAKKI SEYVQALAD NLENLTVNV
 PVPFNNRLEK SRSGDFDIVV GGWTPVYADP IDFLNLLQSK NSNFGKWSN KTFDQLLQEA
 NVTYANKYEE RWKTLQKADQ LVAEEAPLVP LYQLTEARLV ADSVQNLVYG PLGSGYYKSV
 SIGDK

EF018-1 (SEQ ID NO:65)

TGTCATTACA ACGATACCAA TTTTAATCAT TTATCCATTA CTACAAAAAC ACTTTATCGG
 CGGTATGATG GCCGGTGCAG TAAAAGAATA AAGAAAGTAG GGAACAATAT GAAAAAGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TTAGGCGGTT TATTGGTGGC AACGGCGGTC GTTAGTTTATG CGGCCTGTAG CGGTGGGGAA
AAGAAAGCTA GCTCAGATGT CTCAATTAAG GATCGGTATG AATTAGATGA AAAGACGCCT
GCTTGGAAGT TAGATAAGAA GAAAGAACCG ACCAAGATTA AATGGTATAT TAACTCAGAT
TGGACGGCGC TGCCTTTTGG AAAAGACGTG ACCACTGCGC AGATTAAAAA AGACTTAAAT
GTGATATTG AATTTATTTT CGGCGATGAT TCAAAATTAA ATGCCATGAT TTCAAGTGGA
GATATGCCTG ATATCGTGAC ATTAAC TGAA AAAACTGGAC AAGCAGCATT GAAAGCAGAT
TCTTGGGCCT ATTCTTTTAA CGATTTAGCT AAAAAATATG ACCCTATTTT AATGAAAGTT
GTTAACCAAG ATACGTTTAA ATGGTATGCC TTAGAGGATG GAAAAACATA TGGTTACCCCT
AATTACTCTA ATACAAAAGC GGATTATGAA AGTGGAATA TCCCAGTAAA TGATAATTTT
GTTATTCGTG AAGATGTCTA TAATGCATTA GGCAAGCCAG ACGTTTCAAC ACCAGAAAAAT
TTTGAAAAAG TCATGCAACA GATTAAAGAA AAATATCCTG AGATGACCCC AATGGGCTTC
ACCACAGTGG GCGATGGTGC AGGACCATT TTAGACAAAT TACAAGACTT CTAGGTGTT
CCTTTAGAGG ATAAAAATGG TAAATACTAT GATCGAAATT TAGATAAAGA ATATTTAGAA
TGGTTAAAAA CATTTAATGA TGTTTACCGA GCAGGCAATA TTAGTGATGA TAGCTTCACA
GATGATGGGG CAACGTTTGA TGAAAAAGTG AAACAAGGAA ATTAGTCAAC CATGCTCGTT
GCTGGAACCA GTGGTCAAGG TGGGAACCTC ACAGAATTTA TGAAAAATC TGGCACACGT
TATATAGCCA TTGATGGACC AAGTAGCACT TCTGGCCGAA AACCAACATT AAATCAAACC
GGCATTTTCA GTTGGTTAAG TAATTACATT ACGAAAGATG CGAAAGATCC AGCAAAAGTC
ACTCAACTGT TCACATATTT AATTGATGAA CCGGGACAAA TTTTAACAAA ATATGGCGTT
GAAGGAGTTA CTTATGCGTA CAATGATCAA GGAAAAATTG ATTATTTACC AGAAGTGAAA
AAATTAGAAC AAACAGACAA TGATGCCTAC AACAAAAAAT ATGGCATTAG TCGTTTCCTA
TACTTTAACA ACGACCGTGT CAATAAACTA AAAAGTACCA TGGAAAGTGC TTTAACGCAA
ATGCAAGAAT GGGGCAAAGG AAAATTAGTC CCACATTTTC TAATTGAAAA TATTAATCCA
GATGCAGGAA CGCCGGAAGC TCGTGCGAAT GAAGCGATTG AAACCAAAC AAATACAACC
GTTATTTCAA TGATTCGTGC GAAAGATGAT AAAGCCTTTG ACAAATCTTT AGAAGACTAC
AAAGCATTCT TAAATCAAA TAAATGGGAT GCAATTGAAA AAATAAAATC TGAGAAAAATG
GCGGAAAAACA GAGACAAACT TAAGTAA

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EF018-2 (SEQ ID NO:66)

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MKKV LGLLLVATAV VSLAACSGGE
KKASSDVS IK DRYELDEKTP AWKLDKKKEP TKIKWYINSD WTALPFGKDV TTAQIKKDLN
VDIEFISGDD SKLNAMISSG DMPDIVTLTE KTGQAALKAD SWAYSLNDLA KKYDPYLMKV
VNQDTFKWYA LEDGKTYGYP NYSNTKADYE SGNIPVNDNF VIREDVYNAL GKPVDSTPEN
FEKVMQQIKE KYPEMTPMGF TTVGDGAGPF LDKLQDFLGV PLEDKNGKYY DRNLDDKEYLE
WLKTFNDVYR AGNISDDSF TDDGATFDEKV KQGNATMLV AGTSGQGGNF TEFMKKSGTR
YIAIDGPSST SGRKPTLNQT GISGWSNYI TKDAKDPKV TQLFTYLIDE PGQILTKYGV
EGVTYAYNDQ GKIDYLPEVK KLEQTDNDAY NKYGISRFL YFNNDRVNKL KVPMEASLTQ
MQEWGKGKLV PHFVIENINP DAGTPEARAN EAIETKLNTT VISMIRAKDD KAFDKSLEDY
KAFLKSNKWD AIEKIKSEK AENRDCLK

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EF018-3 (SEQ ID NO:67)

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CTGTAG CGGTGGGGAA
AAGAAAGCTA GCTCAGATGT CTCAATTAAG GATCGGTATG AATTAGATGA AAAGACGCCT
GCTTGGAAGT TAGATAAGAA GAAAGAACCG ACCAAGATTA AATGGTATAT TAACTCAGAT
TGGACGGCGC TGCCTTTTGG AAAAGACGTG ACCACTGCGC AGATTAAAAA AGACTTAAAT
GTGATATTG AATTTATTTT CGGCGATGAT TCAAAATTAA ATGCCATGAT TTCAAGTGGA
GATATGCCTG ATATCGTGAC ATTAAC TGAA AAAACTGGAC AAGCAGCATT GAAAGCAGAT
TCTTGGGCCT ATTCTTTTAA CGATTTAGCT AAAAAATATG ACCCTATTTT AATGAAAGTT
GTTAACCAAG ATACGTTTAA ATGGTATGCC TTAGAGGATG GAAAAACATA TGGTTACCCCT
AATTACTCTA ATACAAAAGC GGATTATGAA AGTGGAATA TCCCAGTAAA TGATAATTTT
GTTATTCGTG AAGATGTCTA TAATGCATTA GGCAAGCCAG ACGTTTCAAC ACCAGAAAAAT
TTTGAAAAAG TCATGCAACA GATTAAAGAA AAATATCCTG AGATGACCCC AATGGGCTTC

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ACCACAGTGG GCGATGGTGC AGGACCATTT TTAGACAAAT TACAAGACTT CTTAGGTGTT
CCTTTAGAGG ATAAAAATGG TAAATACTAT GATCGAAATT TAGATAAAGA ATATTTAGAA
TGGTTAAAAA CATTTAATGA TGTTTACCGA GCAGGCAATA TTAGTGATGA TAGCTTCACA
GATGATGGGG CAACGTTTGA TGAAAAAGTG AAACAAGGAA ATTATGCAAC CATGCTCGTT
GCTGGAACCA GTGGTCAAGG TGGGAAC TTCACAAATTTA TGAAAAAATC TGGCACACGT
TATATAGCCA TTGATGGACC AAGTAGCACT TCTGGCCGAA AACCAACATT AAATCAAACC
GGCATTTCAG GTTGGTTAAG TAATTACATT ACGAAAGATG CGAAAGATCC AGCAAAAGTC
ACTCAACTGT TCACATATTT AATTGATGAA CCGGGACAAA TTTTAACAAA ATATGGCGTT
GAAGGAGTTA CTTATGCGTA CAATGATCAA GGAAAAATTG ATTATTTACC AGAAGTGAAA
AAATTAGAAC AAACAGACAA TGATGCCTAC AACAAAAAAT ATGGCATTAG TCGTTTCCTA
TACTTTAACA ACGACCGTGT CAATAAACTA AAAGTACCAA TGGAAAGTGC TTTAACGCAA
ATGCAAGAAT GGGGCAAAGG AAAATTAGTC CCACATTTTCG TAATTGAAAA TATTAATCCA
GATGCAGGAA CGCCGGAAGC TCGTGCGAAT GAAGCGATTG AAACCAAAC AAATACAACC
GTTATTTCAA TGATTTCGTGC GAAAGATGAT AAAGCCTTTG ACAAATCTTT AGAAGACTAC
AAAGCATTCT TAAAATCAAA TAAATGGGAT GCAATTGAAA AAATAAAATC TGAGAAAAATG
GCGGAAAACA GAGACAAACT TAAG

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EF018-4 (SEQ ID NO:68)

CSGGE

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KKASSDVSIK DRYELDEKTP AWKLDKKKEP TKIKWYINSD WTALPFGKDV TTAQIKKDLN
VDIEFISGDD SKLNAMEISSG DMPDIVTLTE KTGQAALKAD SWAYSLNDLA KKYDPYLMKV
VNQDTFKWYA LEDGKTYGYP NYSNTKADYE SGNIPVNDNF VIREDVYNAL GKPVDSTPEN
FEKVMQQIKE KYPEMTPMGF TTVGDGAGPF LDKLQDFLGV PLEDKNGKYY DRNLDKEYLE
WLKTFNDVYR AGNISDDSFY DDGATFDEKV KQGNATMLV AGTSGQGNF TEFMKKSGTR
YIAIDGPSST SGRKPTLNQT GISGWSNYI TKDAKDPKV TQLFTYLIDE PGQILTKYGV
EGVTYAYNDQ GKIDYLPVK KLEQTDNDAY NKKYGISRFL YFNNDRVNKL KVPMESALTQ
MQEWGKGKLV PHFVIENINP DAGTPEARAN EAIETKLNTT VISMIRAKDD KAFDKSLEDY
KAFLKSNKWD AIEKIKSEKM AENRDKLK

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EF019-1 (SEQ ID NO:69)

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TAAAGGAGTT ACACAATGAA ACTTTTAAAA AAGACGGTCC TAATTGGTAC AACCCCTTCTT
CTTGGTTCAT TCTTACTCGC AGCTTGTTGGT AATACGAATA AAGAAGCCAA CAACGCTGAC
AAAACACATG AAGTAACAGA TACCTTAGGC AATAAAGTAA CCGTCCCCGC GAAACCCAAA
CGGATTATTG CGAGTTATTT AGAAGATTAT CTAGTTGCAT TAGGAGAAAA ACCAGTGGCA
CAATGGACAG TTGGACAAGG CAGCATTCAA GATTATTTAG CGAAAGAATT GAAAGATGTC
CCCCTATTTT CCTATGACTT GCCATATGAA GCGGTTCTAA AATTTGAACC TGACTTATTA
TTAATCAGTT CATCTGCTCT AGTTGAAGGC GGTAAATACA AAGAATACAG TAAAATTGCG
CCAACCTTATG TAGTCAAAAA CGGCGAAAAAT GTCACCTGGC GTGATCAATT GGAAGATATT
GCCACTGTTT TAGATAAAAA AGAACAAGCG AAAAAAGTGT TAGAAGATTA TGATACCTTA
ACCAAAGGCG TCCAAGAATA TCTTGGCAAA AAAGATGCTG GCAAATCTGC GGCAGTCTTA
TGGGTAACCA ACAACCAAGT CTTTATGGTT AGCGATAATC GCTCAAGCGG AACCGTGCTC
TATCAGGACT TAGGCCTCCA AGTTCCAAAA TTAGTGGAAG AAATTTCTAA AAACGCTACT
GCGGATTGGA ATCAAGTTTC TTTAGAAAAA TTAGCTGAGC TTGACGCAGA CCACATTTTC
CTTGTAACA GCGATGAATC AGCACCTCTT TTCCAAGAAG CAATTTGGAA GAACTTACCT
GCTGTGAAAA ATAACCAAGT TCATACCTAT GATAAAAAAA GTAGTTGGTT ATACAACGGA
CCTATTGCGA ATACTCAAAT TGTTGAAGAT GTAAAAAAG CGCTCTTAAA TTAA

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EF019-2 ((SEQ ID NO:70)

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MKLLKK TVLIGTTLLL GSFLAACGN TNKEANNADK THEVDTLGN KVTVPKPKR
IIASYLEDYL VALGEKPVAQ WTVGQGSIQD YLAKELKDVP TISYDLPYEA VLKFEPDL

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ISSSALVEGG KYKEYSKIAP TYVVKNGENV TWRDQLEDIA TVLDKKEQAK KVLEDYDTLT
 KGVQEYLGKK DAGKSAAVLW VTNNQVFMVS DNRSSGTVLY QDLGLQVPKL VEEISKNATA
 DWNQVSLEKL AELDADHIFL VNSDESAPLF QEAIWKNLPA VKNNQVHTYD KKSSWLYNGP
 IANTQIVEDV KKALLN

EF019-3 (SEQ ID NO:71)

TTGTGGT AATACGAATA AAGAAGCCAA CAACGCTGAC
 AAAACACATG AAGTAACAGA TACCTTAGGC AATAAAGTAA CCGTCCCCGC GAAACCCAAA
 CGGATTATTG CGAGTTATTT AGAAGATTAT CTAGTTGCAT TAGGAGAAAA ACCAGTGGCA
 CAATGGACAG TTGGACAAGG CAGCATTCAA GATTATTTAG CGAAAGAATT GAAAGATGTC
 CCCACTATTT CCTATGACTT GCCATATGAA GCGGTTCTAA AATTTGAACC TGACTTATTA
 TTAATCAGTT CATCTGCTCT AGTTGAAGGC GGTAAATACA AAGAATACAG TAAAATTGCG
 CCAACTTATG TAGTCAAAAA CGGCGAAAAT GTCACCTGGC GTGATCAATT GGAAGATATT
 GCCACTGTTT TAGATAAAAA AGAACAAGCG AAAAAAGTGT TAGAAGATTA TGATACCTTA
 ACCAAAGGCG TCCAAGAATA TCTTGGCAA AAAGATGCTG GCAAATCTGC GGCAGTCTTA
 TGGGTAACCA ACAACCAAGT CTTTATGGTT AGCGATAATC GCTCAAGCGG AACCGTGCTC
 TATCAGGACT TAGGCCTCCA AGTTCCAAAA TTAGTGGAAG AAATTTCTAA AAACGCTACT
 GCGGATTGGA ATCAAGTTTC TTTAGAAAAA TTAGCTGAGC TTGACGCAGA CCACATTTTC
 CTTGTAAACA GCGATGAATC AGCACCTCTT TTCCAAGAAG CAATTTGGAA GAACTTACCT
 GCTGTGAAAA ATAACCAAGT TCATACCTAT GATAAAAAA GTAGTTGGTT ATACAACGGA
 CCTATTGCGA ATACTCAAAT TGTGAAGAT GTAAAAAAG CGCTCTTAAA T

EF019-4 (SEQ ID NO:72)

CGN TNKEANNADK THEVDTLGN KVTVPKPKR
 IIASYLEDYL VALGEKPVAQ WTVGQGSIQD YLAKELKDVP TISYDLPYEA VLKFEPLDLL
 ISSSALVEGG KYKEYSKIAP TYVVKNGENV TWRDQLEDIA TVLDKKEQAK KVLEDYDTLT
 KGVQEYLGKK DAGKSAAVLW VTNNQVFMVS DNRSSGTVLY QDLGLQVPKL VEEISKNATA
 DWNQVSLEKL AELDADHIFL VNSDESAPLF QEAIWKNLPA VKNNQVHTYD KKSSWLYNGP
 IANTQIVEDV KKALLN

EF020-1 (SEQ ID NO:73)

TGAGGAGATG AGAAAAATGAA AAAGGTAGTT TCAATTTTGT TGATGGTTGT TGCAGTCTTC
 ACATTAACATG CATGTAATGG TTCTAAATTA GATAAAACAG GTGAAGAATT TAAAAATTCT
 ATAATGAAAG ATTCTTCATA TGGTGATGAA TATTCAGAAG ATGGTTTATG TTTTAAATA
 TATAAAGATA AAGACACTAA TCGTTATTTG GCTGATGTTT GGGTTCTGT TAAAGATGAA
 ACTAGCGCAT TGGAGTATTT TTATTATTAT GATGAAGATA AGCGATTAGA TAGTACTAAA
 AGTAAAGTAA CCTTTGATGA TATGAAAGCT AGTGGAACT ATGAAGTAGT GTATAAATCA
 GGGAAATTTA AATAA

EF020-2 (SEQ ID NO:74)

MKKVVS ILLMVAVFT LTACNGSKLD KTGEFFKNSI MKDSSYGDEY SEDGFSFLIY
 KDKDTNRYLA DVWVPVKDET SALEYFYIYD EDKRLDSTKS KVTFDMMKAS GNYEVVYKSG
 KFK

EF020-3 (SEQ ID NO:75)

ATGTAATGG TTCTAAATTA GATAAAACAG GTGAAGAATT TAAAAATTCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATAATGAAAG ATTCTTCATA TGGTGATGAA TATTCAGAAG ATGGTTTTAG TTTTTTAATA
 TATAAAGATA AAGACACTAA TCGTTATTG GCTGATGTTT GGGTTCCTGT TAAAGATGAA
 ACTAGCGCAT TGGAGTATTT TTATTATTAT GATGAAGATA AGCGATTAGA TAGTACTAAA
 AGTAAAGTAA CCTTTGATGA TATGAAAGCT AGTGGAAGCT ATGAAGTAGT GTATAAATCA
 GGGAAATTTA AA

EF020-4 (SEQ ID NO:76)

CNGSKLD KTGEFEKNSI MKDSSYGDEY SEDGFSFLIY
 KDKDNTRYLA DVWVPVKDET SALEFYFYD EDKRLDSTKS KVTFDMMKAS GNYEVVYKSG
 KFK

EF021-1 (SEQ ID NO:77)

TAGTTGTTTA AATACATTAA ACTATTTTTTA GGAGGCTTTA CAGAAATGAA AAAAGCAAAA
 TTATTCGGTT TTAGTTTGAT TGCATTAGGT TTATCAGTTT CACTTGCAGC ATGTGGTGGT
 GGCAAAGGCA AAACCGCTGA AAGCGGCGGT GGCAAAGGGG ATGCAGCGCA TAGTGCTGTA
 ATCATTACAG ATACAGGCGG CGTGGATGAC AAGTCGTTC ACCAATCTTC TTGGGAAGGA
 TTGCAAGCTT GGGGTAAAGA ACATGATTTA CCAGAAGGT CAAAAGGGTA TGCATATATT
 CAATCGAATG ATGCAGCTGA CTATACAACC AATATTGACC AAGCGGTATC AAGTAAATTC
 AACACAATCT TTGGTATTGG CTACTTGCTA AAAGATGCAA TTTCTTCTGC AGCAGATGCC
 AACCTTGATA CAAACTTTGT TTTAATCGAT GATCAAATCG ATGGCAAAA GAATGTCGTT
 TCTGCAACAT TTAGAGATAA TGAAGCAGCT TACTTAGCCG GTGTTGCTGC TGCAAATGAA
 AAAAAACGA ACAAAAGTCGG TTTTGTGGT GGTGAAGAAG GGTGCGTAAT TGACCGTTTC
 CAAGTGCTT TTGAAAAAGG TGTGGCTGAT GCTGCGAAAG AATTAGGTAA AGAAATTAAT
 GTTGATACGA AATATGCGC TTCATTTGCT GATCCTGCCA AAGGGAAAGC TTTAGCTGCT
 GCAATGTACC AAAACGCGT TGATATCATC TTCCATGCTT CTGGTGCGAC TGGACAAGGG
 GTCTTCCAAG AAGCAAAAGA CTTGAATGAA TCAGGTTCCTG GCGACAAAGT TTGGGTAATC
 GCGTGTGACC GCGATCAAGA TGCTGATGGC AAGTACAAAA CAAAAGACGG CAAAGAAGAC
 AACTTCACGT TAACTTCAAC GCTTAAAGGT GTCGGCACAG CGGTTCAAGA TATTGCCAAC
 CGTGCGTTAG AAGACAAATT CCCTGGTGGC GAACATTTAG TTTATGGATT AAAAGATGGT
 GCGTGTGACT TAACAGACGG CTATTTAAAC GACAAAACAA AAGAAGCTGT TAAACAGCA
 AAAGATAAAG TAATCTCAGG TGACGTAAAA GTCCCAGAAA AACCAGAATA A

EF021-2 (SEQ ID NO:78)

MKKAKL FGFSIALGL SVSLAACGGG KGKTAESGGG KGDAHSAVI
 ITDTGGVDDK SFNQSSWEGL QAWGKEHDL ESKGYAYIQ SNDAADYTTN IDQAVSSKFN
 TIFGIGYLLK DAISSAADAN PDTNFVLIDD QIDGKKNVVS ATFRDNEAAY LAGVAAANET
 KTNKVGTVGG EEGVVIDRFQ AGFEKGVADA AKELGKEITV DTKYAASFAD PAKGKALAAA
 MYQNGVDIIF HASGATGQGV FQEAKDLNES GSGDKVWVIG VDRDQDADGK YKTKDGKEDN
 FTLTSTLKV GTAVQDIANR ALEDKFPGE HLTVGLKDGG VDLTDGYLND KTKEAVKTAK
 DKVISGDVKV PEKPE

EF021-3 (SEQ ID NO:79)

ATGTGGTGGT
 GGCAAAGGCA AAACCGCTGA AAGCGGCGGT GGCAAAGGGG ATGCAGCGCA TAGTGCTGTA
 ATCATTACAG ATACAGGCGG CGTGGATGAC AAGTCGTTC ACCAATCTTC TTGGGAAGGA
 TTGCAAGCTT GGGGTAAAGA ACATGATTTA CCAGAAGGT CAAAAGGGTA TGCATATATT
 CAATCGAATG ATGCAGCTGA CTATACAACC AATATTGACC AAGCGGTATC AAGTAAATTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACACAATCT	TTGGTATTGG	CTACTTGCTA	AAAGATGCAA	TTTCTTCTGC	AGCAGATGCC
AACCCTGATA	CAAACCTTGT	TTTAATCGAT	GATCAAATCG	ATGGCAAAAA	GAATGTCGTT
TCTGCAACAT	TTAGAGATAA	TGAAGCAGCT	TACTTAGCCG	GTGTTGCTGC	TGCAAATGAA
ACAAAAACGA	ACAAAGTCGG	TTTTGTGTTG	GGTGAAGAAG	GGGTCGTAAT	TGACCGTTTC
CAAGCTGGTT	TTGAAAAAGG	TGTGGCTGAT	GCTGCGAAAG	AATTAGGTAA	AGAAATTACT
GTTGATACGA	AATATGCGGC	TTCATTTGCT	GATCCTGCCA	AAGGGAAAGC	TTTAGCTGCT
GCAATGTACC	AAAACGGCGT	TGATATCATC	TTCCATGCTT	CTGGTGCGAC	TGGACAAGGG
GTCTTCCAAG	AAGCAAAAGA	CTTGAATGAA	TCAGGTTCTG	GCGACAAAGT	TTGGGTAATC
GGCGTTGACC	GCGATCAAGA	TGCTGATGGC	AAGTACAAAA	CAAAGACCGG	CAAAGAAGAC
AACTTCACGT	TAACCTCAAC	GCTTAAAGGT	GTCGGCACAG	CGGTTCAAGA	TATTGCCAAC
CGTGCGTTAG	AAGACAAATT	CCCTGGTGGC	GAACATTTAG	TTTATGGATT	AAAAGATGGT
GGCGTTGACT	TAACAGACGG	CTATTTAAAC	GACAAAACAA	AAGAAGCTGT	TAAAACAGCA
AAAGATAAAG	TAATCTCAGG	TGACGTAAAA	GTCCAGAAAA	AACCAGAA	

EF021-4 (SEQ ID NO:80)

CGGG KGKTAESGGG KGDAHSAVI

ITDTGGVDDK	SFNQSSWEGL	QAWGKEHDL	EGSKGYAYIQ	SNDAADYTTN	IDQAVSSKFN
TIFGIGYLLK	DAISSAADAN	PDTNFVLIDD	QIDGKKNVVS	ATFRDNEAAY	LAGVAAANET
KTNVKGFVGG	EEGVVIDRFQ	AGFEKGVADA	AKELGKEITV	DTKYAASFAD	PAK GKALAAA
MYQNGVDIIF	HASGATGQGV	FQEAKDLNES	GS GDKVWVIG	VDRDQDADGK	YKTKDGKEDN
FTLTSTLKG	GTAVQDIANR	ALEDKFPGGE	HLVYGLKDGG	VDLTDGYLND	KTKEAVKTAK
DKVISGDVKV	PEKPE				

EFO22-1 (SEQ ID NO:81)

TAAGAGCATA	AAAAAATGAA	GAGTTATAGG	AGAAAGAAGA	TGAAAAAGTA	TTTAAAAATC
ACAATGGTTT	GTATTTTATT	GGTAGGATTT	TTAGCTGGGT	GTACCAATAA	AAATGAAAAAT
AAAAAGAAAC	AGAAAAATAC	CAAAGAAGCC	GTCAACTGA	TGTCACCCTC	GGAATTAACA
ACGCTCAACA	CCTCTGTATT	ATTGGATTTT	CCAGATGCTA	TTGTCCAAAC	TGCAGCGTTT
GAAGGGTTAT	ATAGTTTAGA	TGAACAAGAC	CAATTGGTAC	CAGCCGTAGC	AAAAGCATTG
CCGATGATTT	CAGAAGATGG	AAAAACCTAC	ACGATTTCTT	TGAGAAAAGA	AGCGGTTTGG
AGTAACGATG	ATCCTGTCAC	AGCACATGAT	TTTGAATATG	CTTGAAAAAA	AATGATTGAT
CCTAAAAACG	GCTTTGTTTA	TAGCTTCCTC	ATCGTTGAAA	CAATTCAAAA	TGGTGCAGAA
ATCTCAGCGG	GGAAATTAGC	ACCCAATGAA	CTAGGTGTCA	CAGCTGTGGA	TGATTATACA
TTAAAGGTGA	CGCTCAAAGA	GCCAAAACCG	TACTTTACGT	CCTTGTTAGC	TTTTCCGACA
TTTTTCCCGC	AAAATCNAAA	AGTAGTCGAA	CAATTGGTG	CGGACTATGG	AACTGC TAGT
GATAAAGTCG	TCTATAATGG	TCCGTTCTGT	GTAAAAGATT	GGCAGCAAAC	AAAGATGGAC
TGGCAACTAG	CAAAAAATAA	TCGCTATTGG	GATCACCAGA	ACGTGCGCTC	AGACATTATC
AATTATACAG	TTATCAAAGA	AACATCTACC	GCATTGAATC	TTTTTTGAAGA	TGGACAATTA
GATGTGGCTA	CACTAAGTGG	TGAAGTGGCG	CAACAGAATA	AAAATAATAC	GTTGTATCAT
TCGTATCCAA	CAGCGACAAT	GAAGTATTTG	CGCTTAAATC	AAAAACGGNA	AGGGCAAGCN
ACGCCGCTTG	CAAACGAAAA	CCTGCGTAAA	GCATTGGCTT	TAGGAATAGA	TAAAGAAAAAT
CTAGTCAATA	ATATTATTGC	AGATGGTTCT	AAAGCGCTAC	ATGGTGCGAT	TACGGAAGGC
TTTGTGGCGA	ATCCCACAAC	GGGTCTCGAT	TTTCGTCAAG	AAGCAGGTAA	TTTAATGGTT
TATAACAAAG	AAAAAGCGCA	AAGTTATTGG	AAAAAGCAC	AAGCAGAATT	AGGAGAAAAG
GTTAACGTTG	AATTGATGGT	AACAGATGAT	GGTCTTACA	AAAAAATTGG	TGAAAGTTTG
CAAGGCTCGC	TACAAGAATT	GTTTCTCTGGT	TTGACAATAG	AGCTAACCGC	ATTGCCGACT
GAAGCTGCAT	TGAAGTTTGG	GCGAGAAAGT	GACTATGATT	TATTCTTAAT	TTACTGGACA
CCAGACTATC	AAGACCCAT	TTCTACCCTG	ATGACTTTAT	ACAAGGGCAA	TGATCGCAAT
TATCAGAAC	CTGTCTATGA	CAAATTATTA	GATGAAGCAG	CCACAACCTA	TGCCTTAGAG
CCAGAAAAAA	GATGGGCGAC	ACTGATTGCA	GCTGAAAAAG	AAGTGATTGA	AACGACTGCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GGCATGATTC CACTTAGCCA AAATGAACAA ACAGTCCTGC AAAATGATAA AGTCAAAGGC
TTGAATTTTC ATACCTTTGG CGCTCCATTA ACGTTAAAAA ATGTTTATAA GGAAAAATAA

EF022-2 (SEQ ID NO:82)

MKKYLKIT MVCILLVGFL AGCTNKNENK KKQKNTKEAV QLMSPSELTT
LNTSVLLDFP DAIVQTAAFE GLYSLDEQDQ LVPAAKALP MISEDGKTYT ISLRKEAVWS
NDDPVTAHDF EYAWKKMIDP KNGFVYSFLI VETIQNGAEI SAGKLAPNEL GVTAVDDYTL
KVTLKEPKPY FTSLLAFPTF FPQNXKVVEQ FGADYGTASD KVVYNGPFVW KDWQQTMDW
QLAKNNRYWD HQNVRSIIN YTVIKETSTA LNLFDGQLD VATLSGELAQ QNKNNTLYHS
YPTATMNYLR LNQKRXGQAT PLANENLRKA LALGIDKENL VNNIADGSK ALHGAITEGF
VANPTTGLDF RQEAGNLMVY NKEKAQSYWK KAQAELGEKV NVELMVTDDG SYKKIGESLQ
GSLQELFPGL TIELTALPTE AALNFGRESY YDLFLIYWTP DYQDPISLTM TLYKGNDNRNY
QNPVYDKLLD EAATTYALEP EKRWATLIAA EKEVIETTAG MIPLSQNEQT VLQNDKVKGL
NFHTFGAPLT LKNVYKEK

EF022-3 (SEQ ID NO:83)

GT GTACCAATAA AAATGAAAAT
AAAAAGAAAC AGAAAAATAC CAAAGAAGCC GTTCAACTGA TGTCACCCCTC GGAATTAACA
ACGCTCAACA CCTCTGTATT ATTGGATTTT CCAGATGCTA TTGTCCAAAC TGCAGCGTTT
GAAGGGTTAT ATAGTTTAGA TGAACAAGAC CAATTGGTAC CAGCCGTAGC AAAAGCATTG
CCGATGATTT CAGAAGATGG AAAAACCTAC ACGATTTCTT TGAGAAAAAG AGCGGTTTGG
AGTAACGATG ATCCTGTCAC AGCACATGAT TTTGAATATG CTTGAAAAAA AATGATTGAT
CCTAAAAACG GCTTTGTTTA TAGCTTCCTC ATCGTTGAAA CAATTCAAAA TGGTGCAGAA
ATCTCAGCGG GGAAATTAGC ACCCAATGAA CTAGGTGTCA CAGCTGTGGA TGATTATACA
TTAAAGGTGA CGCTCAAAGA GCCAAAACCG TACTTTACGT CCTGTGTTAGC TTTTCCGACA
TTTTTCCCGC AAAATCNAAG AGTAGTCGAA CAATTGGGTG CGGACTATGG AACTGCTAGT
GATAAAGTCG TCTATAATGG TCCGTTCTGT GTAAAAGATT GGCAGCAAAC AAAGATGGAC
TGGCAACTAG CAAAAAATAA TCGCTATTGG GATCACCAGA ACGTGCCTC AGACATTATC
AATTATACAG TTATCAAAGA AACATCTACC GCATTGAATC TTTTGAAGA TGGACAATTA
GATGTGGCTA CACTAAGTGG TGAAGTGGCG CAACAGAATA AAAATAATAC GTTGATCAT
TCGTATCCAA CAGCGACAAT GAATATTTG CGCTTAAATC AAAAACGGNA AGGGCAAGCN
ACGCCGCTTG CAAACGAAAA CCTGCGTAAA GCATTGGCTT TAGGAATAGA TAAAGAAAAT
CTAGTCAATA ATATTATTGC AGATGGTTCT AAAGCGCTAC ATGGTGCAT TACGGAAGGC
TTTGTGGCGA ATCCACAAC GGGTCTCGAT TTTCTGCAAG AAGCAGGTAA TTTAATGGTT
TATAACAAAG AAAAAGCGCA AAGTTATTGG AAAAAAGCAC AAGCAGAATT AGGAGAAAAG
GTAAACGTTG AATTGATGGT AACAGATGAT GGTCTTTACA AAAAAATTGG TGAAAGTTTG
CAAGGCTCGC TACAAGAATT GTTTCCTGGT TTGACAATAG AGCTAACCGC ATTGCCGACT
GAAGCTGCAT TGAACTTTGG GCGAGAAAGT GACTATGATT TATTCTTAAT TTACTGGACA
CCAGACTATC AAGACCCTAT TTCTACCCTG ATGACTTTAT ACAAGGGCAA TGATCGCAAT
TATCAGAACC CTGTCTATGA CAAATTATTA GATGAAGCAG CCACAACCTA TGCCTTAGAG
CCAGAAAAAA GATGGGCGAC ACTGATTGCA GCTGAAAAAG AAGTGATTGA AACGACTGCT
GGCATGATTC CACTTAGCCA AAATGAACAA ACAGTCCTGC AAAATGATAA AGTCAAAGGC
TTGAATTTTC ATACCTTTGG CGCTCCATTA ACGTTAAAAA ATGTTTATAA GGAAAA

EF022-4 (SEQ ID NO:84)

CTNKNENK KKQKNTKEAV QLMSPSELTT
LNTSVLLDFP DAIVQTAAFE GLYSLDEQDQ LVPAAKALP MISEDGKTYT ISLRKEAVWS
NDDPVTAHDF EYAWKKMIDP KNGFVYSFLI VETIQNGAEI SAGKLAPNEL GVTAVDDYTL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KVTLKEPKPY FTSLLAFPTF FPQNXKVVEQ FGADYGTASD KVVYNGPFV V KDWQQT KMDW
 QLAKNNRYWD HQNVRSDIIN YTVIKETSTA LNLFDGQLD VATLSGELAQ QNKNNNTLYHS
 YPTATMNYLR LNQKRXGQAT PLANENLRKA LALGIDKENL VNNIIADGSK ALHGAITEGF
 VANPTTGLDF RQEAGNLMVY NKEKAQSYWK KAQAELGEKV NVELMVTDDG SYKKIGESLQ
 GSLQELFPGL TIELTALPTE AALNFGRES D YDLFLIYWTP DYQDPISTLM TLYKGNDRNY
 QNPVYDKLLD EAATTYALEP EKRWATLIAA EKEVIETTAG MIPLSQNEQT VLQNDKVKGL
 NFHTFGAPLT LKNVYKEK

EF023-1 (SEQ ID NO:85)

TAAAATGGAG GGATCGGTAT GAAGAAATTA AAAATGTTAG GATGCGTCGG GTTGCTTTTA
 GCTTTAACGG CTGTTCAGGC GGAACGGGA AACTCGGCTG ATAGTAACAA AGCAGCGGAA
 CAAAAAATTG CAATTAGTTC TGAAGCGGCT ATTTTCGACAA TGAACACACA CACAGCGGGG
 GATACGACCT CGACTTTAGT CATGAATCAA GTTTATGAAG GACTCTATGT TTTAGGTAAA
 GAAGATGAAT TAGAGTTGGG GGTGCTGCTC GAAGAACCAG CGATTTCTGA AGATGAAACC
 GTTTATACAT TTAAGATTAG AGAAGATGCC AAATGGTCGA ATGATGATCC AGTAACAGCA
 AACGACTTTG TTTATGCATG GCAACAAGTT GCTTCCCCTA AATCAGGATC GATTTCATCA
 GCTTTATTTT TTGATGTCAT TAAAAATGCT AAGGAAATTG CTTTAGAAGG CGCAGATGTG
 AATACTCTTG GGGTTAAGGC GCTAGATGAT AAAACGTTAG AAATAACTTT AGAACGGCCC
 ACCCCTTATT TGAATCATT ACTTTCGTTT CCTGTTTTGT TTCCACAAA TGAAAAATAT
 ATCAAAGAAC AAGGGGATAA ATATGCTACT GATGCAGAAC ATTTGATTTA TAATGGTCCT
 TTTAAATTGA AAGAAATGGGA TAATGCCTCT TCTGATGACT GGACCTACGA AAAAAATGAT
 ACGTATTGGG ATGCTGAAAA AGTTAAATTA ACAGAAGCGA AAGTTTCAGT AATTAAGAGC
 CCAACGACAG CGGTGAATTT GTTTGACTCG AATGAATTGG ATGTAGTGAA TAAGCTAAGT
 GGTGAATTTA TTCTGGTTA TGTGATAAAT CCAGCCTTTC TTTCAATTCC TCAATTTCGTC
 ACATACTTTT TAAAAATGAA CAGCGTTCGT GATGGAAAAG AAAATCCGGC TTTAGCGAAC
 AACAAATATC GTAAAGCGTT GGCACAAGCT TTTGATAAAG AAAGTTTGT AAAAGAAGTC
 TTGCAAGATC AATCAACGGC TACAGATCAA GTAATCCGC CGGGACAAAC GATTGCGCCA
 GATGGAACAG ATTTACACAA ACTAGCTGCT AAGAAAAATA ACTACTTAAC CTACGATACA
 GCGAAAGCAA AAGAATTCTG GGAAAAAGGG AAAAAAGAAA TTGGGCTGGA TAAAAACAAA
 TTAGAATTTT TAACAGATGA TACAGACAGC GCCAAAAAAG CTGCTGAGTT TTTCCAATTT
 CAATTGGAAG AAAATCTAGA TGGATTAGAA GTGAATGTTA CTCAAGTCC TTTTACTATT
 CGTGTGATC GTGATCAAAC GAGAGACTAT GATTTAGAAT TATCTGGTTG GGAACCGAT
 TATCGTGATC CATTAACAGT TATGCGCATC TTTACTTCGG ATAGTACCTT GGGCGGCGTA
 ACGTTCAAGA GTGATACGTA TGATCAATTA ATTCAAGAAA CTAGAACAAC ACATGCGGCT
 GATCAAGAGG CTCGTTTAAA TGACTTTGCT CAAGCACAAAG ATATTTTGGT GAATCAGGAA
 ACGGTTTTAG CACCAATCTA CAATCGAAGC ATTTCTGTAT TAGCTAATCA AAAAAATCAAG
 GATCTGTATT GGCATTCATT TGGACCCACG TACAGTTTAA AATGGGCTTA TGTTAACTAA

EF023-2 (SEQ ID NO:86)

MKKLK MLGCVLLLLA LTACQAGTGN SADS NKAAEQ KIAISSEAAI STMEPHTAGD
 TTSTLVMNQV YEGLYVLGKE DELELGVAEE EPAISEDETV YTFKIREDAK WSNDDPVTAN
 DFVYAWQQVA SPKSGSIHQALFFDVIKNAK EIALEGADVN TLGVKALDDK TLEITLERPT
 PYLKSLLSFP VLFPPQNEKYI KEQGDKYATD AEHLIYNGPF KLKEWDNASS DDWTYEKNNDT
 YWDAEKVKLT EAKVSVIKSP TTAVNLFDSN ELDVVKLSG EFIPGYVDNP AFLSIPQFVT
 YFLKMNSVRD KENPALANN NIRKALAQAF DKESFVKEVL QDQSTATDQV IPPQTIAPD
 GTDFTKLA AKNNYLT YDTA KAKEFWKEGK KEIGLDKIKL EFLTDDTDSA KKAEEFFQFQ
 LEENLDGLEV NVTQVPFTIR VDRDQTRDYD LELSGWGT DY RDPLTVMRIF TSDSTLGGVT
 FKSDTYDQLI QETRTHAAD QEARLNDFAQ AQDILVNQET VLAPIYNRSI SVLANQKIKD
 LYWHSFGPTY SLKWAYVN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF023-3 (SEQ ID NO:87)

GGGAACGGGA AACTCGGCTG ATAGTAACAA AGCAGCGGAA
CAAAAAATTG CAATTAGTTC TGAAGCGGCT ATTTTCGACAA TGGAAACCACA CACAGCGGGG
GATACGACCT CGACTTTAGT CATGAATCAA GTTTATGAAG GACTCTATGT TTTAGGTAAA
GAAGATGAAT TAGAGTTGGG GGTCGCTGCC GAAGAACCAG CGATTTCTGA AGATGAAACC
GTTTATACAT TTAAGATTAG AGAAGATGCC AAATGGTCGA ATGATGATCC AGTAACAGCA
AACGACTTTG TTTATGCATG GCAACAAGTT GCTTCCCCTA AATCAGGATC GATTCATCAA
GCTTTATTTT TTGATGTCAT TAAAAATGCT AAGGAAATTG CTTTAGAAGG CGCAGATGTG
AATACTCTTG GGGTTAAGGC GCTAGATGAT AAAACGTTAG AAATAACTTT AGAACGGCCC
ACCCCTTATT TGAAATCATT ACTTTCGTTT CCTGTTTTGT TTCCACAAAA TGAAAAATAT
ATCAAAGAAC AAGGGGATAA ATATGCTACT GATGCAGAAC ATTTGATTTA TAATGGTCCT
TTTAAATTGA AAGAATGGGA TAATGCCTCT TCTGATGACT GGACCTACGA AAAAAATGAT
ACGTATTGGG ATGCTGAAAA AGTTAAATTA ACAGAAGCGA AAGTTTCAGT AATTAAGAGC
CCAACGACAG CCGTGAATTT GTTTGACTCG AATGAATTGG ATGTAGTGAA TAAGCTAAGT
GGTGAATTTA TTCCTGGTTA TGTTGATAAT CCAGCCTTTC TTTCAATTCC TCAATTCGTC
ACATACTTTT TAAAAATGAA CAGCGTTCGT GATGGAAAAG AAAATCCGGC TTTAGCGAAC
AACAAATATC GTAAAGCGTT GGCACAAGCT TTTGATAAAG AAAGTTTGT AAAAGAAGTC
TTGCAAGATC AATCAACGGC TACAGATCAA GTAATTCCGC CGGGACAAAC GATTGCGCCA
GATGGAACAG ATTTTCACAAA ACTAGCTGCT AAGAAAAATA ACTACTTAAC CTACGATACA
GCGAAAGCAA AAGAATTCTG GGAAAAAGGG AAAAAAGAAA TTGGGCTGGA TAAAAATCAA
TTAGAATTTT TAACAGATGA TACAGACAGC GCCAAAAAG CTGCTGAGTT TTTCCAATTT
CAATTGGAAG AAAATCTAGA TGGATTAGAA GTGAATGTTA CTCAAGTTCC TTTTACTATT
CGTGTGATC GTGATCAAAC GAGAGACTAT GATTTAGAAT TATCTGGTTG GGGAACCGAT
TATCGTGATC CATTAAACAGT TATGCGCAT TTTACTTCGG ATAGTACCTT GGGCGCGCTA
ACGTTCAAGA GTGATACGTA TGATCAATTA ATTCAAGAAA CTAGAACAAC ACATGCGGCT
GATCAAGAGG CTCGTTTAAA TGACTTTGCT CAAGCACAAG ATATTTTGGT GAATCAGGAA
ACGTTTTAG ACCCAATCTA CAATCGAAGC ATTTCTGTAT TAGCTAATCA AAAAAATCAAG
GATCTGTATT GGCATTCATT TGGACCCACG TACAGTTTAA AATGGGCTTA TGTTAAC

EF023-4 (SEQ ID NO:88)

GTGN SADSINKAAEQ KIAISSEAAI STMEPHTAGD
TTSTLVMNQV YEGLYVLGKE DELELGVAEE EPAISEDETV YTFKIREDAK WSNDPVTAN
DFVYAWQQVA SPKSGSIHQALFFDVIKNAK EIALEGADVNLGLVKALDDK TLEITLERPT
PYLKSLLSFP VLFPQNEKYI KEQGDKYATD AEHLIYNGPF KLKEWDNASS DDWTYEKNDT
YWDAEKVKLT EAKVSVIKSP TTAVNLFDSN ELDVVNKLSE EFIPGYVDNP AFLSIPQFVT
YFLKMNSVRD KENPALANN NIRKALAQAF DKESFVKEVL QDQSTATDQV IPPGQTIAPD
GTDFTKLAAK KNNYLTYDTA KAKEFWEK GKKEIGLDKIKL EFLTDDTDSA KKAEEFFQFQ
LEENLDGLEV NVTQVPFTIR VDRDQTRDYD LELSGWGTDY RDPLTVMRIF TSDSTLGGVT
FKSDTYDQLI QETRTTHAAD QEARLNDFAQ AQDILVNQET VLAPIYNRSI SVLANQKIKD
LYWHSFGPTY SLKWAYVN

EF024-1 (SEQ ID NO:89)

TAATGGCCGT TTCGTCTACT AATAAAGAGG ATGAAGCTAC TCAAATGGCG TTGGCAATGG
AACAAGGATC ATAAAAAAGG AGAAGTGAGC ATGAAAAAAG TACTACCTTT TATTGCCTTA
GTCGGCTTGT TATTGTTGTC AGGTTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
GGTGGTAAAT GGAAAGTGGA AGAAACACGT GCAACTTACA CTTTTTTTGA TGACGGTAAA
TTTTTCAGCTA ATGACTCAGA GGATAGTGTT AGTGGGACAT ACACTTATGA TGAAAAAAT
AAAAAATAA CCTTTGACNT TACTAGCAGN AACTCTTTCA TTATGGAAAA AGTNGANTNC
AANGNTANCA AGATTACAGG GGAAATTGGC GAAAAACAAA GAACACTTAT AAAACAAAAA
ACAGAATAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF024-2 (SEQ ID NO:90)

M KKVLPFIALV GLLLLSGCGT DMKKILTADG
 GKWKVEETRA TYTFFDDGKF SANDSEDSVS GTYTYDEKNK KITFDXTSXN SFIMEKVXXX
 XXKITGEIGE KQRTLIKQKT E

EF024-3 (SEQ ID NO:91)

ATT GACTGCCGAT
 GGTGGTAAAT GGAAAGTGGG AGAAACACGT GCAACTTACA CTTTTTTTGA TGACGGTAAA
 TTTTCAGCTA ATGACTCAGA GGATAGTGT AGTGGGACAT ACACCTTATGA TGAAAAAAAT
 AAAAAAATAA CCTTTGACNT TACTAGCAGN AACTCTTTCA TTATGGAAAA AGTNGANTNC
 AANGNTANCA AGATTACAGG GGAAATTGGC GAAAAACAAA GAACACTTAT AAAACAAAAA
 ACAGAA

EF024-4 (SEQ ID NO:92)

LTADG
 GKWKVEETRA TYTFFDDGKF SANDSEDSVS GTYTYDEKNK KITFDXTSXN SFIMEKVXXX
 XXKITGEIGE KQRTLIKQKT E

EF025-1 (SEQ ID NO:93)

TGAATGAAAC ATATTAAAGG AATGTTGGTT TTTATCGGAT TATTTATTTT GGTGGTTGT
 GCGCCAGATC AAGAGCCAAC GAAACAAACA ACAAGTGGTC CGCAAGAGAC AAAGCAAAGTG
 AAGCAAAGTTA CCGTCACCAA TCAAACGACT TCTGCGGTGG AAAACAAGC GCCGACTAAA
 AATGACGAAC TGATTGCTAA TCAATTGACT TTTGATTCTC ATGAATACAC GTACGAAGTG
 GTTACAGGGG CCACACAAAC GACATTTGGA ACAACCCAC CAGCAAAATA TACACCGGAA
 GAAAAAAGA AAAAAATGTT TTGGTCCAAT CAACCGCCTT TGGGATTAAT GACGGGTAAC
 TATTATAAAA ATGAAGGTGT ATTTACTGGC GGAAATTACG GCATTGTAGA GATTATTACG
 GAACCTGAAA CGCAAAGGAT TCTGAATGTT GAGTTTACAG AGTTTGCTAG TGATCCTTAT
 TATGATACAC GCTATTCCGG TGTCAACAAA CGCCTGTCGG ATTATCCTGA ATTTCAAGCA
 AGCAACACGC GTACAGACGA TACGTTAGTC ACCGTTGTTA ATGGTATTAC TTATGTAGAA
 AAACAAATGC GTGACGAAAA TCGTGTTACA GGTAATTTTT ATACGGTACG CGGTCATCA
 ACTTCTGCGC GTGAAGGATT AATGCCTTTA GCAGCAGAGA TGGACACTTG GCTAAAAGAG
 CCATCGAAAG AAACGTATAT CGGTTACGCA GAAGATTTAG GCAATGGCCT AATCGCTCGA
 CTTCAGTGA TAACAGAAGA GCAGAAAAATA AAACATGTCA GCTATGATGA ATACTTTTCA
 GATGAACAGG AAAAAATCAC AGAAACAGCC TCGGCGCCTT TTATCGTCAA TCGAAATATT
 ATTCACCAGG ATACAATAAA CAAACCAACA ATTCTTTTAT TCATTTTGTA G

EF025-2 (SEQ ID NO:94)

MKHIKGLVF IGLFILVGCA PDQEPKQTT SGPQETKQVK QVTVTNQTS AVEKQAPTKN
 DELIANQLTF DSHEYTYEVV TGATQTTFGT TPPAKYTPPE KKKMFWSNQ PPLGLMTGNY
 YKNEGVFTGG NYGIVEIITE PETQRILNVE FTEFASDPY DTRYSGVNKR LSDYPEFQAS
 NTRTDDTLVT VVNGITYVEK QMRDENRVTG NFYTVRGSST SAREGLMPLA AEMDTWLKEP
 SKETYIGYAE DLGNGLIARL QVITEEQKIK HVSYDEYFSD EQEKITETAC GLFIVNRNII
 HQDTINKPTI LLFIL

EF025-3 (SEQ ID NO:95)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAC GAAACAAACA ACAAGTGGTC CGCAAGAGAC AAAGCAAGTG
AAGCAAGTTA CCGTCACCAA TCAAACGACT TCTGCGGTGG AAAACAAGC GCCGACTAAA
AATGACGAAC TGATTGCTAA TCAATTGACT TTTGATTCTC ATGAATACAC GTACGAAGTG
GTTACAGGGG CCACACAAAC GACATTTGGA ACAACCCAC CAGCAAAATA TACACCGGAA
GAAAAAAGA AAAAAATGTT TTGGTCCAAT CAACCGCCTT TGGGATTAAT GACGGGTAAC
TATTATAAAA ATGAAGGTGT ATTTACTGGC GGAAATTACG GCATTGTAGA GATTATTACG
GAACCTGAAA CGCAAAGGAT TCTGAATGTT GAGTTTACAG AGTTTGCTAG TGATCCTTAT
TATGATACAC GCTATTCTGGG TGTCAACAAA CGCCTGTCGG ATTATCCTGA ATTTCAAGCA
AGCAACACGC GTACAGACGA TACGTTAGTC ACCGTTGTTA ATGGTATTAC TTATGTAGAA
AAACAAATGC GTGACGAAAA TCGTGTTACA GGTAAATTTT ATACGGTACG CGGTTTCATCA
ACTTCTGCGC GTGAAGGATT AATGCCTTTA GCAGCAGAGA TGGACACTTG GCTAAAAGAG
CCATCGAAAG AAACGTATAT CGGTTACGCA GAAGATTTAG GCAATGGCCT AATCGCTCGA
CTTCAAGTGA TAACAGAAGA GCAGAAAATA AAACATGTCA GCTATGATGA ATACTTTTCA
GATGAACAGG AAAAAATCAC AGAAACAGCC TCGGCGCTTT TTATCGTCAA TCGAAATATT
ATTCACCAGG ATACAATAAA CAAACCAACA ATTCTTTTAT TCATTTTG

EF025-4 (SEQ ID NO:96)

TKQTT SGPQETKQVK QVTVTNQTTT AVEKQAPTQN
DELIANQLTF DSHEYTYEVV TGATQTTFGT TPPAKYTPEE KKKKMFWSNQ PPLGLMTGNY
YKNEGFTGG NYGIVEIITE PETQRILNVE FTEFASDPYY DTRYSGVNKR LSDYPEFQAS
NTRDDTLVT VVNGITYVEK QMRDENRVTG NFYTVRGSST SAREGLMPLA AEMDTWLKEP
SKETYIGYAE DLGNGLIARL QVITEEQKIK HVSYDEYFSD EQEKITETAC GLFIVNRNII
HQDTINKPTI LLFIL

EF026-1 (SEQ ID NO:97)

TGAGTGATG ATTACTCATT TCCCTTTGAA TCAGTTATGA TAAAGGAAGA AATAAATAAA
TTTTTTGGAG GGATTTTCAT GAAAATGTCT AAAGTACTCA CCACTGTTTT GACGGCAACT
GCTGCTCTTG TGTGCTTAG TGCTTGTTCA TCTGATAAAA AAACAGATAG TAGTTCCTAGT
AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
AATGTCACCTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
TCCAACGATG TCTATCGTAA ATTAGCACCT TATTTCCCAAG ATGATAATAA AAAAGTAACT
GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
AAAGATGCTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAATTAA

EF026-2 (SEQ ID NO:98)

MKMSK VLTTLTATA ALVLLSACSS DKKTDSSSSS
KETANSSTEVS VGASISAKP EELEMAISDK GNWIVAATDN VTDFDKEVTV GTFHDKGKDS
NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSENFNIVH GTVKGDIEVK ANGFTLNGTK
VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF026-3 (SEQ ID NO:99)

AACAGATAG TAGTTCCTAGT
AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
AATGTCACCTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TCCAACGATG TCTATCGTAA ATTAGCACTT TATTCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAAT

EF026-4 (SEQ ID NO:100)

TDSSSSS

KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSENFNIVH GTVKGDIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF027-1 (SEQ ID NO:101)

TTTGGTATGA AACAGAAAAA GTGGTTAATC GGACTTGTTG CACTGGGCTT GGTTTTAGCA
 GCATGTGGAA GTGGCGGTTC GAAAACGACC TCAAACGAAC CAGCTACACA GAAAATTAAC
 GTCGCATCTG GTGGTGAAGT CTCGACATTA GACAGCGCTC ATTATACAGA TGTCTATAGT
 TCCGATATGA TTGGTCAAGT AGTTGAAGGC TTGTATCGAC AAGATAAAAA CGGAGATCCT
 GAGCTAGCTA TGGCGAAAAGC AGAGCCACAA GTTAGTGAAG ACGGGTTAGT CTATACATTC
 AAGTTACGAG AAGCAAAATG GACAAACGGG GATCCAGTTA AAGCAGGGGA TTTTGTAGTT
 GCGTTTAGAA ACGTGGTCTGA TCCAGCATAC GGTTCAGTA GCAGTAATCA AATGGATATT
 TTTAAAAATG GCGGTGCGGT GCGGGAAGGA CAAGCCACGA TGGAAGAATT TGGTGTCAAA
 GCAATCGATG ACCAGACACT AGAACTAACA TTGGAATAAT CAATTCCCTTA TTTAGCCCAA
 GTCTTGGTTG GGACACCTTT TATGCCTAAA AATGAAGCCT TTGCCAAAGA AAAAGGTACT
 GCCTATGGGA CTCTGTCAGA TAATTTTGTT GGCAATGGGC CGTTTGTAAT TTCAGGTTGG
 GATGGCAATT CCGAAACTTG GAAATTGAAG AAGAATGATC ATTATTGGGA TAAAGAACAC
 GTAAATTTGA ATGAAATTGA TGTCAAGTA GTGAAAGAAA TTGGCACAGG AGCCAATCTT
 TTTGATAATG GCGACTTAGA TTACACTGTT TTAGCAGATA CTTATGCACT TCAGTATAAA
 GAGTCAAAAC AAGCGCATTT TGTACCTAAA GCCATGGTGG GTTATTTAAG CCCCATCAT
 CGCCGTGAAA TTACCGGCAA CGAACATGTT CGAAAAGCTT TTTTACAAGC GATTGACAAA
 GAACTTTTGG CAAAAGAAAT TTTAGGAGAT GGCTCGACAG CTTTAAATGG NTTTGTACCA
 GCTAATTTTG CAAAAATCCA GATACAGGTG AAGATTTCCTG CAAAGAAAAT GGTGATTTAT
 TGCCATATAA TATTAAAGAA GCCCAAGCTA ACTGGAACAA TT

EF027-2 (SEQ ID NO:102)

MKQKKWLI GLVALGLVLA ACGSGGSKTT SNEPATQKIN VASGGELSTL DSAHYTDVYS
 SDMIGQVVEG LYRQDKNGDP ELAMAKAEPQ VSEDGLVYTF KLREAKWTNG DPVKAGDFV
 AFRNVVDPAY GSSSNQMDI FKNGRAVREG QATMEEFVK AIDDQLELT LENPIPYLAQ
 VLVGTPFMPK NEAFAKEKGT AYGTSADNFV GNGPFVISGW DGNSETWKLK KNDHYWDKEH
 VKLNEIDVQV VKEIGTGANL FDNGDLDTYV LADTYALQYK ESKQAHFVPK AMVGYLSPNH
 RREITGNEHV RKAFLQAIDK ETFAKEILGD GSTALNGFVP ANFAKIQIQV KISAKKMIY
 CHIILKKPKL TGTI

EF027-3 (SEQ ID NO:103)

AACGACC TCAAACGAAC CAGCTACACA GAAAATTAAC
 GTCGCATCTG GTGGTGAAGT CTCGACATTA GACAGCGCTC ATTATACAGA TGTCTATAGT
 TCCGATATGA TTGGTCAAGT AGTTGAAGGC TTGTATCGAC AAGATAAAAA CGGAGATCCT
 GAGCTAGCTA TGGCGAAAAGC AGAGCCACAA GTTAGTGAAG ACGGGTTAGT CTATACATTC
 AAGTTACGAG AAGCAAAATG GACAAACGGG GATCCAGTTA AAGCAGGGGA TTTTGTAGTT
 GCGTTTAGAA ACGTGGTCTGA TCCAGCATAC GGTTCAGTA GCAGTAATCA AATGGATATT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TTTAAAAATG GCGGTGCGGT GCGGGAAGGA CAAGCCACGA TGGAAGAATT TGGTGTCAAA
GCAATCGATG ACCAGACACT AGAACTAACA TTGGAAAATC CAATTCCCTTA TTTAGCCCAA
GTCTTG GTTGGGACACCTTT TATGCCTAAA AATGAAGCCT TTGCCAAAGA AAAAGGTACT
GCCTATGGGA CTTCTGCAGA TAATTTTGTT GCGAATGGGC CGTTTGTAAT TTCAGGTTGG
GATGGCAATT CCGAAACTTG GAAATTGAAG AAGAATGATC ATTATTGGGA TAAAGAACAC
GTAAAAATTGA ATGAAATTGA TGTTCAGTA GTGAAAGAAA TTGGCACAGG AGCCAATCTT
TTTGATAATG GCGACTTAGA TTACACTGTT TTAGCAGATA CTTATGCACT TCAGTATAAA
GAGTCAAAAC AAGCGCATTT TGTACCTAAA GCCATGGTGG GTTATTTAAG CCCCAATCAT
CGCCGTGAAA TTACCGGCAA CGAACATGTT CGAAAAGCTT TTTTACAAGC GATTGACAAA
GAAACTTTTG CAAAAGAAAT TTTAGGAGAT GGCTCGACAG CTTTAAATGG NTTTGTACCA
GCTAATTTTG CAAAATCCA GATACAGGTG AAGATTTCCG CAAAGAAAAT GGTGATTTAT
TGCCATATAA TATTAAAGAA GCCCAAGCTA A

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EF027-4 (SEQ ID NO:104)

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TT SNEPATQKIN VASGGELSTL DSAHYTDVYS
SDMIGQVVEG LYRQDKNGDP ELAMAKAEPQ VSEDGLVYTF KLREAKWTNG DPVKAGDFVV
AFRNVVDPAY GSSSSNQMDI FKNGRAVREG QATMEEFVK AIDDQLELT LENPIPYLAQ
VLVGTPFMPK NEAFAKEKGT AYGTSADNFV GNGPFVISGW DGNSETWKLK KNDHYWDKEH
VKLNEIDVQV VKEIGTGANL FDNGDLDTYV LADTYALQYK ESKQAHFVPK AMVGYLSPNH
RREITGNEHV RKAFLQAIDK ETFAKEILGD GSTALNGFVP ANFAKIQIQV KISAKKMIY
CHIILKKPKL

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EF028-1 (SEQ ID NO:105)

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TAACAGAAGC AATACAACAA CTTAACACTT TGTTTACTTG TTATTTATCA GAAATCAACT
AAGACTTGTT ATAGTCAATG TATGGGTAGA TATGAAGGAG GAAACAAGGA AATGAAGAAA
AGAGCTTTGC TAGGGGTAC CTTATTAACA TTCACAACAT TAGCGGGTTG TACAAATTTA
TCTGAACAGA AAAGCGGCGA AAAACAAACA GAGGTTGCTG AAGCGAAGGC AACTGAATCT
GAAAAAGCAT CAGTAAAAAA TGTTATTTTT ATGATTGGAG ATGGCATGGG GAATCCGTAT
ACAACGGGCT ATCGCTATTT CAAAGCCAAT CACTCAGACA AGCGTGTTCC CCAAACAGCT
TTTGATACCT ATTTGGTCGG ACAGCAAGCC ACTTATCCAG AAGATGAAGA AGAGATGTC
ACCGATTGAG CTTCCGCAGC GACAGCGATG GCTGCCGGAG TGAAAACCTA TAATAATGCT
ATTGCACTCG ATAATGACAA GTCCAAAACA GAAACAGTGC TCGAACGTGC GAAAAAGTG
GGGAAATCAA CGGGTCTTGT AGCAACATCT GAAATAACAC ATGCAACCCC TGCTGCATAT
GGCGCACATA ATGTTTCACG CAAAATATG GCAGAAATCG CCGATGACTA TTTTGATGAT
CAAATCGACG GACAACACAA AGTCGATGTG TTAATTGGCG GCGGCTCCGA ATTAATTGCG
CGGAAAGATC GTGATTTAGT CAAAGAATTT TCCCAAGCGG GTTATGGTCA TGTCACAGAC
AAAAAGTCGT TAAATGAGAA CCAAGACGAC AAAATTTTAG GCTTGTTTGC ACCAGCGGG
CTACCTAAAA TGATTGACCG AACGGAAGAA GTCCCTTCAT TAGCTGATAT GACAGAAGCG
GCTCTTCAAC GGTAGATAA AAATGAAAAA GGTTTCTTTT TAATGGTTGA AGGTAGTCAA
ATTGATTGGG CCGGGCATAG CAATGATATT GTTGGCGCGA TGAGCGAAAT GCAAGACTTC
GAAGCGCGCT TTGAAAAGGC CATCGATTTT GCCAAAAAAG ATGGTGAACA TTGGTGGTTA
CAACTGCAGA TCATTCAACA GGGGGCTTGT CTTTAG

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EF028-2 (SEQ ID NO:106)

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MKKR ALLGVTLTTF TTAGCTNLS
EQSGEKQTE VAEAKATESE KASVKNVIFM IGDGMGNPYT TGYRYFKANH SDKRVPQTAF
DTYLVGQQAT YPEDEEENV DSASAATAMA AGVKTYNNAI ALDNDKSKTE TVLERAKKVG
KSTGLVATSE ITHATPAAYG AHNVS RNMA EIADDYFDDQ IDGQHKVDVL LGGGSELFAR
KDRDLVKEFS QAGYGHVTDK KSLNENQDDK ILGLFAPGGL PKMIDRTEEV PSLADMTEAA
LQRLDKNEKG FFLMVEGSQI DWAGHSNDIV GAMSEMQDFE AAFEKAIDFA KKDGEHWWLQ

```

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LQIIQQGACL

EF028-3 (SEQ ID NO:107)

ACAGA AAAGCGGCGA AAAACAAACA GAGGTTGCTG AAGCGAAGGC AACTGAATCT
 GAAAAAGCAT CAGTAAAAAA TGTTATTTTT ATGATTGGAG ATGGCATGGG GAATCCGTAT
 ACAACGGGCT ATCGCTATTT CAAAGCCAAT CACTCAGACA AGCGTGTTC CCAAACAGCT
 TTTGATACCT ATTTGGTCGG ACAGCAAGCC ACTTATCCAG AAGATGAAGA AGAGAATGTC
 ACCGATTTCAG CTTCCGCAGC GACAGCGATG GCTGCCGAG TGAAAACCTA TAATAATGCT
 ATTGCACTCG ATAATGACAA GTCCAAAACA GAAACAGTGC TCGAACGTGC GAAAAAGTG
 GGGAAATCAA CGGCTCTTGT AGCAACATCT GAAATAACAC ATGCAACCCC TGCTGCATAT
 GGCGCACATA ATGTTTCACG CAAAAATATG GCAGAAATCG CCGATGACTA TTTTGATGAT
 CAAATCGACG GACAACACAA AGTCGATGTG TTACTTGGCG GCGGCTCCGA ATTATTTGCC
 CGGAAAGATC GTGATTTAGT CAAAGAATTT TCCCAAGCGG GTTATGGTCA TGTCACAGAC
 AAAAAGTCGT TAAATGAGAA CCAAGACGAC AAAATTTTAG GCTTGTTTGC ACCAGGCGGG
 CTACCTAAAA TGATTGACCG AACGGAAGAA GTCCCTTCAT TAGCTGATAT GACAGAAGCG
 GCTCTTCAAC GGTTAGATAA AAATGAAAAA GGTTTCCTTT TAATGGTTGA AGGTAGTCAA
 ATTGATTGGG CCGGGCATAG CAATGATATT GTTGGCGCGA TGAGCGAAAT GCAAGACTTC
 GAAGCGGCGT TTGAAAAGGC CATCGATTTT GCCAAAAAAG ATGGTGAACA TTGGTGGTTA
 CAACTGCAGA TCATTCAACA GGGGGCTTGT CTT

EF028-4 (SEQ ID NO:108)

QKSGEKQTE VAEAKATESE KASVKNVIFM IGDGMGNPYT TGYRYFKANH SDKRVPQTAF
 DTYLVGQQAT YPEDEENVNT DSASAATAMA AGVKTYNNAI ALDNDKSKTE TVLERAKKVG
 KSTGLVATSE ITHATPAAYG AHNVSARKNMA EIADDYFDDQ IDGQHKVDVL LGGGSELFAR
 KDRDLVKEFS QAGYGHVTDK KSLNENQDDK ILGLFAPGGL PKMIDRTEEV PSLADMTEAA
 LQRLDKNEKG FFLMVEGSQI DWAGHSNDIV GAMSEMQDFE AAFEKAIDFA KKDGEHWWLQ
 LQIIQQGACL

EF029-1 (SEQ ID NO:109)

TGAAGGAGGG AGAAAATGAA AAAGTTAATC GGTA AAAAGT GGCTGCTGCT TACAGCAGTA
 GCCACTTTTT TATTATCAGG ATGCGCAAGT CTTGAACAAA AAGCACAGGA TAGTGTA AAA
 GAAGTTACTG AAAATGTTAC TCAAACATATT TCAAACGATC AACGTATACC AGCTGATTTT
 GTTAGGCACG TGGATGGCGA TACCACAGTA TTAAAAATTG ACGGAAAAGA ACAAAAAGTT
 CGGTTTTTAT TAATTGACAC ACCCGAGACT GTGAAACCGA AAACAAAAGT TCAGCCGTTT
 GGATTGGAAG CTAGCAAACG CACAAAAGAG CTTTTGTCTA CTGCTTCAGA AATTACGTTT
 GAATATGATA AGGGCGATAA AACAGATCGT TACGGACGAG CGTTGGGCTA CATATTCGTA
 GATGGAACAT TACTACAAA AACGCTTGTA AGTGAAGGAT TAGCTCGTGT TGCCTATGTA
 AAAGAGCCTA CAACTAAGTA TTTGGCAGAA CTAGAGCAAG CCCAAGAACA GGCTAAAAAT
 GAGTCACTCG GAATCTGGAG CATACCAGGT TATGTGACAC AACGGGGGTT TAGTAAATAA

EF029-2 (SEQ ID NO:110)

MKKLIG KKWLLLTAVA TFLLSGCASL EQKAQDSVKE VTENVQTIS NDQRIPADFV
 RHVDGDTTVL KIDGKEQKVR FLLIDTPETV KPRTKVQPF LEASKRTKEL LSTASEITFE
 YDKGDKTDY GRALGYIFVD GTLLQKTLVS EGLARVAYVK EPTTKYLAEL EQAQEQAKNE
 SLGIWSIPGY VTQRGFSK

EF029-3 (SEQ ID NO:111)

AAATGTTAC TCAAACATATT TCAAACGATC AACGTATACC AGCTGATTTT
 GTTAGGCACG TGGATGGCGA TACCACAGTA TTAAAAATTG ACGGAAAAGA ACAAAAAGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGGTTTTTAT TAATTGACAC ACCCGAGACT GTGAAACCGA AAACAAAAGT TCAGCCGTTT
 GGATTGGAAG CTAGCAAACG CACAAAAGAG CTTTTGTCTA CTGCTTCAGA AATTACGTTT
 GAATATGATA AGGGCGATAA AACAGATCGT TACGGACGAG CGTTGGGCTA CATATTCGTA
 GATGGAACAT TACTACAAA AACGCTTGTA AGTGAAGGAT TAGCTCGTGT TGCCTATGTA
 AAAAGAGCCTA CAACTAAGTA TTTGGCAGAA CTAGAGCAAG CCCAAGAACA GGCTAAAAAT
 GAGTCACTCG GAATCTGGAG CATACCAGGT TATGTGACAC AACGGGGGTT TAGTAAA

EF029-4 (SEQ ID NO:112)

NVTQTIS NDQRIPADFV
 RHVDGDTTVL KIDGKEQKVR FLLIDTPETV KPKTKVQPFQ LEASKRTKEL LSTASEITFE
 YDKGDKTDRY GRALGYIFVD GTLLQKTLVS EGLARVAYVK EPTTKYLAEL EQAQEQAKNE
 SLGIWSIPGY VTQRGFSK

EF030-1 (SEQ ID NO:113)

TGATTGACAC ATAGGGGGAA TAGTATGAAA AAGTTAAAAA TGATGGGGAT TATGTTATTT
 GTTAGTACGG TCTTGGTAGG TTGTGGCACA ACAGCAGANA CAAAAATAGA CGAGAAAAGCA
 ACTGAGAAAA CCAGTGTCTC GAAAAAAGTT TTAAATTTAA TGGAGAACTC GGAAATCGGT
 TCAATGGATT CTATTTTTTAC ACAAGATGAA GCCAGTATTA ACGCACAGTC CAATGTCTTT
 GAAGGGTTAT ATCAATTGGA TGAAAAAGAT CAACTAATAC CTGCTGCTGC TAAAGAGATG
 CCAGAAATTT CTGAGGATGG CAAACGATAT ACCATTAAAC TAAGAGAAGA TGGCAAGTGG
 TCCAATGGTG ATGCTGTAAC AGCCAATGAT TTCGTTTTTG CTGGCGTAA ATTAGCGAAT
 CCAAAAAACC AAGCCAATTA CTTTTCTTG TTAGAAGGAA CGATTCTGAA CGGAACAGCT
 ATTACAAAAG AGGAAAAAGC ACCAGAGGAA TTGGGTGTCA AAGCGCTTGA TGATTATACT
 TTGGAGGTTA CTTTAGAAAA GCCTGTACCA TATTTTACGT CGTTATTGGC ATTTTCTCCA
 TTTTCCCCAC AAAACGAAGC ATTCGTGAAA GAAAAAGGAC AAGCCTATGG CACTTCTAGT
 GAAATGATTG TATCTAATGG TCCGTTTTTA ATGAAAAATT GGGATCAGTC AGCGATGTCC
 TGGGATTTTG TGCGTAATCC CTACTATTAC GATAAAGAAA AAGTAAATC AGAAACGATT
 CATTTTGAAG TTCTTAAAGA AACCAATACC GTTTATAATT TGTACGAATC AGGTGAATTA
 GATGTGGCTG TCTTAACAGG AGATTTTGCT AAACAAAATC GAGACAACCC AGACTATGAA
 GCAATCGAAC GGTCAAAAGT CTATTCCTTA CGTTTAAACC AAAAAAGAAA CGAAAAACCA
 TCCATTTTTG CAAATGAGAA TGTCGCGAAA GCTTTAGCTT ATGCTTTGGA TAAAAAAGT
 TTAGTCGATA ATATTTTAGC AGATGGCTCA AAAGAAATTT ATGGGTACAT TCCAGAAAAA
 TTTGTATATA ACCCAGAAAC GAATGAAGAT TTTTCGTCAAG AAGCAGGCGC TCTTGTCAAA
 ACAGACGCCA AAAAAGCCAA AGAGTATTTA GATAAAGCAA AAGCAGAGCT AAACGGAGAT
 GTAGCCATTG AACTTCTTTC AAGAGATGGT GATAGTGACC GA

EF030-2 (SEQ ID NO:114)

MKK LKMMGIMLFV STVLVCGT AXTKIDEKAT EKTSVSKVL NLMENSEIGS
 MDSIFTQDEA SINAQSNVFE GLYQLDEKDQ LIPAAAKEMP EISEDGKRYT IKLREDGKWS
 NGDAVTANDF VFAWRKLANP KNQANYFFLL EGTILNGTAI TKEEKAPPEL GVKALDDYTL
 EVTLEKPVY FTSLLAFSPF FPQNEAFVKE KGQAYGTSSE MIVSNGPFLM KNWDQSAMSW
 DFVRNPYYYD KEVKVSETH FEVLKETNTV YNLYESGELD VAVLTGDFAK QNRDNPDYEA
 IERSKVYSLR LNQRNEKPS IFANENVRKA LAYALDKKSL VDNILADGSK EIYGYIPEKF
 VYNPETNEDF RQEAGALVKT DAKKAKEYLD KAKAELNGDV AIELLSRDGD SDR

EF030-3 (SEQ ID NO:115)

GAGAAAGCA
 ACTGAGAAAA CCAGTGTCTC GAAAAAAGTT TTAAATTTAA TGGAGAACTC GGAAATCGGT
 TCAATGGATT CTATTTTTTAC ACAAGATGAA GCCAGTATTA ACGCACAGTC CAATGTCTTT
 GAAGGGTTAT ATCAATTGGA TGAAAAAGAT CAACTAATAC CTGCTGCTGC TAAAGAGATG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGAAATTT CTGAGGATGG CAAACGATAT ACCATTAAAC TAAGAGAAGA TGGCAAGTGG
TCCAATGGTG ATGCTGTAAC AGCCAATGAT TTCGTTTTTG CTGGCGTAA ATTAGCGAAT
CCCCAAAACC AAGCCAATTA CTTTTTCTTG TTAGAAGGAA CGATTCTGAA CGGAACAGCT
ATTACAAAAG AGGAAAAAGC ACCAGAGGAA TTGGGTGTCA AAGCGCTTGA TGATTATACT
TTGGAGGTTA CTTTAGAAAA GCCTGTACCA TATTTTACGT CGTTATTGGC ATTTTCTCCA
TTTTTCCCAC AAAACGAAGC ATTCGTGAAA GAAAAAGGAC AAGCCTATGG CACTTCTAGT
GAAATGATTG TATCTAATGG TCCGTTTTTA ATGAAAAATT GGGATCAGTC AGCGATGTCG
TGGGATTTTG TGCCTAATCC CTACTATTAC GATAAAGAAA AAGTAAATC AGAAACGATT
CATTTTGAAG TTCTTAAAGA AACCAATACC GTTTATAATT TGTACGAATC AGGTGAATTA
GATGTGGCTG TCTTAACAGG AGATTTTGTCT AAACAAAATC GAGACAACCC AGACTATGAA
GCAATCGAAC GGTCAAAAGT CTATTCCTTA CGTTTAAACC AAAAAAGAAA CGAAAAACCA
TCCATTTTGT CAAATGAGAA TGTCCGCAAA GCTTTAGCTT ATGCTTTGGA TAAAAAAGT
TTAGTCGATA ATATTTTAGC AGATGGCTCA AAAGAAATTT ATGGGTACAT TCCAGAAAAA
TTTGATATATA ACCCAGAAAC GAATGAAGAT TTTCGTCAAG AAGCAGGCGC TCTTGTCAAA
ACAGACGCCA AAAAAGCCAA AGAGTATTTA GATAAAGCAA AAGCAGAGCT AAACGGAGAT
GTAGCCATTG AACTTCTTTC AAGAGATGGT

EF030-4 (SEQ ID NO:116)

EKAT EKTSVSKKVL NLMENSEIGS

MDSIFTQDEA SINAQSNVFE GLYQLDEKDQ LIPAAAKEMP EISEDGKRYT IKLREDGKWS
NGDAVTANDF VFAWRKLANP KNQANYFFLL EGTILNGTAI TKEEKAPEEL GVKALDDYTL
EVTLEKPVYP FTSLLAFSPF FPQNEAFVKE KGQAYGTSSE MIVSNGPFLM KNWDQSAMSW
DFVRNPYYD KEVKVSETH FEVLKETNTV YNLYESGELD VAVLTGDFAK QNRDNPDYEA
IERSKVYSLR LNQKRNEKPS IFANENVRKA LAYALDKKSL VDNILADGSK EIYGYIPEKF
VYNPETNEDE RQEAGALVKT DAKKAKEYLD KAKAELNGDV AIELLSRDG

EF031-1 (SEQ ID NO:117)

TGAGAAATTA GTTATTTTAG AAAAATAAAA ACCATTTTGG AGGAAGATTT AAAAATGAAA
AAACGCGTAA TTTTAGGGAC ATTAGTCGCT GCAACGTTAT TAATGACTGC TTGTGGAAAC
AGCGAAGCAA CTACGAAAAG CGAGAGCAAA GGTGGAAGTA ATGCTTTAGT CGTTTCAACT
TTCGGATTAA GTGAAGATAT TGTCAAAAAA GACATTATCG CTCCATTTGA AAAAGAGAAT
GAAGCGAAAG TTACCTTAGA AGTAGGCAAT AGCGCAGACC GCTTTACGAA ATTAATAAAT
AATCCCAATG CGGGAATTGA TGTCATTGAA TTAGCACAAAG CAAATGCAGC ACAAGGTGGA
AAAGATGGGT TATTTGAAAA AATTACAGAA AAAGAAGTAC CTAATTTAAG TCAGTTAACG
CCGGGAGCAA AAGAGGTTTT TGAAAGTGGT GCTGGCGTAC CAATCGCTGT AAACAGTATC
GGGATTGTTT ACAACAAAGA AAAATTAGGC AAAGAAATTA AAACTGGGA TGACTTATGG
TCAGCTGATT TGAAAGGTAA AATTTCTGTT CCAGACGTTG CCACGACGGC AGGTCCTTTA
ATGTTATACG TTGCTAGTGA ACATGCTGGT CAAGATATTA CAAAAGATAA CGGGAAGGCC
GCTTTTGAAG CGATGAAAGA ATTAATAACCA AACGTTGTTA AAACGTATTC AAAATCGTCA
GACTTAGCNA ATATGTTCCA ATCTGGTGAA ATTGAAGCAG CTGTGGTTGC TGATTTTGCG
GTTGATATTA TTCAAGGCGC ACAGAAAACG TGA

EFO031-2 (SEQ ID NO:118)

MKK RVILGTLVAA TLLMTACGNS EATTKSESKG GSNALVVSTF

GLSEDIVKDD IIPFEKENE AKVTLEVGN SADRFTKLKNN PNAGIDVIEL AQANAAQGGK
DGLFEKITEK EVPNLSQLTP GAKEVFESGA GVPIAVNSIG IVYNKEKLGK EIKNWDDLWS
ADLKGKISVP DVATTAGPLM LYVASEHAGQ DITKDNGKAA FEAMKELKPN VVKTYKSSD
LANMFQSGEI EAAVVADFAV DIIQGAQKT

EF031-3 (SEQ ID NO:119)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AA CTACGAAAAG CGAGAGCAAA GGTGGAAGTA ATGCTTTAGT CGTTTCAACT
 TTCGGATTAA GTGAAGATAT TGTCAAAAA GACATTATCG CTCCATTTGA AAAAGAGAAT
 GAAGCGAAAAG TTACCTTAGA AGTAGGCAAT AGCGCAGACC GCTTTACGAA ATTAAGAAAT
 AATCCCAATG CCGGAATTGA TGTCATTGAA TTAGCACAAAG CAAATGCAGC ACAAGGTGGA
 AAAGATGGGT TATTTGAAAA AATTACAGAA AAAGAAGTAC CTAATTTAAG TCAGTTAACG
 CCGGGAGCAA AAGAGGTTTT TGAAAGTGGT GCTGGCGTAC CAATCGCTGT AAACAGTATC
 GGGATTGTTT ACAACAAAGA AAAATTAGGC AAAGAAATTA AAACTGGGA TGACTTATGG
 TCAGCTGATT TGAAAGGTAA AATTTCTGTT CCAGACGTTG CCACGACGGC AGGTCCTTTA
 ATGTTATACG TTGCTAGTGA ACATGCTGGT CAAGATATTA CAAAAGATAA CGGGAAGGCC
 GCTTTTGAAG CGATGAAAGA ATTAACCA AACGTTGTTA AAACGTATTC AAAATCGTCA
 GACTTAGCNA ATATGTTCCA ATCTGGTGAA ATTGAAGCAG CTGTGGTTGC TGATTTGCG
 GTTGATATTA TTCAAGGCGC ACAGAAAA

EF031-4 (SEQ ID NO:120)

TTKSESKG GSNALVVSTF
 GLSEDIVKDD IIAPEKENE AKVTLEVGN SADRFTKLKNN PNAGIDVIEL AQANAAQGGK
 DGLFEKITEK EVPNLSQLTP GAKEVFESGA GVPIAVNSIG IVYNKEKLGK EIKNWDLLWS
 ADLKGKISVP DVATTAGPLM LYVASEHAGQ DITKDNGKAA FEAMKELKPN VVKTYSSKSSD
 LANMFQSGEI EAAVVADFAV DIIQGAQK

EF032-1 (SEQ ID NO:121)

TGAATAAATT ATTTAGGAGG AATTATGATG AAAAAATTAA TTAGTTTAGG ATTGGTTTGT
 GTTTGTGGTA TTCTACTACT TACTGCTTGT NCGGGAAATA ATGATAATAA AGATACTGAA
 AAGTCAACCA GTCAATCTAG CAGCACAGTT AAACAACCGA ATTCAAAAGA CTTTGTGTCG
 TCAGGGGAAT ATTCAGTTGG AAAAGATATT GATCCTGGAG ATTACTATGC TGTATTAACT
 CAACTAGATG ATAAATCGAG CATAGTTCTT ATTACCGTCA AATCAGGCGG AGAAAATAGT
 AACCATGACT TATACGGAGT GGGAAACAAG AAAAAAGTAT CTCTTAAAAA GGGAGATACT
 CTCACATTCG AAAGTCCGA CAAAGATTTT GTTGTTAGAT TTTTAAATGA AAAAGATTTT
 CAAGAATATA TGAAAAATCC AGTATCNAGT ACTGAAACTA GCAAACANAA AACAGTAAAC
 TCTGATGTTT CTAAGAGTAG TAGCCAAGAT AATAAACAAT CTGATGTATC TGAAAAAATA
 GAAGTAAAGTA CTGAAGCGAA GTCTGATGTA GCTACTAATA CTTTACCGAG CGAAGATAAA
 AATACTAATG ACATTACTAA GCTAGCAGAT GAGCCAACCT TAGAACAACA AACCGTCTTA
 GATACTTTAG CTAAGCATCA ATTTAATGAT ATGTATCCTT ATAAAGGAAG CAAAATGCAT
 TCAATTATCG GCGTCATCCC AACCATGGAC GCAAAAAGAT GGTAA

EF032-2 (SEQ ID NO:122)

MK KLISLGLVCV CGISLLTACX GNNDNKDTEK STSQSSSTVK QPNSKDFVAS
 GEYSVGKIDID PGDYYAVLTQ LDDKSSIVLI TVKSGGENSN HDLYGVGNKK KVSLLKGDITL
 TFETADKDFV VRFLNEKDFQ EYMKNPVSSS ETSKXKTVNS DVSKSSSQDN KQSDVSEKKE
 VSTEAKSDVA TNTLPSEDKN TNDITKLADE PTLEQQTVLD TLAKHQFNNDM YPYKSGSMHS
 IIGVIPTMDA KRW

EF032-3 (SEQ ID NO:123)

TA ATGATAATAA AGATACTGAA
 AAGTCAACCA GTCAATCTAG CAGCACAGTT AAACAACCGA ATTCAAAAGA CTTTGTGTCG
 TCAGGGGAAT ATTCAGTTGG AAAAGATATT GATCCTGGAG ATTACTATGC TGTATTAACT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAACTAGATG ATAAATCGAG CATAGTTCCTT ATTACCGTCA AATCAGGCGG AGAAAATAGT
 AACCATGACT TATACGGAGT GGGAAACAAG AAAAAAGTAT CTCTTAAAAA GGGAGATACT
 CTCACATTCG AAAC TGCCGA CAAAGATTTT GTTGTTAGAT TTTTAAATGA AAAAGATTTT
 CAAGAATATA TGAAAAATCC AGTATCNAGT ACTGAAACTA GCAAACANAA AACAGTAAAC
 TCTGATGTTT CTAAAAGTAG TAGCCAAGAT AATAAACAAT CTGATGTATC TGAAAAAAAA
 GAAGTAAGTA CTGAAGCGAA GTCTGATGTA GCTACTAATA CTTTACCGAG CGAAGATAAA
 AATACTAATG ACATTACTAA GCTAGCAGAT GAGCCAACCT TAGAACAACA AACCGTCTTA
 GATACTTTAG CTAAGCATCA ATTTAATGAT ATGTATCCTT ATAAAGGAAG CAAAATGCAT
 TCAATTATCG GCGTCATCCC AACCATGGAC GCAAAAAGAT GG

EF032-4 (SEQ ID NO:124)

NDNKDTEK STSQSSSTVK QPNSKDFVAS
 GEYSVGKDID PGDYYAVLTQ LDDKSSIVLI TVKSGGENSN HDLYGVGNKK KVSLKKGDTL
 TFETADKDFV VRFLNEKDFQ EYMKNPVSST ETSKXKTVNS DVSKSSSQDN KQSDVSEKKE
 VSTEAKSDVA TNTPSEDKN TNDITKLADE PTLEQQTVDL TLAKHQFNDM YPYKSGSKMHS
 IIGVIPTMDA KRW

EF033-1 (SEQ ID NO:125)

TGACTGCTTT TTTTCTATTG GAGAAAAAAG TGGTTTTTTT GTATTGTTTT GACGTTGAGA
 CAAAGGAGGT TCATTTTCAGA AAATTTTCCC CAAAATAAAA TAGACGAATG CGAGGATGAA
 AAAATGAAAA AATTTACTTT AACAAATGATG ACTTTAGGTT TAGTAGCAAC ACTTGGCTTA
 GCAGGATGTG GTAAACAGGA AAAGAAAGCA ACTACCTCTT CTGAAAAAAC AGAAGTAACG
 TTACCAACCA AAGACCGTAG CGGCAAAGAA ATTACTTTAC CCAAAGAAGC AACCAAAATT
 ATTTCCCTAG TGCCATCAAC AACAGAAAGTG ATTGAAGACT TAGGTAAAAC CGACCAATTA
 ATCGCAGTTG ATACTCAAAG TAGTACAATG ATGACTGATT TAAAAAAATT ACCACAAATG
 GATATGATGG CTGTCGATGC CGAAAAATTG ATTGCCTTGA AACCACAAAT TGTTTATGTG
 AATGACATCA ATTTAGCTAG CTCAGAAAAGT GTTTGGAAGC AAGTGGAAGA TGCTGGAATT
 ACAGTCGTTA ATATCCCCAC TAGTACAAGC ATCAAAGCAA TCAAAGAAGA CGTCCAATTC
 ATCGCTGATA GCTTATCTGA ACATGAAAAA GGACAAAAGT TAATCAAAAC AATGGATCAA
 GAAATCGACG AGTAG

EF033-2 (SEQ ID NO:126)

MKKFTLTMMT LGLVATLGLA
 GCGKQEKKAT TSSEKTEVTL PTKDRSGKEI TLPKEATKII SLVPSTTEVI EDLGKTDQLI
 AVDTQSSTMM TDLKKLPQMD MMAVDAEKLI ALKPQIVYVN DINLASSES V WKQVEDAGIT
 VVNIPTSTSI KAIKEDVQFI ADSLSEHEKG QKLIKTMDOE IDE

EF033-3 (SEQ ID NO:127)

CTCTT CTGAAAAAAC AGAAGTAACG
 TTACCAACCA AAGACCGTAG CGGCAAAGAA ATTACTTTAC CCAAAGAAGC AACCAAAATT
 ATTTCCCTAG TGCCATCAAC AACAGAAAGTG ATTGAAGACT TAGGTAAAAC CGACCAATTA
 ATCGCAGTTG ATACTCAAAG TAGTACAATG ATGACTGATT TAAAAAAATT ACCACAAATG
 GATATGATGG CTGTCGATGC CGAAAAATTG ATTGCCTTGA AACCACAAAT TGTTTATGTG
 AATGACATCA ATTTAGCTAG CTCAGAAAAGT GTTTGGAAGC AAGTGGAAGA TGCTGGAATT
 ACAGTCGTTA ATATCCCCAC TAGTACAAGC ATCAAAGCAA TCAAAGAAGA CGTCCAATTC
 ATCGCTGATA GCTTATCTGA ACATGAAAAA GGACAAAAGT TAATCAAAAC AATGGATCAA
 GAAATCGACG AGTAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF033-4 (SEQ ID NO:128)

SSEKTEVT L PTKDRSGKEI TLPKEATKII SLVPSTTEVI EDLGKTDQLI
 AVDTQSSTMM TDLKKLPQMD MMAVDAEKLI ALKPQIVYVN DINLASSES V WKQVEDAGIT
 VVNIPTSTSI KAIKEDVQFI ADSLSEHEKG QKLIKTMDOE IDE

EF034-1 (SEQ ID NO:129)

TAGGAGGGAG TAATCATGAA AAAAATCGGG TATTTTAGTT GTATTATTTT TTTCATGTTT
 TTGGTAGGTT GTAGTAATAA CAAAAAGAA AACGGCAATC TTTTGAATGC CAGTTCGTTT
 CCTTTAATAC TCACCACGAT TATTGAAAAA GAAGAAGACC TAACGAAAGG TTCAATTTTT
 TTCAACAAGG ATAAAACCAT GACGCTTGAA AAAGAATATT TAGTTAATCC CAATAATGAA
 GACACAAAAA AAACAAGTAG AACAGAAAAA AAGGTATATA AAAATATTAA AATACAAGAA
 AATAAAGAGA GCTATGAAAT TATAGGTCAA TTGGACAAAA AAACGAAAAA AATAGAGTTT
 AAAAAAGTTG ATGAAGGTAA ACGTATATCT GATGCAGAAG GTAATGTGTA TGGTGATTTT
 GGTGGTAAAT AG

EF034-2 (SEQ ID NO:130)

MKKIGY FSCIIFMFL VGCSNNKKEN GNLLNASSFP LILTTIIEKE EDLTKGSIF
 NKDKTMTLEK EYLVNPNED TKKTSRTEKK VYKNIQEN KESYEIIGQL DKKTCKIEFK
 KVDEGKRISD AEGNVYGDFG GK

EF034-3 (SEQ ID NO:131)

AGAA AACGGCAATC TTTTGAATGC CAGTTCGTTT
 CCTTTAATAC TCACCACGAT TATTGAAAAA GAAGAAGACC TAACGAAAGG TTCAATTTTT
 TTCAACAAGG ATAAAACCAT GACGCTTGAA AAAGAATATT TAGTTAATCC CAATAATGAA
 GACACAAAAA AAACAAGTAG AACAGAAAAA AAGGTATATA AAAATATTAA AATACAAGAA
 AATAAAGAGA GCTATGAAAT TATAGGTCAA TTGGACAAAA AAACGAAAAA AATAGAGTTT
 AAAAAAGTTG ATGAAGGTAA ACGTATATCT GATGCAGAAG GTAATGTGTA TGGTGATTTT
 GGTGGTAAAT AG

EF034-4 (SEQ ID NO:132)

KEN GNLLNASSFP LILTTIIEKE EDLTKGSIF
 NKDKTMTLEK EYLVNPNED TKKTSRTEKK VYKNIQEN KESYEIIGQL DKKTCKIEFK
 KVDEGKRISD AEGNVYGDFG GK

EF035-1 (SEQ ID NO:133)

TAAACGAGAG GTGAGTTTAT GAAAACAAAA ATCGGAAAAA CAGTTATCTT GTCAGCATTT
 TTATTCACAA GTTTCCTTTT ACTGAGTGGT TGTACCTCGG CTGGCGAAGA GATGGAAAAA
 ACAATTGATC GACAGAAAGA AAAAGTCGAT AAAACGGTCG ATAAGCAGAA ACATAAAAAAT
 GAAAATTCCA TGGAAAGTTA CGACGAAAAA GTTGACCGTT CTTTAGATAG TCAAGAAGAC
 AAAATCGATA CTACTGAGTA A

EF035-2 (SEQ ID NO:134)

MKTKI GKTIVLSAFL FTSFLLLSGC TSAGEEMEKT IDRQKEKVDK TVDKQKHKNE
 NSMESYDEKV DRSLDSQEDK IDTTE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF035-3 (SEQ ID NO:135)

GATGGAAAAA

ACAATTGATC GACAGAAAGA AAAAGTCGAT AAAACGGTCG ATAAGCAGAA ACATAAAAAT
 GAAAATTCCA TGGAAAGTTA CGACGAAAAA GTTGACCGTT CTTTAGATAG TCAAGAAGAC
 AAAATCGATA CTA CTGAG

EF035-4 (SEQ ID NO:136)

MEKT IDRQKEKVDK TVDKQKHKNE
 NSMESYDEKV DRSLDSQEDK IDTTE

EF036-1 (SEQ ID NO:137)

TAATTTTCAA GTCCTACATA TAATGGTAAA ATAGAATGGA TTGAAATTAA TTGGAGGAAT
 AATGAATCGA TGAAAAAAG AATTGCTATTA TTTATTGGTT TGGCAAGTAT ACTTACTTTG
 ACAGGATGTG CAAAATGGAT TGATCGTGGT GAATCCATCA CAGCGGTAGG CTCATCAGCT
 TTACAACCAT TAGTAGAGAC AGCGAGTGAG GAATATCAAA GCCAAAATCC GGGAAGATTT
 ATTAATGTCC AAGGTGGCGG AAGCGGAACA GGTCTGAGTC AAGTCCAATC TGGCGCGGTA
 GACATTGGTA ATTCTGATTT ATTTGCAGAA GAGAAAAAGG GCATCAAAGC GGAAGACTTA
 ATTGATCATA AAGTTGCTGT CGTTGGGATT ACACCAATCG TTAACAAAAA TGTCGGTGTC
 AAAGATATCT CAATGGAAAA TTAAAGAAA ATCTTTT TAG GTGAAGTAAC AAAGTGGAAA
 GAACTTGGCG GGAAAGACCA AAAAATTGTT ATTTTGAATA GAGCGGCCCG TAGTGGTACG
 CGTGCGACTT TTGAAAAGTG GGTCTTGGGA GATAAACAG CCATTCGTGC GCAAGAACAA
 GATTCCAGCG GCATGGTTCG TTCCATTGTT TCTGATACAC CAGGAGCGAT TAGTTATACC
 GCATTTTCAT ATGTTACTGA TGAAGTAGCT ACGTTAAGTA TTGATGGTGT TCAGCCAACA
 GATGAAAATG TAATGAACAA TAAATGGATT ATTTGGTCTT ATGAACACAT GTACACTCGT
 AAAAAATCAA GTGATTTAAC CAAAGAGTTT TTAGACTTTA TGTTGTCAGA TGATATCCAA
 GAACGTGTGA TTGGTCAATT AGGGTATATT CCTGTTTCGA AAATGGAAAT TGAACGGGAT
 TGGCAAGGAA ATGTCATTAA ATAA

EF-36-2 (SEQ ID NO:138)

MKKRLLLF IGLASILTLT GCAKWIDRGE SITAVGSSAL
 QPLVETASEE YQSQNPGRFI NVQGGSGTG LSQVQSGAVD IGNSDLFAEE KKGIIKAEDLI
 DHKVAUVGIT PIVNKNVGVK DISMENLKKI FLGEVTNWKE LGGKDQKIVI LNRAAGSGTR
 ATFEKWVLGD KTAIRAQEQD SSGMVRISVS DTPGAISYTA FSYVTDEVAT LSIDGVQPTD
 ENVMNKNWII WSYEHMYTRK NPSDLTKEFL DFMLSDDIQE RVIGQLGYIP VSKMEIERDW
 QGNVIK

EF036-3 (SEQ ID NO:139)

GAT TGATCGTGGT GAATCCATCA CAGCGGTAGG CTCATCAGCT
 TTACAACCAT TAGTAGAGAC AGCGAGTGAG GAATATCAAA GCCAAAATCC GGGAAGATTT
 ATTAATGTCC AAGGTGGCGG AAGCGGAACA GGTCTGAGTC AAGTCCAATC TGGCGCGGTA
 GACATTGGTA ATTCTGATTT ATTTGCAGAA GAGAAAAAGG GCATCAAAGC GGAAGACTTA
 ATTGATCATA AAGTTGCTGT CGTTGGGATT ACACCAATCG TTAACAAAAA TGTCGGTGTC
 AAAGATATCT CAATGGAAAA TTAAAGAAA ATCTTTT TAG GTGAAGTAAC AAAGTGGAAA
 GAACTTGGCG GGAAAGACCA AAAAATTGTT ATTTTGAATA GAGCGGCCCG TAGTGGTACG
 CGTGCGACTT TTGAAAAGTG GGTCTTGGGA GATAAACAG CCATTCGTGC GCAAGAACAA
 GATTCCAGCG GCATGGTTCG TTCCATTGTT TCTGATACAC CAGGAGCGAT TAGTTATACC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCATTTTCAT ATGTTACTGA TGAAGTAGCT ACGTTAAGTA TTGATGGTGT TCAGCCAACA
 GATGAAAATG TAATGAACAA TAAATGGATT ATTTGGTCTT ATGAACACAT GTACACTCGT
 AAAAATCCAA GTGATTTAAC CAAAGAGTTT TTAGACTTTA TGTTGTCAGA TGATATCCAA
 GAACGTGTGA TTGGTCAATT AGGGTATATT CCTGTTTCGA AAATGGAAAT TGAACGGGAT
 TGGCAAGGAA ATGTCATTAA A

EF036-4 (SEQ ID NO:140)

IDRGE SITAVGSSAL

QPLVETASEE YQSQNPGRFI NVQGGSGTG LSQVQSGAVD IGNSDLFAEE KKGIIKAEDLI
 DHKVAVVGIT PIVNKNVGK DISMENLKKI FLGEVTNWKE LGGKDQKIVI LNRAAGSGTR
 ATFEKWVLGD KTAIRAQEQD SSGMVRSIVS DTPGAISYTA FSYVTDEVAT LSIDGVQPTD
 ENVMNNKWII WSYEHMYTRK NPSDLTKEFL DFMLSDDIQE RVIGQLGYIP VSKMEIERDW
 QGNVIK

EF037-1 (SEQ ID NO:141)

TGAGTGTATG ATTACTCATT TCCCTTTGAA TCAGTTATGA TAAAGGAAGA AATAAATAAA
 TTTTTTGGAG GGATTTTCAT GAAAATGTCT AAAGTACTCA CCACTGTTTT GACGGCAACT
 GCTGCTCTTG TGTTGCTTAG TGCTTGTTCA TCTGATAAAA AAACAGATAG TAGTTCTAGT
 AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACCTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACTT TATTCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA ATAA

EF037-2 (SEQ ID NO:142)

MKMSK VLTTVLATA ALVLLSACSS DKKTDSSSSS

KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSNFNIVH GTVKGDIEVK ANGFTLNGTK
 VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF037-3 (SEQ ID NO:143)

AACAGATAG TAGTTCTAGT

AGCAAAGAAA CAGCTAATTC AAGTACAGAA GTAGTCTCTG GTGCTTCAAT TAGTGCCAAG
 CCTGAAGAGC TCGAAATGGC GTTAAGTGAT AAAGGAAATT GGATTGTGCG AGCTACTGAC
 AATGTCACCTT TTGATAAAGA GGTAACAGTT GCTGGTACTT TCCATGATAA GGGGAAAGAT
 TCCAACGATG TCTATCGTAA ATTAGCACTT TATTCCCAAG ATGATAATAA AAAAGTAACT
 GCTGAATATG AAATCACGGT TCCTAAGCTA ATCGTTTCTT CTGAAAATTT CAACATCGTT
 CACGGGACTG TCAAAGGTGA TATTGAGGTG AAAGCAAATG GCTTTACTTT AAATGGTACC
 AAAGTTAATG GCAATATTAC TTTTGATAAA CAAGAATACA AAGATTCTGC TGACTTAGAA
 AAAGATGGTG CCACTGTTAC TGGTGAAGTC ACCGTAGCCA A

EF037-4 (SEQ ID NO:144)

TDSSSSS

KETANSSTEV VSGASISAKP EELEMALSDK GNWIVAATDN VTFDKEVTVA GTFHDKGKDS
 NDVYRKLALY SQDDNKKVTA EYEITVPKLI VSSNFNIVH GTVKGDIEVK ANGFTLNGTK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VNGNITFDKQ EYKDSADLEK DGATVTGEVT VANN

EF038-1 (SEQ ID NO:145)

TAATGGCCAT TTCGTCTACT AATAAAGAGG ATGAAGCTAC TCAAATGGCG TTGGCAATGG
 AACAAAGGATC ATAAAAAAGG AGAAGTGAGC ATGAAAAAAG TACTACCTTT TATTGCCTTA
 GTCGGCTTGT TATTGTTGTC AGGTTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
 GGTGGTAAAT GGGAACTAGA AAATAAAAGT CCAACTACTA CTTACACTTT TTTTGATGAT
 GAAACTTTTT CGAGGTATAA TTCAAAAATT AGTGATAGTG GAACGTACTC TTACGATGAA
 AATAATAAAA AACTCACTTT GGATATAAAA AATAAAGAAC AATTAATAAT GGAAAATGTT
 GAATATAAAG ACGGTAAATT AAAAGGTGAA ATTGGAGGCG AGAAGGACTC TGATAAAAAA
 TNGAATAAGA GGTGTCTTTG A

EF038-2 (SEQ ID NO:146)

M KLLKWRWQWN KDHHKGEVSM KVLPLFIALV GLLLLSGCGT DMKKILTADG
 GKWELENKSP TTTYTFFDDE TFSRYNSKIS DSGTYSYDEN NKKLTLDIKN KEQLIMENVE
 YKDGKLGKEI GGEKDSKX NKRCL

EF038-3 (SEQ ID NO:147)

TTGTGGA ACAGATATGA AAAAGATATT GACTGCCGAT
 GGTGGTAAAT GGGAACTAGA AAATAAAAGT CCAACTACTA CTTACACTTT TTTTGATGAT
 GAAACTTTTT CGAGGTATAA TTCAAAAATT AGTGATAGTG GAACGTACTC TTACGATGAA
 AATAATAAAA AACTCACTTT GGATATAAAA AATAAAGAAC AATTAATAAT GGAAAATGTT
 GAATATAAAG ACGGTAAATT AAAAGGTGAA ATTGGAGGCG AGAAGGACTC TGATAAAAAA
 TNGAATAAGA GGTGTCTTTG A

EF038-4 (SEQ ID NO:148)

CGT DMKKILTADG
 GKWELENKSP TTTYTFFDDE TFSRYNSKIS DSGTYSYDEN NKKLTLDIKN KEQLIMENVE
 YKDGKLGKEI GGEKDSKX NKRCL

EF039-1 (SEQ ID NO:149)

TAAATATATC AAAAAGAAAA AAGGGGATTA CCAACCATGA AAAAGAAAAA AGTTTTTAGT
 GCGCTTACCT TATTAACCTT TAGTACGTTG TTGATTGCAG GCTGTGCTGG CGGAGCCAAC
 TCTGCAACAG ATAAATCAAG TGCAGCTAGC TCAAGCACTG CAGTCTCTAG TTCAGCAGAA
 GCAGCTAAAG AGCAATCAAA AGGACAAGAA TTAACAGAAA TTTTATCCAG TACTGATTGG
 CAAGGCACAA AAGTTTACGA CAAAAATNAT AATAATTTAA CAGCAGAAAA TGCTAATTTT
 ATTGGTTTTAG CAAAATATGA TGGTGAAACA GGTTTTTTATG AATTTTTCGA CAAAGAAACA
 GGTGAAACCC GTGGCGATGA AGGCACATTC TTTGTGACAG ACGATGGCGA AAAGCGTATC
 TTAATTTTCGG ATACACAAAA CTATCAAGCG GTGGTCGATT TAACGGAAGT GACGAAAGAT
 AAATTTACCT ATAAGCGAAT GGGTAAAGAT AAAGACGGGA AAGATGTAGA AGTCTTTGTA
 GAACATATCC CTTATTCTGA CGAGAAATTA ACCTTTACGA ACGGCCGTAA AGATTTAGAA
 ACAGAAACTG GCAAGATTGT TACCAATGAA CCTGGGGATG ACATTTTAGG GGCCACATTA
 TGGAATGGCA CGAAAGTTTT AGATGAAGAC GGTAACGATG TTAAGTGAAGC AAATAAAATG
 TTTATTAGTT TAGCGAAATT TGATAATAAA ACAAGTAAAT ATGAATTCTT TGATTTAGAA
 ACGGGTAAAA CACGTGGAGA TTTTGGTTAC TTCCAAGTAA TTGATAATAA CAAAATCCGT
 GCTCACGTTT CAATTGGTGA CAATAAATAT GGAGCTGCAT TAGAATTAAC AGAATTAAT
 GATAACGTT TTACGTATAC ACGAATGGGT AAAGACAACA ATGGCAAAGA AATTAAAGTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTTGTAGAAC ATGAACCATA TGAAGGAGAC TTTACGCCAG ACTTCACGTT CTAA

EF039-2 (SEQ ID NO:150)

MKKKKVFSA LTLTTFSTLL IAGCAGGANS ATDKSSAASS STAVSSSAEA
 AKEQSKGQEL TEILSSTDWQ GTKVYDKNXN NLTAENANFI GLAKYDGETG FYEFFDKETG
 ETRGDEGTFF VTDDGEKRIL ISDTQNYQAV VDLTEVTKDK FTYKRMGKDK DGKDVEVFVE
 HIPYSDEKLT FTNGRKDLET ETGKIVTNEP GDDILGATLW NGTKVLDEDG NDVTEANKMF
 ISLAKFDNKT SKYEFFDLET GKTRGDFGYF QVIDNNKIRA HVSIGDNKYG AALELTELND
 KRFTYTRMGK DNNGKEIKVF VEHEPYEGDF TPDFTF

EF039-3 (SEQ ID NO:151)

TGCAACAG ATAAATCAAG TGCAGCTAGC TCAAGCACTG CAGTCTCTAG TTCAGCAGAA
 GCAGCTAAAG AGCAATCAAA AGGACAAGAA TTAACAGAAA TTTTATCCAG TACTGATTGG
 CAAGGCACAA AAGTTTACGA CAAAAATNAT AATAATTTAA CAGCAGAAAA TGCTAATTTT
 ATTGGTTTAG CAAAATATGA TGGTGAAACA GGTTTTTATG AATTTTTTCGA CAAAGAAACA
 GGTGAAACCC GTGGCGATGA AGGCACATTC TTTGTGACAG ACGATGGCGA AAAGCGTATC
 TTAATTTTCGG ATACACAAAA CTATCAAGCG GTGGTCGATT TAACGGAAGT GACGAAAGAT
 AAATTTACCT ATAAGCGAAT GGGTAAAGAT AAAGACGGGA AAGATGTAGA AGTCTTTGTA
 GAACATATCC CTTATTCTGA CGAGAAATTA ACCTTTACGA ACGGCCGTAA AGATTTAGAA
 ACAGAAACTG GCAAGATTGT TACCAATGAA CCTGGGGATG ACATTTTAGG GGCCACATTA
 TGGAATGGCA CGAAAGTTTT AGATGAAGAC GGTAAACGATG TTAAGTGAAGC AAATAAAATG
 TTTATTAGTT TAGCGAAATT TGATAATAAA ACAAGTAAAT ATGAATTCTT TGATTTAGAA
 ACGGGTAAAA CACGTGGAGA TTTTGGTTAC TTCCAAGTAA TTGATAATAA CAAAATCCGT
 GCTCACGTTT CAATTGGTGA CAATAAATAT GGAGCTGCAT TAGAATTAAC AGAATTAAT
 GATAAACGTT TTACGTATAC ACGAATGGGT AAAGACAACA ATGGCAAAGA AATTAAAGTC
 TTTGTAGAAC ATGAACCATA TGAAGGAGAC TTTACGCCAG ACTTCACGTT CTAA

EF039-4 (SEQ ID NO:152)

ATDKSSAASS STAVSSSAEA
 AKEQSKGQEL TEILSSTDWQ GTKVYDKNXN NLTAENANFI GLAKYDGETG FYEFFDKETG
 ETRGDEGTFF VTDDGEKRIL ISDTQNYQAV VDLTEVTKDK FTYKRMGKDK DGKDVEVFVE
 HIPYSDEKLT FTNGRKDLET ETGKIVTNEP GDDILGATLW NGTKVLDEDG NDVTEANKMF
 ISLAKFDNKT SKYEFFDLET GKTRGDFGYF QVIDNNKIRA HVSIGDNKYG AALELTELND
 KRFTYTRMGK DNNGKEIKVF VEHEPYEGDF TPDFTF

EF040-1 (SEQ ID NO:153)

TAGATTAGAA CCACTGGAGA AAAATCTCAT ATTTCTCTCG AGGAAAGGAA GTTGAGCACA
 ATGAACAAAA AAATTTTAAT GGGGCTATTA AGTGTCGTGA CCATTCCATT ACTTGCTGCG
 TGTCAGGAG GAGAAACACC TTCCGCAGCG TCAAAAAATA GTCAAACGGT GACTACTCAA
 AGTAGTGCAA AAACGTGAAAG CACCAGTACA ACCCGTTCGG TAGCTCAAAC AACATCAAAA
 GAGGAAGTGA AAGAACCGAT GAAGACCTAT GAAGTGGGTG CGCTTTTAGA AGCAGCCAAT
 CAACGAGATA CGAAGAAGGT CAAGGAAATT TTACAAGATA CTACTTATCA AGTGGATGAA
 GTCGACACAG AAGGCAACAC ACCGCTCAAT ATCGCTGTTT ACAATAATGA CATTGAGATT
 GCAAAAGCGT TGATTGATCG GGGTGCCGAT ATTAATCTGC AAAACAGCAT TAGTGATAGT
 CCCTATCTTT ATGCGGGAGC GCAAGGACGT ACGGAGATTT TAGCGTATAT GTTAAACAT
 GCGACCCAG ATTTAAATAA GCATAACCGT TACGGTGGCA ATGCGTTAAT TCCGGCAGCT
 GAAAAAGGAC ATATTGACAA TGTGAAGCTC TTGTTAGAAG ATGGACGAGA AGACATAGAT
 TTCCAAAATG ACTTTGGCTA TACAGCATTG ATTTAGGCAG TGGGGTTACG TGAAGGGAAC
 CAACTTTACC AAGATATTGT AAAATTGTTA ATGGAAAAATG GTGCGGATCA ATCCATTAAA
 GACAATTCTG GTCGAACAGC AATGGACTAT GCCAATCAAA AAGGTTATAC GGAAATTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAATTTTAG CACAGTACAA CTAA

EF040-2 (SEQ ID NO:154)

M NKKILMGLLS VVTIPLLAAC QGGETPSAAS KNSQTVTTQS
 SAKTESTSTT RSVAQTTSKE EVKEPMKTYE VGALLEEAAHQ RDTKKVKEIL QDTTYQVDEV
 DTEGNTPLNI AVHNNIDIEIA KALIDRGADI NLQNSISDSP YLYAGAQRRT EILAYMLKHA
 TPDNLKHNRY GGNALIPAAE KGHIDNVKLL LEDGREDIDF QNDFGYTALI EAVGLREGNQ
 LYQDIVKLLM ENGADQSIKD NSGRTAMDYA NQKGYTEISK ILAQYN

EF040-3 (SEQ ID NO:155)

AGCG TCAAAAAATA GTCAAACGGT GACTACTCAA
 AGTAGTGCAA AAACGTAAAG CACAGTACA ACCCGTTCGG TAGCTCAAAC AACATCAAAA
 GAGGAAGTGA AAGAACCGAT GAAGACCTAT GAAGTGGGTG CGCTTTTAGA AGCAGCCAAT
 CAACGAGATA CGAAGAAGGT CAAGGAAATT TTACAAGATA CTACTTATCA AGTGGATGAA
 GTCGACACAG AAGGCAACAC ACCGCTCAAT ATCGCTGTTC ACAATAATGA CATTGAGATT
 GCAAAAGCGT TGATTGATCG GGGTGCCGAT ATTAATCTGC AAAACAGCAT TAGTGATAGT
 CCCTATCTTT ATGCGGGAGC GCAAGGACGT ACGGAGATTT TAGCGTATAT GTTAAACAT
 GCGACCCAG ATTTAAATAA GCATAACCGT TACGGTGGCA ATGCGTTAAT TCCGGCAGCT
 GAAAAAGGAC ATATTGACAA TGTGAAGCTC TTGTTAGAAG ATGGACGAGA AGACATAGAT
 TTCCAAAATG ACTTTGGCTA TACAGCATTG ATTGAGGCAG TGGGGTTACG TGAAGGGAAC
 CAACTTTACC AAGATATTGT AAAATTGTTA ATGGAAAATG GTGCGGATCA ATCCATTAAA
 GACAATTCTG GTCGAACAGC AATGGACTAT GCCAATCAAA AAGGTTATAC GGAAATTAGT
 AAAATTTTAG CACAGTACAA C

EF040-4 (SEQ ID NO:156)

AS KNSQTVTTQS
 SAKTESTSTT RSVAQTTSKE EVKEPMKTYE VGALLEEAAHQ RDTKKVKEIL QDTTYQVDEV
 DTEGNTPLNI AVHNNIDIEIA KALIDRGADI NLQNSISDSP YLYAGAQRRT EILAYMLKHA
 TPDNLKHNRY GGNALIPAAE KGHIDNVKLL LEDGREDIDF QNDFGYTALI EAVGLREGNQ
 LYQDIVKLLM ENGADQSIKD NSGRTAMDYA NQKGYTEISK ILAQYN

EF041-1 (SEQ ID NO:157)

TAATTATTAA NTTCTGATTT TTCAGAAAAT ACAGATTGCA TTATTTTAGG AGGCAACACT
 ATGAAATTGA AAAAGTCATT AACATTCCGT GTGATTACAT TATTTAGCGT AACAACTTTA
 GCGGCTTGTC GAGGCGGCGG AACGTCAGAT AGCTCAAGCG CGTCTGGTGG CGGTAAGGCA
 AGTGGCGAAC AAGTTTTACG TGTCACAGAA CAACAAGAAA TGCCAACAGC TGATTTATCA
 CTAGCAACAG NCAGAATTAG TTTTATTGCA TTAAATAATG TATATGAAGG AATTTATCGT
 TTAGACAAAG ATAACAAAGT CCAACCTGCA GGTGCAGCGG AAAAAGCAGA AGTTTCTGAA
 GATGGACTAA CATACAAAAT TAAATTAAAT AAAGATGCAA AATGGTCAGA CGGTAAACCA
 GTGACTGCTA ATGACTATGT TTACGGATGG CAACGAACAG TTGATCCAGC GACAGCTTCT
 GAATATGCTT ATCTGTATGC CTCTGTAAAA AATGGTGATG CCATTGCTAA AGGGGAAAAA
 GATAATCAG AATTAGGAAT TAAAGCAGTC AGTGATACAG AATTAGAAAT CACTTTAGAA
 AAAGCAACAC CATACTTTGA TTACTTATTA GCTTTCCCAT CATTCTTCCC GCAACGTCAA
 GACATTGTGG AAAAAATATG TAAAAATTAT GCATCAAACA GCGAAAGTGC TGTCTACAAT
 GGTCCATTCG TCTTAGACGG CTTTGATGGT CCTGGTACAG ATACAAAATG GTCATTCAAG
 AAAAACGATC AATATTGGGA TAAAGATACT GTGAACTGG ACTCAGTAGA TGTGAATGTC
 GTGAAAGAAT CACCAACCGC GTTGAACCTG TTCCAAGATG GACAAACAGA CGATGTCGTT
 CTTTCTGGTG AATTAGCCCA ACAAATGGCC AATGACCCAG CTTTTGTAG TCAAAAAGAA
 GCATCAACAC AATATATGGA ACTAAATCAA CGTGATGAAA AATCACCATT TAGAAATGCG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACTTACGTA AAGCAATTTC TTACTCAATC GACCGTAAAG CGTTAGTTGA ATCAATCCTT
AGGGGATGG

EF041-2 (SEQ ID NO:158)

M KLKSLTFTGV ITLFSVTTLA ACGGGGTS DS SSASGGGKAS
GEQVLRVTEQ QEMPTADLSL ATXRISFIAL NNVYEGIYRL DKDNKVQPAG AA EKA EVSED
GLTYKIKLNK DAKWSDGKPV TANDYVYGWQ RTVDPATASE YAYLYASVKN GDAIAKGEKD
KSELGIKAVS DTELEITLEK ATPYFDYLLA FPSFFPQRQD IVEKYGKNYA SNSESA VYNG
PFVLDGFDGP GTDTKWSFKK NDQYWDKDTV KLDSVDVNVV KESPTALNLF QDGQTD DVVL
SGELAQQMAN DPAFVSQKEA STQYMELNQR DEKSPFRNAN LRKAISYSID RKALVESILR
GW

EF041-3 (SEQ ID NO:159)

TTGTG GAGGCGGCGG AACGTCAGAT AGCTCAAGCG CGTCTGGTGG CGGTAAGGCA
AGTGGCGAAC AAGTTTTACG TGTCACAGAA CAACAAGAAA TGCCAACAGC TGATTTATCA
CTAGCAACAG NCAGAATTAG TTTTATTGCA TTAAATAATG TATATGAAGG AATTTATCGT
TTAGACAAAG ATAACAAAGT CCAACCTGCA GGTGCAGCGG AAAAAGCAGA AGTTTCTGAA
GATGGACTAA CATACAAAAT TAAATTAAAT AAAGATGCAA AATGGTCAGA CCGTAAACCA
GTGACTGCTA ATGACTATGT TTACGGATGG CAACGAACAG TTGATCCAGC GACAGCTTCT
GAATATGCTT ATCTGTATGC CTCTGTAAAA AATGGTGATG CCATTGCTAA AGGGGAAAAA
GATAAATCAG AATTAGGAAT TAAAGCAGTC AGTGATACAG AATTAGAAAT CACTTTAGAA
AAAGCAACAC CATACTTTGA TTACTTATTA GCTTTCCCAT CATCTTCCC GCAACGTCAA
GACATTGTGG AAAAATATGG TAAAAATTAT GCATCAACA GCGAAAGTGC TGTCTACAA
GGTCCATTCG TCTTAGACGG CTTTGATGGT CCTGGTACAG ATACAAAATG GTCATTCAAG
AAAAACGATC AATATTGGGA TAAAGATACT GTGAAACTGG ACTCAGTAGA TGTGAATGTC
GTGAAAGAAT CACCAACCGC GTTGAACCTG TTCCAAGATG GACAAACAGA CGATGTCGTT
CTTTCTGGTG AATTAGCCCA ACAAATGGCC AATGACCCAG CTTTTGTAG TCAAAAAGAA
GCATCAACAC AATATATGGA ACTAAATCAA CGTGATGAAA AATCACCATT TAGAAATGCG
AACTTACGTA AAGCAATTTC TTACTCAATC GACCGTAAAG CGTTAGTTGA ATCAATCCTT
AGGGGATGG

EF041-4 (SEQ ID NO:160)

CGGGGTS DS SSASGGGKAS
GEQVLRVTEQ QEMPTADLSL ATXRISFIAL NNVYEGIYRL DKDNKVQPAG AA EKA EVSED
GLTYKIKLNK DAKWSDGKPV TANDYVYGWQ RTVDPATASE YAYLYASVKN GDAIAKGEKD
KSELGIKAVS DTELEITLEK ATPYFDYLLA FPSFFPQRQD IVEKYGKNYA SNSESA VYNG
PFVLDGFDGP GTDTKWSFKK NDQYWDKDTV KLDSVDVNVV KESPTALNLF QDGQTD DVVL
SGELAQQMAN DPAFVSQKEA STQYMELNQR DEKSPFRNAN LRKAISYSID RKALVESILR
GW

EF044-1 (SEQ ID NO:161)

TAAGATAAAA TTAGTTATAG CGTCTATAGG AGGAATAGTA TGAAAAAATT AGTTTGTGTT
ATTTTAGTTA TTTTTTTAAC AGGTTGTAGT TCTCAAAAAG CGAATGAACC TAAAAACAA
GAAAATTCTA CCAATCATAC AACATCAATA AAAAGCAGTA CTAATCATT CAGTTCTAGC
ATAGAAACAA GCTCTAATAA TAAACTAAAA GAAACTTCAG AAAGTGCCAG CACCACTCAA
ACTTCGTCAA AGTCGAAAAA TGAAGTATCT ACAAATGTCG AAGAAGCAAA TTCTTTAGAA
GCAACACCTT ATGCTGTCTGA TCTTAGTAGC TTAAACAATC CACTCGTATT TAATTTTAAA
GGAATGAATG TGCCAACCTC AATTACGTTA GAGAACTTAA ATTCAACACC AACTGCTACC
TTCCGAACTA AATTGTTTGG GGCTGAAAAA GGTCAAGTGA AAGAAGCCAT TAATAAATAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAGCTATCTA TAAATACAAT TCCTACAAAA GAGATTAGAA TATTTTCAGC GGCCGATAAC
 AGTATTCGCA CCGTTAAAGT AAATACAGAA TTAATTTTAG GAACTAATAT TTCTTCAAAC
 GATGAACAAA ATAGATCGGG CACTTTATAC TTATTCAACA ATAAAAATGG TTCGATATCT
 TTAATCACTC CTAACACGCG TGGCAATGTT ACGGATGATC AAAAAGACGT TATGCTAGAA
 GTAATTCAAT AA

EF044-2 (SEQ ID NO:162)

MKKLVCVI LVIFLTGCSQ KANEPKKQE NSTNHTTSIK SSTNHYSSSI
 ETSSNNKLKE TSESASTTQT SSKSKNEVST NVEEANSLEA TPYAVDLSSL NNPLVFNFKG
 MNVPTSITLE NLNSTPTATF RTKLFGAENG QVKEAINKYE LSINTIPTKE IRIFSAADNS
 IRTVKVNTEL ILGTNISSND EQNRSGTLYL FNNKNGSISL ITPNYAGNVT DDQKDVMLEV
 IQ

EF044-3 (SEQ ID NO:163)

TTGTAGT TCTCAAAAAG CGAATGAACC TAAAAACAA
 GAAAATTCTA CCAATCATAC AACATCAATA AAAAGCAGTA CTAATCATT A CAGTTCTAGC
 ATAGAAACAA GCTCTAATAA TAAACTAAAA GAACTTCAG AAAGTGCCAG CACCACTCAA
 ACTTCGTCAA AGTCGAAAAA TGAAGTATCT ACAAATGTCG AAGAAGCAAA TTCTTTAGAA
 GCAACACCTT ATGCTGTCTGA TCTTAGTAGC TTAAACAATC CACTCGTATT TAATTTTAAA
 GGAATGAATG TGCCAACTTC AATTACGTTA GAGAACTTAA ATTCAACACC AACTGCTACC
 TTCCGAAC TAATTGTTTGG GGCTGAAAAT GGTCAAGTGA AAGAAGCCAT TAATAAATAT
 GAGCTATCTA TAAATACAAT TCCTACAAAA GAGATTAGAA TATTTTCAGC GGCCGATAAC
 AGTATTCGCA CCGTTAAAGT AAATACAGAA TTAATTTTAG GAACTAATAT TTCTTCAAAC
 GATGAACAAA ATAGATCGGG CACTTTATAC TTATTCAACA ATAAAAATGG TTCGATATCT
 TTAATCACTC CTAACACGCG TGGCAATGTT ACGGATGATC AAAAAGACGT TATGCTAGAA
 GTAATTCAA

EF044-4 (SEQ ID NO:164)

CSS KANEPKKQE NSTNHTTSIK SSTNHYSSSI
 ETSSNNKLKE TSESASTTQT SSKSKNEVST NVEEANSLEA TPYAVDLSSL NNPLVFNFKG
 MNVPTSITLE NLNSTPTATF RTKLFGAENG QVKEAINKYE LSINTIPTKE IRIFSAADNS
 IRTVKVNTEL ILGTNISSND EQNRSGTLYL FNNKNGSISL ITPNYAGNVT DDQKDVMLEV
 IQ

EF045-1 (SEQ ID NO:165)

TAGCCAAAAA ATGAGGGAGG AAAAGAGATG AACAAGAAAC GGATTTTAGG TGCAATCACG
 TTAGCTTCTG TGTTAGTATT CGGGTTAGCT GCATGTGGTG GCGGCAATAA AGGCGGGGGC
 AATAAAGCAA CGGAAACAGA AGACATTTCA AAAATGCCAA TCGCTGTTAA AAATGATAAA
 AAAGCAATTG ATGGCGGTAC ATTAGATGTC GCTGTAGTTA TGGATACACA ATTCCAAGGA
 CTTTTCCAGC AAGAATTTTA TCAAGACAAC TATGATGCAC AATACATGCT TCCAACGGTA
 CAGCCATTAT TTAACAAATGA TGCAGACTTT AAGATTGTCG ATGGGGGTCC TGCGGATCTG
 AAATTAGATG AAGATGCCAA TACAGCAACC ATTAAATTAC GTGACAATTT GAAATGGTCT
 GACGGTAAAG ATGTGACAGC CGATGACGTG ATTTTCTCTT ATGAAGTCAT TGGTCATAAA
 GACTATACAG GGATTCGTTA TGATGATAAC TTTACGAATA TTGTTGGCAT GGAAGACTAC
 CATGATGGTA AATCGCCAAC CATTTCTGGC ATAGAAAAAG TCAATGATAA AGAAGTTAAA
 ATCACTTATA AAGAAGTTCA CCCAGGAATG CAACAATTAG GTGGCGGTGT TTGGGGCTCA
 GTTTTACCAA AACATGCCCT TGAAGGAATT GCTGTAAAG ACATGGAATC AAGCGATGCA
 GTTCGTAAAA ACCCTGTGAC TATTGGACCA TACTACATGA GTAATATTGT GACAGGTGAA
 TCTGTTGAAT ACCTACCAA TGAGCATTAC TACGGTGGTA AACCTAAATT AGATAAATTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGTTCAAAT CTGTTCCCTTC TGCGAGCATT GTAGAAGCGA TGAAAGCGAA ACAATACGAT
 ATTGCATTAT CAATGCCAAC AGATACGTAT CCAACATACA AAGATACTGA AGGGTATCAA
 ATCTTAGGAC GTCCCGAACA AGCCTACACG TATATTGGCT TTAAATATGGG TACGTTTGAC
 AAAGAAACAA ATACAGTGAA ATACAATCCA AAAGCTAAAA TGGCAGATAA AAGCTTACGT
 CAAGCCATGG GCTATGCAAT TGACAATGAT GCAGTCGGCC AAAAATTCTA CAACGGCTTA
 CGAACAGGGG CAACAACGTT AATCCCACCA GTCTTCAAGA GCTTGCATGA TAGCGAAGCG
 AAAGGCTATA CGCTTGATTT AGACAAAGCG AAAAAATTAT TAGACGATGC TGGTTATAAA
 GACGTAGACG GCGATGGCAT TCGCGAAGAC AAAGAAGGCA AACCCTAGA AATCAAGTTT
 GCTTCAATGT CAGGCGGCGA AACTGCACAA CCCTTGCTG ATTACTATGT CCAACAATGG
 AAAGAAATTG GCTTAAACGT AACGTATACA ACAGGACGCT TAATTGATTT CCAAGCATTC
 TATGATAAAT TGAAAAATGA TGACCCAGAA GTAGATATCT ATCAAGGCGC GTGGGGCACA
 GGTTCAGATC CTTACCAAC CGGCTTATAT GGTCCAACT CAGCCTTTAA CTATACACGT
 TTTGAGTCAG AAGAAAATAC TAAATTACTT GATGCGATTG ATTCAAAAGC ATCATTTGAT
 GAAGAAAAAC GTAAAAAAGC CTTCTACGAT TGGCAAGAGT ATGCCATTGA TGAAGCGTTT
 GTAATCCCAA CGCTTTACAG AAATGAAGTC TTGCCTGTCA ACGACCGTGT AGTTGACTTT
 ACTTGGGCAG TTGATACGAA AGATAATCCA TGGGCAACGG TGGGTGTCAC AGCAGACTCA
 CGGAAATAA

EF045-2 (SEQ ID NO:166)

MN KKRILGAILT ASVLVFGGLA CGGGNKGSGN KATETEDISK MPIAVKNDKK
 AIDGGTLDDA VVMDTQFQGL FQQEFYQDNY DAQYMLPTVQ PLFNNDADFK IVDGGPADLK
 LDEDANTATI KLRDNLKWSG GKDVTTADDVI FSYEVIGHKD YTGIRYDDNF TNIVGMEDYH
 DGKSPTISGI EKVDNKEVKI TYKEVHPGMQ QLGGGVWGSV LPKHAFEGIA VKDMESSDAV
 RKNPVTIGPY YMSNIVTGES VEYLPNEHY GGPVKLDKLV FKSVPASIV EAMKAKQYDI
 ALSMPTDTYP TYKDTEGYQI LGRPEQAYTY IGFKMGTFDK ETNTVKYNPK AKMADKSLRQ
 AMGYAIDNDA VGQKFYNGLR TGATTLIPPV FKSLLHDEAK GYTLDDLKAK KLLDDAGYKD
 VDGDGIREDK EGKPLEIKFA SMSGGETAQP LADYYVQQWK EIGLNVYTTT GRLIDFQAFY
 DKLKNDDEPV DIYQGAWGTG SDPSPTGLYG PNSAFNYTRF ESEENTKLLD AIDSASFDE
 EKRKKAFYDW QEYAIDEAFV IPTLYRNEVL PVNDRVVDFT WAVDTKDNPW ATVGVTADSR
 K

EF045-3 (SEQ ID NO:167)

ATGTGGTG GCGGCAATAA AGGCGGGGGC
 AATAAAGCAA CGGAAACAGA AGACATTTCA AAAATGCCAA TCGCTGTAA AAATGATAAA
 AAAGCAATTG ATGGCGGTAC ATTAGATGTC GCTGTAGTTA TGGATACACA ATTCCAAGGA
 CTTTTCCAGC AAGAATTTTA TCAAGACAAC TATGATGCAC AATACATGCT TCCAACGGTA
 CAGCCATTAT TTAACAATGA TGCAGACTTT AAGATTGTCTG ATGGGGGTCC TCGGATCTG
 AAATTAGATG AAGATGCCAA TACAGCAACC ATTAAATTAC GTGACAATTT GAAATGGTCT
 GACGGTAAAG ATGTGACAGC CGATGACGTG ATTTTCTCTT ATGAAGTCAT TGGTCATAAA
 GACTATACAG GGATTCGTTA TGATGATAAC TTTACGAATA TTGTTGGCAT GGAAGACTAC
 CATGATGGTA AATCGCCAAC CATTTCTGGC ATAGAAAAAG TCAATGATAA AGAAGTTAAA
 ATCACTTATA AAGAAGTTCA CCCAGGAATG CAACAATTAG GTGGCGGTGT TTGGGGCTCA
 GTTTTACCAA AACATGCCTT TGAAGGAATT GCTGTTAAAG ACATGGAATC AAGCGATGCA
 GTTCGTAAAA ACCCTGTGAC TATTGGACCA TACTACATGA GTAATATTGT GACAGGTGAA
 TCTGTTGAAT ACCTACCAA TGAGCATTAC TACGGTGGTA AACCTAAATT AGATAAATTA
 GTGTTCAAAT CTGTTCCCTTC TGCGAGCATT GTAGAAGCGA TGAAAGCGAA ACAATACGAT
 ATTGCATTAT CAATGCCAAC AGATACGTAT CCAACATACA AAGATACTGA AGGGTATCAA
 ATCTTAGGAC GTCCCGAACA AGCCTACACG TATATTGGCT TTAAATATGGG TACGTTTGAC
 AAAGAAACAA ATACAGTGAA ATACAATCCA AAAGCTAAAA TGGCAGATAA AAGCTTACGT
 CAAGCCATGG GCTATGCAAT TGACAATGAT GCAGTCGGCC AAAAATTCTA CAACGGCTTA
 CGAACAGGGG CAACAACGTT AATCCCACCA GTCTTCAAGA GCTTGCATGA TAGCGAAGCG
 AAAGGCTATA CGCTTGATTT AGACAAAGCG AAAAAATTAT TAGACGATGC TGGTTATAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GACGTAGACG GCGATGGCAT TCGCGAAGAC AAAGAAGGCA AACCACCTAGA AATCAAGTTT
 GCTTCAATGT CAGGCGGCGA AACTGCACAA CCACTTGCTG ATTACTATGT CCAACAATGG
 AAAGAAATTG GCTTAAACGT AACGTATACA ACAGGACGCT TAATTGATTT CCAAGCATTC
 TATGATAAAT TGAAAAATGA TGACCCAGAA GTAGATATCT ATCAAGGCGC GTGGGGCACA
 GGTTCAGATC CTTACCAAC CGGCTTATAT GGTCCAACT CAGCCTTTAA CTATACACGT
 TTTGAGTCAG AAGAAAAATAC TAAATTACTT GATGCGATTG ATTCAAAAAGC ATCATTGTAT
 GAAGAAAAAC GTAAAAAAGC CTTCTACGAT TGGCAAGAGT ATGCCATTGA TGAAGCGTTT
 GTAATCCCAA CGCTTTACAG AAATGAAGTC TTGCCTGTCA ACGACCGTGT AGTTGACTTT
 ACTTGGGCAG TTGATACGAA AGATAATCCA TGGGCAACGG TGGGTGTCAC AGCAGACTCA
 CGGAAA

EF045-4 (SEQ ID NO:168)

CGGGNKGSGN KATETEDISK MPIAVKNDKK
 AIDGGTLDVA VVMDTQFQGL FQQEFYQDNY DAQYMLPTVQ PLFNNADDFK IVDGGPADLK
 LDEDANTATI KLRDNLKWSG GKDVTADDVI FSYEVIGHKD YTGIRYDDNF TNIVGMEDYH
 DGKSPTISGI EKVNDEKVI TYKEVHPGMQ QLGGGVWGSV LPKHAFEGIA VKDMESSDAV
 RKNPVTIGPY YMSNIVTGES VEYLPNEHYG GKKPKLDKLV FKSVPASIV EAMKAKQYDI
 ALSMPTDTYP TYKDTEGYQI LGRPEQAYTY IGFKMGTFDK ETNTVKYNPK AKMADKSLRQ
 AMGYAIDNDA VGQKFYNGLR TGATTLIPPV FKSLHDSEAK GYTLDLKAK KLLDDAGYKD
 VDGDGIREDK EGKPLEIKFA SMSGGETAQP LADYVYQQWK EIGLNVYTT GRLIDFQAFY
 DKLKNDDEPV DIYQGAWGTG SDPSPTGLYG PNSAFNYTRF ESEENTKLLD AIDSKASFDE
 EKRKKAFYDW QEYAIDEAFV IPTLYRNEVL PVNDRVVDFT WAVDTKDNPW ATVGVTADSR
 K

EF046-1 (SEQ ID NO:169)

TAGGAGGATA TAATGAAAAA AAAACTTATT GTACTATTGT TAGCCTTATT TTTAACGGCA
 TGTAGTAATA ATACTGGGGG AAAAAATAGC GACGCTTCAT CTACTGAAGT ATCAACTAAG
 CAGCAAACTA CCCAGTCTTC TAAAAAAGAT AGTAGTAATC CGGACACAAC ACCAACTTCT
 ACATCATCTA TAACAATTGA AACAAACCGAG AATTTAAAGA ATAGAGAATT GAATCCAACA
 GATGATGTTT CAAAAACTAG ACGACAATTG TATGAACAAG GAATTAACAG TTCAACAATT
 ACGGATAAAG AACTAAAGGA ATATATATCA GAGGCTAAAG AACAAAAGAA AGATGTCATT
 AATTATATTA AGCAAAAA

EF046-2 (SEQ ID NO:170)

MKKKLIV LLLALFLTAC SNNTGGKNSD ASSTEVSTKQ QTTQSSKKDS SNPDTTPTST
 SSITTIETTEN LKNRELNPTD DVSKTRRQLY EQGINSSTIT DKELKEYISE AKEQKKDVIN
 YIKQK

EF046-3 (SEQ ID NO:171)

A
 TGTAGTAATA ATACTGGGGG AAAAAATAGC GACGCTTCAT CTACTGAAGT ATCAACTAAG
 CAGCAAACTA CCCAGTCTTC TAAAAAAGAT AGTAGTAATC CGGACACAAC ACCAACTTCT
 ACATCATCTA TAACAATTGA AACAAACCGAG AATTTAAAGA ATAGAGAATT GAATCCAACA
 GATGATGTTT CAAAAACTAG ACGACAATTG TATGAACAAG GAATTAACAG TTCAACAATT
 ACGGATAAAG AACTAAAGGA ATATATATCA GAGGCTAAAG AACAAAAGAA AGATGTCATT
 AATTATATTA AGCAAAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF046-4 (SEQ ID NO:172)

C SNNTGGKNSD ASSTEVSTKQ QTTQSSKKDS SNPDTTPTST
 SSITIEETTEN LKNRELNPTD DVSKTRRQLY EQGINSSTIT DKELKEYISE AKEQKKDVIN
 YIKQK

EF047-1 (SEQ ID NO:173)

TAGGGAAAAC AAGGAGGAAT TCTTATGAAA AAGATAGGGC TTATTTCTAG TGCTTTTCTT
 TTAACCCCTTG CTTTAGCAGC ATGCGGCGGC GGAAAAAGTA CAGAAAATAC GGATAGTCGT
 TCCAGTGCTG CGGAAAGTAC CACAGTCGAG AGTACAAAAG CATCTGCTAC AAAAGAATCA
 AGTAGCAAAG CAACAACAAA ATCTAGTGAT GCGAAACCGT CAGGAACAAC AACAGCTGAT
 TCGAAAGCAA CAGCTTCTTC TACGAAGGAA GCGGCAAATA ATGGCTCAGC AGAGAAGCAA
 TCACCAGCGA AAAATGCGAA TCCAGATGAC CAAGCCAACC AAGTGCTTAA CCAGCTAGCA
 AACATGTTTC CTGGTCAAGG CTTACCGCAG GCAATTTTAA CGAGTCAAAC GAATAACTTT
 TTAACCTGCAG CGACAACTTC ACAAGCGGAT CAAAACAATT TCCGTGTTTT ATATTATGCA
 GAAAAAGAAG CGATTCCAGT GAATGATGCA CGTGTCATC AGTTAACGCC AATTAGTTCT
 TTTGAGAAAA AAACATATGG CTCTGATGCC GAAGCAAAAA ATGCAGTGAA CCAAATCATT
 GACAATGGCG GTCAACCAGT AGATTTAGGT TACAATATTA CTGGGTATAA ACAAGGGGCG
 GCAGGTTCTA GTTACTTATC TTGGCAAGAA GGCAATTGGA GTTTAGTCGT ACGGGCCTCA
 AATATCAATG GTGAATCGCC TGATGATTTA GCGAAAAATG TTGTCAACAT TTTGGAACAA
 GAAACATTAC CAGCACCAGT TACCGTTGGT CAAATCACAC TGAACGTGGC AGGAACCACT
 GACTATAATC GAAACTCAGT AGTTTGGCAA GCCGGTACAG TCGTTTACTC TGTCCATCAT
 TTTGACCCAA TTCAAGCAGT GAAGATGGCA ACATCAATGT AA

EF047-2 (SEQ ID NO:174)

MKK IGLISSAFLL TLALAACGGG KSTENTDSRS SAAESTTVES TKASATKESS
 SKATTKSSDA KPSGTTTADS KATASSTKEA ANNGSAEKQS PAKNANPDDQ ANQVLNQLAN
 MFPQGQLPQA ILTSQTNNFL TAATTSQADQ NNFRVLYYAE KEAIPVNDAR VNQLTPISSF
 EKPTYGSDAE AKNAVNIQIID NGGQPVLDGY NITGYKQGA GSSYLSWQEG NWSLVVRASN
 INGESPDDLA KNVVNILEQE TLPAPNTVGQ ITLNVAGTTD YNRNSVWVQA GTVVYSVHHF
 DPIQAVKMAT SM

EF047-3 (SEQ ID NO:175)

ATGCGGCGGC GGAAAAAGTA CAGAAAATAC GGATAGTCGT
 TCCAGTGCTG CGGAAAGTAC CACAGTCGAG AGTACAAAAG CATCTGCTAC AAAAGAATCA
 AGTAGCAAAG CAACAACAAA ATCTAGTGAT GCGAAACCGT CAGGAACAAC AACAGCTGAT
 TCGAAAGCAA CAGCTTCTTC TACGAAGGAA GCGGCAAATA ATGGCTCAGC AGAGAAGCAA
 TCACCAGCGA AAAATGCGAA TCCAGATGAC CAAGCCAACC AAGTGCTTAA CCAGCTAGCA
 AACATGTTTC CTGGTCAAGG CTTACCGCAG GCAATTTTAA CGAGTCAAAC GAATAACTTT
 TTAACCTGCAG CGACAACTTC ACAAGCGGAT CAAAACAATT TCCGTGTTTT ATATTATGCA
 GAAAAAGAAG CGATTCCAGT GAATGATGCA CGTGTCATC AGTTAACGCC AATTAGTTCT
 TTTGAGAAAA AAACATATGG CTCTGATGCC GAAGCAAAAA ATGCAGTGAA CCAAATCATT
 GACAATGGCG GTCAACCAGT AGATTTAGGT TACAATATTA CTGGGTATAA ACAAGGGGCG
 GCAGGTTCTA GTTACTTATC TTGGCAAGAA GGCAATTGGA GTTTAGTCGT ACGGGCCTCA
 AATATCAATG GTGAATCGCC TGATGATTTA GCGAAAAATG TTGTCAACAT TTTGGAACAA
 GAAACATTAC CAGCACCAGT TACCGTTGGT CAAATCACAC TGAACGTGGC AGGAACCACT
 GACTATAATC GAAACTCAGT AGTTTGGCAA GCCGGTACAG TCGTTTACTC TGTCCATCAT
 TTTGACCCAA TTCAAGCAGT GAAGATGGCA ACATCAATGT AA

EF047-4 (SEQ ID NO:176)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGGG KSTENTDSRS SAAESTTIVES TKASATKESS

SKATTKSSDA KPSGTTTADS KATASSTKEA ANNGSAEKQS PAKNANPDDQ ANQVLNQLAN
 MFPQGGLPQA ILTSQTNNFL TAATTSQADQ NNFRVLYYAE KEAIPVNDAR VNQLTPISSE
 EKKTYGSDAE AKNAVNQIID NGGQPVDLGY NITGYKQGAA GSSYLSWQEG NWSLVVRASN
 INGESPDDL A KNVVNILEQE TLPAPNTVGQ I T L N V A G T T D Y N R N S V V W Q A G T V V Y S V H H F
 DPIQAVKMAT SM

EF048-1 (SEQ ID NO:177)

TAAGGAGAAA AGTTCATGAA AAAAAGAAAG GTTTTATTTA CAGCAGTTAT GGTATTGGCA
 GGATTACAGT TGCTAAGTGG TTGCGGCAAA ACAGAAGCTT CCGCAAATGA TACGGTAGTC
 TTGCGCTATG CGTATGCTAG TAATAGCCAA CCAGTTATCG ATTCTATGAA GAAATTCGGT
 GAATTAGTAG AGGAAAAAAC AGATGGTAAA GTTCAAATTG AATATTTTCC AGATGGTCAA
 TTAGGAGGAG AAACAGAACT AATTGAATTA ACACAAACAG GTGCAATTGA TTTTGCAAAG
 GTCAGTGGAT CAGCATTAGA AAGTTTTTCT AAAGATTATT CTGTATTTGC CATTCCGTAT
 ATTTTTTGATA ATGAAAAACA TTTTTTTAAA GTAATGGATA ATCAAGCGCT AATGCAACCA
 GTGTATGATT CTACAAAAAA ATTAGGATTT GTTGGTTTAA CTTATTATGA CTCTGGTCAA
 CGAAGTTTTT ATATGAGCAA AGGGCCTGTT ACATCTCCAG ATGATTTGAA AGGTAAAAAA
 ATTCGGGTCA TGCAAAGTGA AACC GCCATC AAAATGGTAG AACTTTTAGG GGGTTCGCCA
 GTACCTATGG GTAGTTCGGA AGTATATACT TCTCTACAAT CTAATCTAAT CAACGGTGCA
 GAGAATAATG AGTTCGTTTT ATATACAGCT GGT CATGGTG GTGTGGCTAA GTATTATTCT
 TATGATGAGC ATACTCGAGT GCCAGATATT GTGATTATGA ACGAGGGAAC AAAAGAACGT
 TTGACAGCGA AACAAGAACA AGCGATTGAA GAAGCAGCAA AAGAATCGAC CGCTTTTGAA
 AAAACGGTCT TTAAAGAAGC GGTGGAAGAA GAAAAGAAAA AAGCACAAAGC AGAATATGGC
 GTTGTGTTCA ATCAAGTAGA CAGTGAACCA TTCCAAAAAC TTGTTCAACC GTTGCATGAA
 TCATTCAAAA ATAGCTCAGA ACATGGCGAA CTGTATCAGG CTATTGCCA GTTGGCGGAC
 TAA

EF048-2 (SEQ ID NO:178)

MKKRKV LFTAVMVLG LQLLSGCGKT EASANDTVVL RYAYASNSQP VIDSMKKFGE
 LVEEKTGDKV QIEYFPDQQL GGETELIELT QTGAIDFAKV SGSALSFASK DYSVFAIPYI
 FDNEKHFFKV MDNQALMQPV YDSTKKLGFV GLTYYDSGQR SFYMSKGPVT SPDDLKGGKI
 RVMQSETAIK MVELLGGSPV PMGSSEVYTS LQSNLINGAE NNEFVLYTAG HGGVAKYYSY
 DEHTRVPDIV IMNEGTKERL TAKQEQAIEE AAKESTAF EK TVFKEAVEEE KKKAQAEYGV
 VFNQVDSEPF QKL VQPLHES FKNSSEHGEL YQAIRQLAD

EF048-3 (SEQ ID NO:179)

TTGCGGCAAA ACAGAAGCTT CCGCAAATGA TACGGTAGTC
 TTGCGCTATG CGTATGCTAG TAATAGCCAA CCAGTTATCG ATTCTATGAA GAAATTCGGT
 GAATTAGTAG AGGAAAAAAC AGATGGTAAA GTTCAAATTG AATATTTTCC AGATGGTCAA
 TTAGGAGGAG AAACAGAACT AATTGAATTA ACACAAACAG GTGCAATTGA TTTTGCAAAG
 GTCAGTGGAT CAGCATTAGA AAGTTTTTCT AAAGATTATT CTGTATTTGC CATTCCGTAT
 ATTTTTTGATA ATGAAAAACA TTTTTTTAAA GTAATGGATA ATCAAGCGCT AATGCAACCA
 GTGTATGATT CTACAAAAAA ATTAGGATTT GTTGGTTTAA CTTATTATGA CTCTGGTCAA
 CGAAGTTTTT ATATGAGCAA AGGGCCTGTT ACATCTCCAG ATGATTTGAA AGGTAAAAAA
 ATTCGGGTCA TGCAAAGTGA AACC GCCATC AAAATGGTAG AACTTTTAGG GGGTTCGCCA
 GTACCTATGG GTAGTTCGGA AGTATATACT TCTCTACAAT CTAATCTAAT CAACGGTGCA
 GAGAATAATG AGTTCGTTTT ATATACAGCT GGT CATGGTG GTGTGGCTAA GTATTATTCT
 TATGATGAGC ATACTCGAGT GCCAGATATT GTGATTATGA ACGAGGGAAC AAAAGAACGT
 TTGACAGCGA AACAAGAACA AGCGATTGAA GAAGCAGCAA AAGAATCGAC CGCTTTTGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAACGGTCT TTAAAGAAGC GGTGAAGAA GAAAAGAAAA AAGCACAAGC AGAATATGGC
 GTTGTGTTCA ATCAAGTAGA CAGTGAACCA TTCCAAAAAC TTGTTCAACC GTTGCATGAA
 TCATTCAAAA ATAGCTCAGA ACATGGCGAA CTGTATCAGG CTATTCGCCA GTTGGCGGAC
 TAA

EF048-4 (SEQ ID NO:180)

CGKT EASANDTVVL RYAYASNSQP VIDSMKKFGE
 LVEEKTGDKV QIEYFPDGQL GGETELIELT QTGAIDFAKV SGSALSFASK DYSVFAIPYI
 FDNEKHFFKV MDNQALMQPV YDSTKKLGFV GLTYYDSGQR SFYMSKGPVT SPDDLKGGKI
 RVMQSETAIK MVELLGSPV PMGSSEVYTS LQSNLINGAE NNEFVLYTAG HGGVAKYYSY
 DEHTRVPDIV IMNEGTERL TAKQEQAIEE AAKESTAFEK TVFKEAVEEE KKKAQAEYGV
 VFNQVDSEPF QKLVQPLHES FKNSSEHGEL YQAIRQLAD

EF049-1 (SEQ ID NO:181)

TGAGACTCTT TCTTTTTTCAA AATGAGGTAT GGTATAGTTA TAACAGANAT AAAACTANAA
 AAAACAGGAG TGCATAAGAG AATGAAGAAA AAATAATCT TAGCTGCAGC GGGCGCAATG
 GCCGTTTTTA GTTTAGCAGC GTGTTCAAGC GGTTCAAAAG ATATCGCAAC AATGAAAGGT
 TCAACAATTA CTGTTGATGA TTTTATAAAC CAAATTAAAG AACAAAGCAC TAGCCAACAA
 GCGTTTAGCC AAATGGTTAT TTATAAAGTC TTTGAAGAAA AATATGGCGA CAAAGTAACT
 GACAAAGANA TTCAAAAAAA CTTTGACGAA GCCAAAGAAC AAGTAGAAGC ACAAGGCGGA
 AAGTTCTCTG ATGCATTAAA ACAAGCTGGT TTAAGTAAA AAACATTCAA GAAACAGTTA
 AAACAAAGAG CAGCCTATGA TGCAGGTCTA AAAGCCCACT TAAAAATTAC AGATGAAGAC
 TTAAAAACAG CTTGGGCAAG TTTCCATCCA GAAGTAGAAG CACAAATTAT CCAAGTTGCT
 TCAGAAGATG ATGCCAAAGC TGTCAGAAAA GAAATCACTG ACGGCGGCGA TTTACAAAAA
 ATTGCTAAAG AAAAATCAAC AGATACTGCT ACGAAAAAAG ATGGCGGTAA AATTAAATTT
 GATTACAAAG CAACAACCTGT TCCTGCCGAA GTTAAAGAAG CTGCCTTCAA ATTAAAGAT
 GGCGAAGTGT CAGAACCAAT TGCTGCAACA AATATGCAAA CCTACCAAAC AACCTACTAT
 GTAGTGAAAA TACGCAAAAA CAAAGCAAAA GGCAATGACA TGAAACCTTA TGAAAAAGAG
 ATCAAGAAAA TTGCTGAAGA AACAAAAATTA GCCGATCAAA CATTTGTTTC GAAAGTCATT
 AGTGACGAAT TAAAAGCGGC CAATGTGAAA ATTAAAGATG ATGCCTTCAA GAACGCTTTA
 GCAGGCTACA TGCAAACTGA ATCTTCAAGC GCTTCTTCAAG AGAAAAAGA ATCAAAATCA
 AGTGATTCTA AAACAAGCGA TACCAAAACA AGCGACTCTG AAAAAGCAAC AGATTCTTCA
 AGCAAAACAA CAGAATCTTC TTCTAAATAA

EF049-2 (SEQ ID NO:182)

MKKK LILAAAGAMA VFSLAACSSG SKDIATMKGS
 TITVDDFYNQ IKEQSTSQQA FSQMVYKVF EEKYGDKVTD KXIQKNFDEA KEQVEAQGGK
 FSDALKQAGL TEKTFKKQLK QRAAYDAGLK AHLKITDEDL KTAWASFHPE VEAQIIQVAS
 EDDAKAVKKE ITDGGDFTKI AKEKSTDAT KKGKIKFD SQATTVPFV KEAAFKLKDG
 EVSEPIAATN MQTYQTTYV VKMTKNKAKG NDMKPYEKEI KKIAEETKLA DQTFVSKVIS
 DELKAANVKI KDDAFKNALA GYMQTESSA SSEKKESKSS DSKTSDTKTS DSEKATDSSS
 KTESSSK

EF049-3 (SEQ ID NO:183)

GTGTTCAAGC GGTTCAAAAG ATATCGCAAC AATGAAAGGT
 TCAACAATTA CTGTTGATGA TTTTATAAAC CAAATTAAAG AACAAAGCAC TAGCCAACAA
 GCGTTTAGCC AAATGGTTAT TTATAAAGTC TTTGAAGAAA AATATGGCGA CAAAGTAACT
 GACAAAGANA TTCAAAAAAA CTTTGACGAA GCCAAAGAAC AAGTAGAAGC ACAAGGCGGA
 AAGTTCTCTG ATGCATTAAA ACAAGCTGGT TTAAGTAAA AAACATTCAA GAAACAGTTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

AAACAAAGAG CAGCCTATGA TGCAGGTCTA AAAGCCCACT TAAAAATTAC AGATGAAGAC
TTAAAAACAG CTTGGGCAAG TTTCCATCCA GAAGTAGAAG CACAAATTAT CCAAGTTGCT
TCAGAAGATG ATGCCAAAGC TGTCAAGAAA GAAATCACTG ACGGCGGCGA TTTACAAAAA
ATTGCTAAAG AAAAATCAAC AGATACTGCT ACGAAAAAAG ATGGCGGTAA AATTAAATTT
GATTCACAAG CAACAACGTG TCCTGCCGAA GTTAAAGAAG CTGCCTTCAA ATTTAAAGAT
GGCGAAGTGT CAGAACCAAT TGCTGCAACA AATATGCAAA CCTACCAAAC AACCTACTAT
GTAGTGAAAA TGACGAAAAA CAAAGCAAAA GGCAATGACA TGAAACCTTA TGAAAAAGAG
ATCAAGAAAA TTGCTGAAGA AACAAAATTA GCCGATCAAA CATTTGTTTC GAAAGTCATT
AGTGACGAAT TAAAAGCGGC CAATGTGAAA ATTAAAGATG ATGCCTTCAA GAACGCTTTA
GCAGGCTACA TGCAAACTGA ATCTTCAAGC GCTTCTTCAG AGAAAAAGA ATCAAAATCA
AGTGATTCTA AAACAAGCGA TACCAAAACA AGCGACTCTG AAAAAGCAAC AGATTCTTCA
AGCAAAACAA CAGAATCTTC TTCTAAATAA

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EF049-4 (SEQ ID NO:184)

CSSG SKDIATMKGS

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TITVDDFYNQ IKEQSTSQQA FSQMVYKVF EEKYGDKVTD KXIQKNFDEA KEQVEAQGGK
FSDALKQAGL TEKTFKKQLK QRAAYDAGLK AHLKITDEDL KTAWASFHPE VEAQIIQVAS
EDDAKAVKKE ITDGGDFTKI AKEKSTDAT KKDGGKIKFD SQATTVP AEV KEAAFKLKD G
EVSEPIAATN MQTYQTTYV VKMTKNKAKG NDMKPYEKEI KKIAEETKLA DQTFVSKVIS
DELKAANVKI KDDAFKNALA GYMQTESSA SSEKKESKSS DSKTSDTKTS DSEKATDSSS
KTTESSSK

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EF050-1 (SEQ ID NO:185)

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TAGGGTCTGG AAAAGCAGTC AACTGACTTC TTTTCCAAGC CCTTTTTTAC TTCATCGCAG
AAAGGATGNA AAAAAATGAA CATGCCCAAA AATATCNGTT ATTTTCTTT GCTAATGGGT
CTTGTTCTAT TATTAAGTGC TTGCCAAATT GGGGCAACTA CGAAGGATGA CAACCAAGCC
GCCACAAAAG AAGCAACTGT TGAGTTAAAC CGCACAAACA CACCAACGCT TTTTTTTCAT
GGTTACGCAG GAACTAAAAA TTCGTTTGGC TCGTTACTGC ATCGCTTGA GAAACAAGGT
GCCACAAC TC AAGAATTAGT GCTACTCGTT AAACCTGATG GGACCGTGGT TAAAGAGCGA
GGAGCTTTAA GTGGCAAAGC GACGAATCCC AGTGTTCAAG TTCTATTGA AGATAATAAA
AACAATGAAT GGAATCAAAC AGAATGGATA AAAAACACAT TACTCTATTT ACAAAAAAAT
TATCAAGTGA ACAAAGCCAA TATTGTCGGG CACTCTATGG GTGGTGTTAG TGGTTTACGT
TATTTAGGAA CCTATGGGCA AGATACATCG TTACCTAAAA TTGAAAAAT CGTCAGCATT
GGAGCACCTT TCAATGATTT TATTGATACG AGTCAACAGC AAACCATCGA AACGGAAC TA
GAAAACGGCC CCACAGAAAA AAGTAGCCGC TATTTGGATT ATCAAGAGAT GATTAATGTT
GTTCCAGAAA AACTGCCCAT TTTATTAATT GGTGGTCAAT TAAGTCCAAC AGATTTAAGT
GATGGAACGG TGCCGTTATC TAGTGCCCTTA GCAGTCAACG CCTTGCTAAG ACAGCGAGGA
ACTCAAGTCA CTAGCCAGAT TATTAAAGGA GAAAATGCAC AACATAGTCA ATTACATGAA
AATCCTGAAG TAGATCAATT GCTAATCGAA TTTCTATGGC CGAGTAAAAA ATAG

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EF050-2 (SEQ ID NO:186)

MNMPKN IXYFSLLMGL VLLLSACQIG ATTKDDNQAA

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TKEATVELNR TTPTLFFHG YAGTKNSFGS LLHRLEKQGA TTQELVLLVK PDGTVVKERG
ALSGKATNPS VQVLFEDNKN NEWNQTEWIK NTLlyLQKNY QVNKANIVGH SMGGVSGRLY
LGTYGQDTSI PKIEKFVSI APFNDFIDTS QQQTIELE NGPTEKSSRY LDYQEMINVV
PEKLPILLIG QLSPTDLSD GTVPLSSALA VNALLRQRGT QVTSQIIKGE NAQHSQHLHEN
PEVDQLLIEF LWPSKK

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EF050-3 (SEQ ID NO:187)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TTGCCAAATT GGGGCAACTA CGAAGGATGA CAACCAAGCC
GCCACAAAAG AAGCAACTGT TGAGTTAAAC CGCACAAACA CACCAACGCT TTTTTTTCAT
GGTTACGCAG GAACATAAAA TTCGTTTGGC TCGTTACTGC ATCGCTTGGA GAAACAAGGT
GCCACAACCTC AAGAATTAGT GCTACTCGTT AAACCTGATG GGACCGTGGT TAAAGAGCGA
GGAGCTTTAA GTGGCAAAGC GACGAATCCC AGTGTTC AAG TTCTATTTGA AGATAATAAA
AACAAATGAAT GGAATCAAAC AGAATGGATA AAAAACACAT TACTCTATTT ACAAAAAAAT
TATCAAGTGA ACAAAGCCAA TATTGTCGGG CACTCTATGG GTGGTGTTAG TGGTTTACGT
TATTTAGGAA CCTATGGGCA AGATACATCG TTACCTAAAA TTGAAAAAAT CGTCAGCATT
GGAGCACCTT TCAATGATTT TATTGATACG AGTCAACAGC AAACCATCGA AACGGAAC TA
GAAAACGGCC CCACAGAAAA AAGTAGCCGC TATTTGGATT ATCAAGAGAT GATTAATGTT
GTTCCAGAAA AACTGCCCCAT TTTATTAATT GGTGGTCAAT TAAGTCCAAC AGATTTAAGT
GATGGAACGG TGCCGTTATC TAGTGCCTTA GCAGTCAACG CCTTGCTAAG ACAGCGAGGA
ACTCAAGTCA CTAGCCAGAT TATTAAAGGA GAAAATGCAC AACATAGTCA ATTACATGAA
AATCCTGAAG TAGATCAATT GCTAATCGAA TTTCTATGGC CGAGTAAAAA ATAG

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EF050-4 (SEQ ID NO:188)

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CQIG ATTKDDNQAA
TKEATVELNR TTTPTLFFHG YAGTKNSFGS LLHRLEKQGA TTQELVLLVK PDGTVVKERG
ALSGKATNPS VQVLFEDNKN NEWNQTEWIK NTLLEYLQKNY QVNKANIVGH SMGGVSGRLRY
LGTYGQDTSI PKIEKFVSIG APFNDFIDTS QQQTIELE NGPTEKSSRY LDYQEMINVV
PEKLPILLIG GQLSPDLSL GTVPLSSALA VNALLRQRGT QVTSQIIKGE NAQHSQHLHEN
PEVDQLLIEF LWPSKK

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EF051-1 (SEQ ID NO:189)

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TAAAGAAAA GAGGCGTTCA AATGTCTAAA CAAAAAAGG CTGTGTTTCCT GCTTAGTTTCA
TTCAGTTTAG TTGCCCTAAT TGCTGCATGT ACAAATCAGC CGCAAAAAGA AACAGTTTCA
ACAAAAAAG AAGAAATAAC CCTTGCGGCA GCAGCTAGCT TAGAATCAGT CATGGAGAAG
AAAATTATTC CAGCCTTTGA AAAAGAGCAT CCAGATATTC AGGTAACTGG AACCTATGAT
AGTTCTGGAA AATTACAGAT GCAAATTGAA AAAGGCCTAA AAGCCGATGT ATTTTTCTCA
GCTTCGACAA AACAAATGAA TGCATTGGTT GCAGAAAAAC TAATTAATAA AAAAAGTGTC
GTTCTTTTAT TGGAAAACCA GTCGTTCTT ATTGTGCCTA ACCAAGATCA AGCAAAGTGG
CATGATTTTT CTGATTTAAA AAAAGCCCAA ATGATAGCAA TTGGTGATCC TGCAAGTGTT
CCAGCTGGTC AATATGCCGA AGAAGGCTTA AAAGCTTTAG GCGCTTGGTC TTATGTAGAA
AAACACGCAA GCTTTGGCAC GAATGTAACA GAAGTCCTTG AATGGGTAGC TAATGCAAGT
GCAGAAGCTG GCTTAGTTTA TGCACAGAT GCAGCAACCA ATTCAAAAGT AGCGATTGTT
GCGGCCATGC CTGAAGCTGT TTTGAAAAAG CCAATTATCT ATCCAGTTGG TAAAGTTGCC
GCCTCTAAGA AACAAAAATC AGCAGATGCT TTTTAAATT TTTTACAGAG TCAACAATGC
AGAAAAATAT TTGANAATAT TGGCTTTAAG TTAACAAAGT AG

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EF051-2 (SEQ ID NO:190)

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MSKQ KKAFLSLF SLVALIACT NQPKETVST KKEEITLAAA ASLESVMEKK
IIPAFEKEHP DIQVTGTYDS SGKLQMIEK GLKADVFFSA STKQMNALVA EKLINKKSVV
PLENLVLVI VPNQDQAKWH DFSDLKKAQM IAIGDPASVP AGQYAEGLK ALGAWSYVEK
HASFQTNVTE VLEWVANASA EAGLVYATDA ATNSKVAIVA AMPEAVLKKP IIYPVGKVAA
SKKQKSADAF LNFLQSQQR KYFXNIGFKL TK

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EF051-3 (SEQ ID NO:191)

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ATGT ACAAATCAGC CGCAAAAAGA AACAGTTTCA
ACAAAAAAG AAGAAATAAC CCTTGCGGCA GCAGCTAGCT TAGAATCAGT CATGGAGAAG

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAATTATTC CAGCCTTTGA AAAAGAGCAT CCAGATATTC AGGTAACCTGG AACCTATGAT
 AGTTCTGGAA AATTACAGAT GCAAATTGAA AAAGGCCTAA AAGCCGATGT ATTTTCTCA
 GCTTCGACAA AACAAATGAA TGCATTGGTT GCAGAAAAAC TAATTAATAA AAAAAGTGTC
 GTTCCTTTAT TGGAAAACCA GTCGTTCTT ATTGTGCCTA ACCAAGATCA AGCAAAGTGG
 CATGATTTTT CTGATTTAAA AAAAGCCCAA ATGATAGCAA TTGGTGATCC TGCAAGTGTT
 CCAGCTGGTC AATATGCCGA AGAAGGCTTA AAAGCTTTAG GCGCTTGGTC TTATGTAGAA
 AAACACGCAA GCTTTGGCAC GAATGTAACA GAAGTCCTTG AATGGGTAGC TAATGCAAGT
 GCAGAAGCTG GCTTAGTTTA TGCGACAGAT GCAGCAACCA ATTCAAAAGT AGCGATTGTT
 GCGGCCATGC CTGAAGCTGT TTTGAAAAAG CCAATTATCT ATCCAGTTGG TAAAGTTGCC
 GCCTCTAAGA AACAAAAATC AGCAGATGCT TTTTAAATT TTTTACAGAG TCAACAATGC
 AGAAAATATT TTGANAATAT TGGCTTTAAG TTAACAAAGT AG

EF051-4 (SEQ ID NO:192)

CT NQPQKETVST KKEEITLAAA ASLESVMEKK
 IIPAFEKEHP DIQVTGTYDS SGKLQMQIEK GLKADVFFSA STKQMNALVA EKLINKKSVV
 PLENQLVLI VPNQDQAKWH DFSDLKKAQM IAIGDPASVP AGQYAEGLK ALGAWSYVEK
 HASFGTNVTE VLEWVANASA EAGLVYATDA ATNSKVAIVA AMPEAVLKKP IIYPVGKVAA
 SKKQKSADAF LNFLQSQQCR KYFXNIGFKL TK

EF052-1 (SEQ ID NO:193)

TAAAGTAGGA GAAGCGCAAG CGAAAAAAGT GAATCAATCG GCAGCGTATC AAGTAGTGAT
 CCCACAATGG GTACCATGGG TAGCATTATC TTTGACAGTA GCACTTGCTG GATTGATTGC
 TTAATTAGTT CGTCGTGGAG AGAAGTGGAA AAACGAAGGG GAAGTGACAT AATGAGANGA
 NGAAATCTTC NGTTTTTATT ATTGTTGGTT CTATTAATTT ATATTCCTCA ACAAATCTAT
 GCAGAAAAA GGGAGACCAC AGAAGTCGGA ATCGGGTTTA CAAAACTTC AGACATACCA
 TCAAAAAAAT ATCCAGTTGT GAATGTATTG CCGCAAACAA CCATTCAATC GCTATCAATC
 GTTCGTAGCA GAACGCAAAT AAAAAGATTA CCTAAACTG GTGACAATCG AATAACTTGG
 CTAAGCTGGT TTGGCATATT GTTTTAAATA AGTAGTTTTT GGCTGTTTCT ATTTAGACAA
 TTATGTAGAA AAGGAGAATA A

EF052-2 (SEQ ID NO:194)

MRXX
 NLXFLLLLVL LIYIPQTTYA ENRETTEVGI GFTKTS DIPS KKNPVVNVLP QTTIQSLSIV
 RSRTQIKRLP KTGDNRITWL SWFGILFLIS SFWLFLFRQL CRKGE

EF052-3 (SEQ ID NO:195)

AGAAAATA GGGAGACCAC AGAAGTCGGA ATCGGGTTTA CAAAACTTC AGACATACCA
 TCAAAAAAAT ATCCAGTTGT GAATGTATTG CCGCAAACAA CCATTCAATC GCTATCAATC
 GTTCGTAGCA GAACGCAAAT AAAAAGAT

EF052-4 (SEQ ID NO:196)

ENRETTEVGI GFTKTS DIPS KKNPVVNVLP QTTIQSLSIV
 RSRTQIKR

EF053-1 (SEQ ID NO:197)

TAGTCATGGC ACCATAACAA GGAGGAGAGA AGTGAGATGA AAAAATACCT TTTGCTTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TGTTTTTTAG GTCTTTTCAG CTTCTGTCAT TCAGACACTG CGTTTGGAGA AGCAGCTTAT
 GAAAATAGTG GTGTTGTCTC CTTTATGGA ACGTATGAAT ATCCACAGA AGAGTCGACA
 ACAGCGACTA GTAATTCTTC CACAACGACC GAACCCACCA AGCCAGCTGA CGGAGGCGCT
 TCATCCGTCC TTTCTTCTGG CGTATATGGA TCGCGACAAG GAAGATTACC AGCGACAGGT
 ACCACCAATC AAGCACCATT TATTTATTTG GGAATCAGCC TTATCACTAT AGGCATATTA
 TTTATTAAAA GGAGAAGAGA AGATGAAAAA AACAGTATTA GCAGTAGTAG GGATTGTAGG
 ATTTAG

EF053-2 (SEQ ID NO:198)

MKYYLLLS SC FLGLFSFCHS DTAFGEAAAYE NSGVVSFYGT YEYPTEESTT
 ATSNSSTTTE PTKPADGGAS SVLSSGVYGS RQGRLPATGT TNQAPFIYLG ISLITIGILF
 IKRRREDEKN SISSSRDCRI

EF053-3 (SEQ ID NO:199)

TTTGGAGA AGCAGCTTAT
 GAAAATAGTG GTGTTGTCTC CTTTATGGA ACGTATGAAT ATCCACAGA AGAGTCGACA
 ACAGCGACTA GTAATTCTTC CACAACGACC GAACCCACCA AGCCAGCTGA CGGAGGCGCT
 TCATCCGTCC TTTCTTCTGG CGTATATGGA TCGCGACAAG GAAGA

EF053-4 (SEQ ID NO:200)

FGEEAAAYE NSGVVSFYGT YEYPTEESTT
 ATSNSSTTTE PTKPADGGAS SVLSSGVYGS RQGR

EF054-1 (SEQ ID NO:201)

TAAATAAAAA ATTATTTTGA GGAAATTACA ATGAAAAAAA TTATTTTATC AAGCTTGTTT
 AGTGCAGTAC TAGTATTCGG TGGCGGAAGT ATAACAGCAT TCGCTGACGA TTTAGGACCA
 ACAGATCCAG CAACTCCACC AATTACCGAA CCAACTGATT CTAGTGAACC TACGAATCCT
 ACTGAGCCGG TGGATCCTGC AGAACCAGCA GTAATACCAA CTGATCCAAC AGAACCAAGC
 AAGCCAAACG AGCCTACAAC ACCGAGTGAG CCAGAAAAGC CAACAGAACC AACAACGCCA
 ATTGATCCTG GAACGCCGGT TGAACCGACT GAACCAAGCG AGCCAACAGA ACCTAGTCAA
 CCAACCGAGC CTACAACACC AAGCGAACCA GAAAAACCTG TTA CTCCAGA ACAACCGAAA
 GAACCAACTC AACCAGTGAT TCCAGAAAAA CCAGCAGAAC CAGAAACACC AAAAACTCCT
 GAACAGCCCA CTAAACCAAT AGACGTAGTC GTTACACCTA GTGGAGAAAT TGATAAAACG
 AATCAATCGG CAGGAACACA ACCAAGTATT CCTATTGAAA CAAGCAACTT AGCGGAGGTA
 ACACATGTAC CAAGTGAAAC TACTCCAATT ACAACAGAAG CTGGGGAAGA AATTGTAGCA
 GTAGATAAAG GTGTTCCGTT AACCAAAACA CCAGAAGGAT TAAAACCAAT TAGCAGCTCG
 TATAAGGTTT TACCTAGCGG AAACGTTGAG GTAAAAGCAA GTGATGGAAA AATGAAAGTA
 TTGCCACATA CAGGAGAGAA ATTCACTCTC CTTTCTCTG TATTGGGAAG CTTCTTTGTA
 TTAATTTTCA GATTCTTTTT CTTTAAAAAG AATAAGAAAA AAGCTTAA

EF054-2 (SEQ ID NO:202)

M KKIILSSLFS AVLVFGGGSI TAFADDLGPT DPATPPITEP TDSSEPTNPT
 EPVDPAEPPV IPTDPTEPSK PTEPTTPSEP EKPTEPTTPI DPGTFVEPTE PSEPTEPSQP
 TEPTTPSEPE KPVTPEQPK EPTQPIVEKP AEPETPKTPE QPTKPIDVVV TPSGEIDKTN
 QSAGTQPSIP IETSNLAEVT HVPSETTPI TTEAGEEIVAV DKGVP LTKTP EGLKPISSSY
 KVLPSGNVEV KASDGKMKVL PHTGEKFTLL FSVLGSFFVL ISGFFFFKKN KKKA

EF054-3 (SEQ ID NO:203)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

A

ACAGATCCAG CAACTCCACC AATTACCGAA CCAACTGATT CTAGTGAACC TACGAATCCT
 ACTGAGCCGG TGGATCCTGC AGAACCGCCA GTAATACCAA CTGATCCAAC AGAACCAAGC
 AAGCCAACCG AGCCTACAAC ACCGAGTGAG CCAGAAAAGC CAACAGAACC AACAACGCCA
 ATTGATCCTG GAACGCCGGT TGAACCGACT GAACCAAGCG AGCCAACAGA ACCTAGTCAA
 CCAACCGAGC CTACAACACC AAGCGAACCA GAAAAACCTG TTACTCCAGA ACAACCGAAA
 GAACCAACTC AACCAGTGAT TCCAGAAAAA CCAGCAGAAC CAGAAACACC AAAAACTCCT
 GAACAGCCCA CTAAACCAAT AGACGTAGTC GTTACACCTA GTGGAGAAAT TGATAAAACG
 AATCAATCGG CAGGAACACA ACCAAGTATT CCTATTGAAA CAAGCAACTT AGCGGAGGTA
 ACACATGTAC CAAGTGAAAC TACTCCAATT ACAACAGAAG CTGGGGAAGA AATTGTAGCA
 GTAGATAAAG GTGTTCCGTT AACCAAAACA CCAGAAGGAT TAAAACCAAT TAGCAGCTCG
 TATAAGGTTT TACCTAGCGG AAACGTTGAG GTAAAAGCAA GTGATGGAAA AATGAAAGTA

T

EF054-4 (SEQ ID NO:204)

DDLGP DPATPPITEP TDSSEPTNPT
 EPVDP AEP PV IPTDPTEPSK PTEPTTPSEP EKPTEPTTPI DPGTPVEPTE PSEPTEPSQP
 TEPTTPSEPE KPVTPEQPK EPTQPIVEKP AEPETPKTPE QPTKPIDVVV TPSGEIDKTN
 QSAGTQPSIP IETSNLAEVT HVPSETTPIT TEAGEEIVAV DKGVP LTKTP EGLKPISSSY
 KVLPSGNVEV KASDGKMKV

EF055-1 (SEQ ID NO:205)

TAACAAAAGG TTGTTTTGTC TTTCTTGTGT AAAAGGGCAA GAAAGGCTAG CGAGTTAAAA
 GGAGGTTTTT CAATG.AAAAA AAAGCGTTAT TTAATGATTG TGTGTCTACT ATCTTCTCCT
 AGTTTTTTTA TAAATGTTGA AGCGTCTGAT GGTGGTTCTA GTTCGGTGGG GATTGAATTT
 TACCAAAATC CGAGAACACC CGCTCCTAAA GATCCCCAC CGAAAACAGA TGCGCCAGCT
 GCTGATCCCA AGGAACCAGC TGGTCCTCCG CAAGGAGATC AACGAAGTGG TGGTTCGACA
 CAGACCACCA CAACTGGCTC AACGCTCCCT CGTACAGGGA GCAAGAGTCA GGCAAATTTG
 AGCATTCTCN GNTTCGCCTT AATCGGTTTG GCGGGAATCG TACATAGAAA GAAGGGACGA
 CATGAAGCAA ACTAA

EF055-2 (SEQ ID NO:206)

MKKKRYL MIVCLLSSPS FFINVEASDG GSSSVGIEFY
 QNPRTPAPKD PPPKTDAPAA DPKEPAGPPQ GDQRSGGSTQ TTTTGSTLPR TGSKSQANLS
 ILXFALIGLA GIVHRKKGRH EAN

EF055-3 (SEQ ID NO:207)

AGCGTCTGAT GGTGGTTCTA GTTCGGTGGG GATTGAATTT
 TACCAAAATC CGAGAACACC CGCTCCTAAA GATCCCCAC CGAAAACAGA TGCGCCAGCT
 GCTGATCCCA AGGAACCAGC TGGTCCTCCG CAAGGAGATC AACGAAGTGG TGGTTCGACA
 CAGACCACCA CAACTGGCTC AACG

EF055-4 (SEQ ID NO:208)

SDG GSSSVGIEFY
 QNPRTPAPKD PPPKTDAPAA DPKEPAGPPQ GDQRSGGSTQ TTTTGST

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF056-1 (SEQ ID NO:209)

TAAATGAAAA AAAAGCGTTA TTTAATAATT GCGTGTTTAC TATTTTCCCC TAGTTTTTTT
 ATAAATGTTG AAGCATCTGA GGGTGGTTCT AGTTCGGTGG GAATTGAATT TTACCAAAAT
 CCGGCAACAC CCGCTCCTAA AGATGCCCCA CCGAAAACAG ATGAGCCAGC TGCGGATCCC
 AAGGAACCAG CTGGTCCTCT GCAAGGAGAT CAACGAAGTG GTGGTTCGAC ACAGACCACC
 ACAGCTGGCT CGCAGCTCCC TCGTACAGGA AGCAAGAGTC AGGCAAACCT GAGCATTCTT
 GGTCTTGTCT TGATTGGTCT TGTCCGAATG GTCCAGAGAA AGAAGGGACG ACATGAAGCA
 AACTAA

EF056-2 (SEQ ID NO:210)

MKKKRYLIIA CLLFSPSFFI NVEASEGGSS SVGIEFYQNP ATPAPKDAPP KTDEPAADPK
 EPAGPLQGDQ RSGGSTQTTT AGSQLPRTGS KSQANLSILG LVLIGLVGMV QRKKGRHEAN

EF056-3 (SEQ ID NO:211)

ATCTGA GGGTGGTTCT AGTTCGGTGG GAATTGAATT TTACCAAAAT
 CCGGCAACAC CCGCTCCTAA AGATGCCCCA CCGAAAACAG ATGAGCCAGC TGCGGATCCC
 AAGGAACCAG CTGGTCCTCT GCAAGGAGAT CAACGAAGTG GTGGTTCGAC ACAGACCACC
 ACAGCTGGCT CGCAG

EF056-4 (SEQ ID NO:212)

SEGGSS SVGIEFYQNP ATPAPKDAPP KTDEPAADPK
 EPAGPLQGDQ RSGGSTQTTT AGSQ

EF057-1 (SEQ ID NO:213)

TAATGTTTAT TGGCTGGGCC AGTCAATGTT GAAAATGGGG AAGGAGGAAT TCAGATGAAA
 ATCATAAAAA GGTTAGTTT GGTATGTTTA GGGCTATTGA TCATTGGGTT GCNAACAAAA
 AGCGNTATGG CTGAAGAAAA TAATTATGAA TCAAATGGTC AAGCGAGCTT CTATGGTACC
 TACGTTTATG AGAATGAAAA AGAGTCAAAT GACGTAGCGT ATACCCAACA ATCAGAAGAA
 CAGGGAAGAA ACAATTTAGC TGCTTCTGGA CAAGCAGTTT TACCTAAAAC AGGCGAGTCT
 GAAAATCCGC TGTATTCCTT GATAGGAGTT AGTTTGTGG GGATAGTCAT TTATTTAATT
 AATAAAATGA AACGAGAGAA GGAGTTTATT TAA

EF057-2 (SEQ ID NO:214)

MKI IKRFSVLCLG LLIIGLXTKS XMAEENNYES NGQASFYGTY
 VYENEKESND VAYTQQSEEQ GRNNLAASGQ AVLPKTGESE NPLYSLIGVS LLGIVIIYLIN
 KMKREKEFI

EF057-3 (SEQ ID NO:215)

AAA TAATTATGAA TCAAATGGTC AAGCGAGCTT CTATGGTACC
 TACGTTTATG AGAATGAAAA AGAGTCAAAT GACGTAGCGT ATACCCAACA ATCAGAAGAA
 CAGGGAAGAA ACAATTTAGC TGCTTCTGGA CAAGCAGTTT

EF057-4 (SEQ ID NO:216)

EENNYES NGQASFYGTY
 VYENEKESND VAYTQQSEEQ GRNNLAASGQ AV

TABLE 1. Nuclcotide and Amino Acid Sequences of *E. faecalis* Genes.

EF058-1 (SEQ ID NO:217)

TGAAGAACGT TCTATTTGGT TGACGATTGC AGGCCTGCTA ATCATTGGGA TGGTAGTCAT
 TTGGCTATTT TATCAAAAAC AAAAAAGAGG AGAGAGAAAA TGAAGCAATT AAAAAAGTTT
 TGGTACACCG TTAGTACCTT GTTACTAATT TTGCCACTTT TCACAAGTGT ATTAGGGACA
 ACAACTGCAT TTGCAGAAGA AAATGGGGAG AGCGCACAGC TCGTGATTCA CAAAAAGAAA
 ATGACGGATT TACCAGATCC GCTTATTCAA AATAGCGGGA AAGAAATGAG CGAGTTTGAT
 AAATATCAAG GACTGGCAGA TGTGACGTTT AGTATTTATA ACGTGACGAA CGAATTTTAC
 GAGCAACGAG CGGCAGGCGC AAGCGTTGAT GCAGCTAAAC AAGCTGTCCA AAGTTTAACT
 CCTGGGAAAC CTGTTGCTCA AGGAACCACC GATGCAAATG GGAATGTCAC TGTTTCAGTTA
 CCTAAAAAAC AAAATGGTAA AGATGCAGTG TATACCATTA AAGAAGAACC AAAAGAGGGT
 GTAGTTGCTG CTACGAATAT GGTGGTGGCG TTCCAGTTT ACGAAATGAT CAAGCAAACA
 GATGGTTCCCT ATAAATATGG AACAGAAGAA TTAGCGGTTG TTCATATTTA TCCTAAAAAT
 GTGGTAGCCA ATGATGGTAG TTTACATGTG AAAAAAGTAG GAACTGCTGA AAATGAAGGA
 TTAAATGGCG CAGAATTTGT TATTTCTAAA AGCGAAGGCT CACCAGGCAC AGTAAAATAT
 ATCCAAGGAG TCAAAGATGG ATTATATACA TGGACAACGG ATAAAGAACA AGCAAAACGC
 TTTATTACTG GGAAAAGTTA TGAAATTGGC GAAATGATT TCACAGAAGC AGAGAAATGGA
 ACGGGAGAAAT TAACAGTTAA AAATCTTGAG GTTGGTTCGT ATATTTTAGA AGAAGTAAAA
 GCTCCAAATA ATGCAGAATT AATTGAAAAT CAAACAAAAA CACCATTTAC AATTGAAGCA
 AACATCAAAA CACCTGTTGA AAAACAGTC AAAAAAGATA CCTCTAAAGT TGATAAAACA
 ACACCAAGCT TAGATGGTAA AGATGTGGCA ATTGGCGAAA AAATTAAATA TCAAATTTCT
 GTAAATATTC CATTTGGGGAT TGCAGACAAA GAAGGCGACG CTAATAAATA CGTCAAATTC
 AATTTAGTTG ATAAACATGA TGCAGCCTTA ACTTTTGATA ACGTGACTTC TGGAGAGTAT
 GCTTATGCGT TATATGATGG GGATACAGTG ATTGCTCCTG AAAATTATCA AGTGACTGAA
 CAAGCAAAATG GCTTCACTGT GCCCGTTAAT CCAGCGTATA TTCTACGCT AACACCAGGC
 GGCACACTAA AATTCGTTTA CTTTATGCAT TTAAATGAAA AAGCAGATCC TACGAAAGGC
 TTTAAAAATG AGGCGAATGT TGATAACGGT CATACCGACG ACCAAACACC ACCAATGTTT
 GAAGTTGTGA CAGGTGGGAA ACGTTTCATT AAAGTCGATG GCGATGTGAC AGCGACACAA
 GCCTTGCGCG GAGCTTCCTT TGTCGTCCGT GATCAAAACA GCGACACAGC AAATTATTTG
 AAAATCGATG AAACAACGAA AGCAGCAACT TGGGTGAAAA CAAAAGCTGA AGCAACTACT
 TTTACAACAA CGGCTGATGG ATTAGTTGAT ATCACAGGGC TTAAATACGG TACCTATTAT
 TTAGAAGAAA CTGTAGCTCC TGATGATTAT GTCTTGTTAA CAAATCGGAT TGAATTTGTG
 GTCAATGAAC AATCATATGG CACAACAGAA AACCTAGTTT CACCAGAAAA AGTACCAAAC
 AAACACAAAG GTACCTTACC TTCAACAGGT GGCAAAGGAA TCTACGTTTA CTTAGGAAGT
 GCGCAGTCT TGCTACTTAT TGCAGGAGTC TACTTTGCTA GACGTAGAAA AGAAAATGCT
 TAA

EF058-2 (SEQ ID NO:218)

MKQLKKVW YTVSTLLLIL PLFTSVLGTT
 TAFAEENGES AQLVIHKKKM TDLDPDPLIQN SGKEMSEFDK YQGLADVTF S IYNTNEFYE
 QRAAGASVDA AKQAVQSLTP GKPVAQGTDD ANGNVTVQLP KKQNGKDAVY TIKEEPKEGV
 VAATNMVAVF PVYEMIKQTD GSYKYGTEEL AVVHIYPKNV VANDGSLHVK KVGTAENEGL
 NGAEFVSKS EGSPGTVKYI QGVKDGLYTW TTDKEQAKRF ITGKSYEIGE NDFTEAENGT
 GELTVKNLEV GSYILEEVKA PNNAELIENQ TKTPFTIEAN NQTPVEKTVK NDTSKVDKTT
 PSLDGKDVAI GEKIKYQISV NIPLGIADKE GDANKYVKFN LVDKHDAALT FDNVTSGEYA
 YALYDGDVTI APENYQVTEQ ANGFTVAVNP AYIPTLTPGG TLKFVYFMHL NEKADPTKGF
 KNEANVDNGH TDDQTPPTVE VVTGGKRFIK VDGDVTATQA LAGASFVVRD QNSDTANYLK
 IDETTKAATW VKTKAEATTF TTTADGLVDI TGLKYGYTYL EETVAPDDYV LLTNRIEFVV
 NEQSYGTTEN LVSPEKVPNK HKGTLPSTGG KGIYVYLGSG AVLLLIAGVY FARRRRKENA

EF058-3 (SEQ ID NO:219)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AGAAGA AAATGGGGAG AGCGCACAGC TCGTGATTCA CAAAAAGAAA
 ATGACGGATT TACCAGATCC GCTTATTCAA AATAGCGGGA AAGAAATGAG CGAGTTTGAT
 AAATATCAAG GACTGGCAGA TGTGACGTTT AGTATTTATA ACGTGACGAA CGAATTTTAC
 GAGCAACGAG CGGCAGGCGC AAGCGTTGAT GCAGCTAAAC AAGCTGTCCA AAGTTTAACT
 CCTGGGAAAC CTGTTGCTCA AGGAACCACC GATGCAAATG GGAATGTCAC TGTTTCAGTTA
 CCTAAAAAAC AAAATGGTAA AGATGCAGTG TATACCATTA AAGAAGAACC AAAAGAGGGT
 GTAGTTGCTG CTACGAATAT GGTGGTGGCG TTCCCAGTTT ACGAAATGAT CAAGCAAACA
 GATGGTTCCT ATAAATATGG AACAGAAGAA TTAGCGGTTG TTCATATTTA TCCTAAAAAT
 GTGGTAGCCA ATGATGGTAG TTTACATGTG AAAAAAGTAG GAACTGCTGA AAATGAAGGA
 TTAAATGGCG CAGAATTTGT TATTTCTAAA AGCGAAGGCT CACCAGGCAC AGTAAAAATAT
 ATCCAAGGAG TCAAAGATGG ATTATATACA TGGACAACGG ATAAAGAACA AGCAAAACGC
 TTTATTACTG GGAAAAGTTA TGAAATTGGC GAAAATGATT TCACAGAAGC AGAGAATGGA
 ACGGGAGAAAT TAACAGTTAA AAATCTTGAG GTTGGTTCGT ATATTTTAGA AGAAGTAAAA
 GCTCCAAATA ATGCAGAATT AATTGAAAAT CAAACAAAAA CACCATTTAC AATTGAAGCA
 AACAAATCAAA CACCTGTTGA AAAAACAGTC AAAAAAGATA CCTCTAAAGT TGATAAAACA
 ACACCAAGCT TAGATGGTAA AGATGTGGCA ATTGGCGAAA AAATTAAATA TCAATTTTCT
 GTAAATATTC CATTTGGGGAT TGCAGACAAA GAAGGCGACG CTAATAAATA CGTCAAATTC
 AATTTAGTTG ATAAACATGA TGCAGCCTTA ACTTTTGATA ACGTGACTTC TGGAGAGTAT
 GCTTATGCGT TATATGATGG GGATACAGTG ATTGCTCCTG AAAATTATCA AGTGACTGAA
 CAAGCAAATG GCTTCACTGT CGCCGTTAAT CCAGCGTATA TTCTTACGCT AACACCAGGC
 GGCACACTAA AATTCGTTTA CTTTATGCAT TTAAATGAAA AAGCAGATCC TACGAAAGGC
 TTTAAAAATG AGGCGAATGT TGATAACGGT CATACCGACG ACCAAACACC ACCAACTGTT
 GAAGTTGTGA CAGGTGGGAA ACGTTTCATT AAAGTCGATG GCGATGTGAC AGCGACACAA
 GCCTTGCGCG GAGCTTCCTT TGTCGTCCGT GATCAAAACA GCGACACAGC AAATTATTTG
 AAAATCGATG AAACAACGAA AGCAGCAACT TGGGTGAAAA CAAAAGCTGA AGCAACTACT
 TTTACAACAA CGGCTGATGG ATTAGTTGAT ATCACAGGGC TTAAATACGG TACCTATTAT
 TTAGAAGAAA CTGTAGCTCC TGATGATTAT GTCTTGTTAA CAAATCGGAT TGAATTTGTG
 GTCAATGAAC AATCATATGG CACAACAGAA AACCTAGTTT CACCAGAAAA AGTACCAAAC
 AAACACAAAG GTACCTTACC T

EF058-4 (SEQ ID NO:220)

EENGES AQLVIHKKKM TDLDPDPLIQN SGKEMSEFDK YQGLADVTFIS IYNVTNEFYE
 QRAAGASVDA AKQAVQSLTP GKPVAQGTDD ANGNVTVQLP KKQNGKDAVY TIKEEPKEGV
 VAATNMVAVF PVYEMIKQTD GSYKYGTEEL AVVHIYPKNV VANDGSLHVK KVGTAENEGL
 NGAEFVSKS EGSPGTVKYI QGVKDGLYTW TTDKEQAKRF ITGKSYEIGE NDFTEAENG
 GELTVKNLEFV GSYILEEVKA PNNAELIENQ TKPTPTIEAN NQTPVEKTVK NDTSKVDKTT
 PSLDGKDVAI GEKIKYQISV NIPLGIADKE GDANKYVKFN LVDKHDAALT FDNVTSGEYA
 YALYDGDTVI APENYQVTEQ ANGFTVAVNP AYIPTLTTPGG TLKFVYFMHL NEKADPTKGF
 KNEANVDNGH TDDQTPPTVE VVTGGKRFIK VGDVDTATQA LAGASFVVRD QNSDTANYLK
 IDETTKAATW VKTKAEATTF TTTADGLVDI TGLKYGTYYL EETVAPDDYV LLTNRIEFVV
 NEQSYGTTEN LVSPEKVPNK HKGT

EF059-1 (SEQ ID NO:221)

TAGATTGGAA GAATGAAAAT GAAAAAATG ATTATTTATTG CCTTATTCAG TACAAGCCTT
 TTAGCAGGGG GAAGCAGTGT TTCTGCTTAT GCGCAAGAAAT CAGAAGGAAA TCTTGGTGAA
 ACAACAGGGA GTGTTTTACC AGATGAACCG AATGTACCAA CTGACCCAAT AACGCCAAGT
 GAGCCAGAGC AACCAACAGA GCCAAGTACA CCAGAGCAAC CATCGGAACC GTCAACACCA
 ACCGAACCTA GTGAGCCTTC AAAACCGACG GATCCTTCGT TACCAGACGA ACCGAGCGTA
 CCAACAGAGC CAACAACGCC AAGTAAGCCA GAGCAACCAA CAGAGCCAAC AACGCCAAGT
 GTACCAGAGC AACCAACAGA GCCAAGTGTA CCAGAAAAAC CAGTAGAACC AAATAAACCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACCGAGCCAG AAAAGCCTGT GCCAGTTGTT CCGAAAAAC CAGTTGTACC ACAACAACCA
 GAGCAACCAA CAGATGTGGT GGTAAAGCCA AATGGAGAAA TTGCAACAGG AGAATCTACA
 CAACAGCCAA CTGTTCCAAT TGAAACGAAT AACCTTTCAG AAGTAACACA TGTCCCAACT
 GTGACGACAC CGATTGAAAC AGCAAGCGGA GAAGCAATTG TCGCAGTGGA TAAGGGCGTT
 CCTTTAACAC AAACGGCTGA TGGATTAAAA CCGATTAAAA GTGAATATAA AGTATTACCA
 AGTGGAATG TACAAGTGAA AAGTGCTGAC GGAAAAATGA AAGTACTTCC TTACACTGGT
 GAAAAATGG GCATAATTGG GTCAATCGCT GGTGTATGTT TGAAGTGTTC ATCAGGAATC
 TTAATTTATA AAAAACGTAA AGTGTAG

EF059-2 (SEQ ID NO:222)

MKKMI IALFSTSL AGGSSVSAYA QESEGNLGET TGSVLPDEPN VPTDPITPSE
 PEQPTPESTP EQPSEPSTPT EPSEPSKPTD PSLPDEPSVP TEPTTPSKPE QPTEPTTPSV
 PEQPTPEPSVP EKPVEPNKPT EPEKVPVVP EKPVPVQQPE QPTDVVVKPN GEIATGESTQ
 QPTVPIETNN LSEVTHVPTV TTPIETASGE AIVAVDKGVP LTQTADGLKP IKSEYKVLPS
 GNVQVKSADG KMKVLPYTGE KMGIIGSIAG VCLTVLSGIL IYKKRKV

EF059-3 (SEQ ID NO:223)

AGAAGGAAA TCTTGGTGAA
 ACAACAGGGA GTGTTTTACC AGATGAACCG AATGTACCAA CTGACCCAAT AACGCCAAGT
 GAGCCAGAGC AACCAACAGA GCCAAGTACA CCAGAGCAAC CATCGGAACC GTCAACACCA
 ACCGAACCTA GTGAGCCTTC AAAACCGACG GATCCTTCGT TACCAGACGA ACCGAGCGTA
 CCAACAGAGC CAACAACGCC AAGTAAGCCA GAGCAACCAA CAGAGCCAAC AACGCCAAGT
 GTACCAGAGC AACCAACAGA GCCAAGTGTA CCAGAAAAAC CAGTAGAACC AAATAAACCA
 ACCGAGCCAG AAAAGCCTGT GCCAGTTGTT CCGAAAAAC CAGTTGTACC ACAACAACCA
 GAGCAACCAA CAGATGTGGT GGTAAAGCCA AATGGAGAAA TTGCAACAGG AGAATCTACA
 CAACAGCCAA CTGTTCCAAT TGAAACGAAT AACCTTTCAG AAGTAACACA TGTCCCAACT
 GTGACGACAC CGATTGAAAC AGCAAGCGGA GAAGCAATTG TCGCAGTGGA TAAGGGCGTT
 CCTTTAACAC AAACGGCTGA TGGATTAAAA CCGATTAAAA GTGAATATAA AGTATTACCA
 AGTGGAATG TACAAGTGAA AAGTGCTGAC GGAAAAATGA AAGTAC

EF059-4 (SEQ ID NO:224)

EGNLGET TGSVLPDEPN VPTDPITPSE
 PEQPTPESTP EQPSEPSTPT EPSEPSKPTD PSLPDEPSVP TEPTTPSKPE QPTEPTTPSV
 PEQPTPEPSVP EKPVEPNKPT EPEKVPVVP EKPVPVQQPE QPTDVVVKPN GEIATGESTQ
 QPTVPIETNN LSEVTHVPTV TTPIETASGE AIVAVDKGVP LTQTADGLKP IKSEYKVLPS
 GNVQVKSADG KMKV

EF060-1 (SEQ ID NO:225)

TGAAAAATAG ACAAGGAGCA CGCGATGATG ACAATGAAAA GTAAAGGGTC ACTTCTGGTG
 ACGTTGGGAA TACTTTTAAC CGTTGGCATT GCGAGTCTAA TTGTTTCTTC TGAGAGTTTT
 GCAGAAGAAG TAGGGCAAAC GAATATCGGT GTAACGTTCT ATGGAGGAAA AGAGCCACTA
 AAAACGGAAG GTGTCATTAA GCCAATAGAG CAACCAGTCA CTGATAAAGA TAAAAAACG
 TCACAACAAC AAGACAAAGT GAGCAGAAAA ACCACTGCTA AAACGAATCC GACTAATGCA
 CAGACGTCAT TACCAAGGAC AGGTGAACGA AATAGCACGT GGCTTTACAG CCTTGGTATT
 GCCTGTTTAC TCGTAGTACT AACAAGTTTC TATTATTGTA ATAAAAAAG GAAAAAGGAA
 AAATAA

EF060-2 (SEQ ID NO:226)

MMT MKSKGSLVLT LGILLTVGIA SLIVSSESFA EEVGQTNIGV TFYGGKEPLK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TEGVIKPIEQ PVTDKDKKTS QQQDKVSRKT TAKTNPTNAQ TSLPRTGERN STWLYSLGIA
CLLVVLTSFY YLNKKRKKKEK

EF060-3 (SEQ ID NO:227)

AGAAGAAG TAGGGCAAAC GAATATCGGT GTAACGTTCT ATGGAGGAAA AGAGCCACTA
AAAACGGAAG GTGTCATTAA GCCAATAGAG CAACCAGTCA CTGATAAAGA TAAAAAACG
TCACAACAAC AAGACAAAGT GAGCAGAAAA ACCACTGCTA AAACGAATCC GACTAATGCA
CAGACGTCAT

EF060-4 (SEQ ID NO:228)

EEVGQTNIGV TFYGGKEPLK
TEGVIKPIEQ PVTDKDKKTS QQQDKVSRKT TAKTNPTNAQ TS

EF061-1 (SEQ ID NO:229)

TAATGGAACG ACCGACAGAA GAAGATTTTG AACTTACAAA TTAAAATTAA AATGGAGGAA
ATAATGATGA AAAAAATTCT TTTTGCTAGT TTATTTAGTG CCACACTACT ATTTGGGGGA
AGTGAAATTT CTGCTTTTGC ACAAGAAATT ATCCCTGATG ATACTACGAC ACCGCCCATT
GAAGTACCAA CAGAACCAAG TACACCAGAA AAGCCAACAG ATCCAACACC GCCAATTGAG
CCACCTGTAG ACCCTGTAGA GCCACCTATT ACACCAACGG AGCCAACAGA ACCGACAGAG
CCGACAACAC CAACAGAACC TACAACCTCT ACAGAGCCAA GTGAACCAGA ACAACCAACG
GAGCCAAGTA AACCAGTAGA ACCTGAAAAA CCAGTTACAC CAAGCAAACC AGCAGAACCC
GAAAAAACTG TGACACCAAC TAAACCAACA GAATCTGAAA AACCAGTACA ACCAGCAGAA
CCAAGCAAGC CAATCGACGT TGTGTAAACG CCAACAGGGG AATTAAATCA CGCTGGAAAT
GGTACACAAC AGCCAACAGT CCCTATTGAA ACAAGTAATT TGGCAGAAAT CACGCACGTG
CCTAGTGTA CAACACCTAT TACAACCTACA GACGGAGAAA ACATTGTAGC TGTAAGAAAA
GGTGTTCAC TTACACAAAC AGCAGAAGGG TTAAAACCTA TTCAATCNAG TTACAAAGTA
TTGCCTAGCG GAAATGTAGA AGTAAAAGGT AAGGACGGTA AAATGAAGGT TTTACCATAC
ACAGGTGAAG AAATGAATAT CTTTTTATCT GCCGTAGCGG TATCTTGTCT GTAG

EF061-2 (SEQ ID NO:230)

MMKKILFASL FSATLLFGGS EISAFQEII PDDTTTPPIE
VPTEPSTPEK PTDPTPIEP PVDPEPPIT PTEPTEPTEP TTPTEPTTPT EPSEPEQPTE
PSKPVEPEKP VTPSKPAEPE KTVTPTKPTE SEKPVQPAEP SKPIDVVVTP TGELNHAGNG
TQOPTVPIET SNLAEITHVP SVTTPITTTD GENIVAVEKG VPLTQTAEGL KPIQSSYKVL
PSGNVEVKGK DGKMKVLPYT GEEMNIFLSA VAVSCL

EF061-3 (SEQ ID NO:231)

GAAATTT CTGCTTTTGC ACAAGAAATT ATCCCTGATG ATACTACGAC ACCGCCCATT
GAAGTACCAA CAGAACCAAG TACACCAGAA AAGCCAACAG ATCCAACACC GCCAATTGAG
CCACCTGTAG ACCCTGTAGA GCCACCTATT ACACCAACGG AGCCAACAGA ACCGACAGAG
CCGACAACAC CAACAGAACC TACAACCTCT ACAGAGCCAA GTGAACCAGA ACAACCAACG
GAGCCAAGTA AACCAGTAGA ACCTGAAAAA CCAGTTACAC CAAGCAAACC AGCAGAACCC
GAAAAAACTG TGACACCAAC TAAACCAACA GAATCTGAAA AACCAGTACA ACCAGCAGAA
CCAAGCAAGC CAATCGACGT TGTGTAAACG CCAACAGGGG AATTAAATCA CGCTGGAAAT
GGTACACAAC AGCCAACAGT CCCTATTGAA ACAAGTAATT TGGCAGAAAT CACGCACGTG
CCTAGTGTA CAACACCTAT TACAACCTACA GACGGAGAAA ACATTGTAGC TGTAAGAAAA
GGTGTTCAC TTACACAAAC AGCAGAAGGG TTAAAACCTA TTCAATCNAG TTACAAAGTA
TTGCCTAGCG GAAATGTAGA AGTAAAAGGT AAGGACGGTA AAATGAAGGT TT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF061-4 (SEQ ID NO:232)

QEII PDDTTTPPIE

VPTEPSTPEK PTDPTPIEP PVDPEPPIT PTEPTEPTEP TTPTEPTTPT EPSEPEQPTE
 PSKPVEPEKP VTPSKPAEPE KTVTPTKPTE SEKPVQPAEP SKPIDVVVTP TGELNHAGNG
 TQQPTVPIET SNLAEITHVP SVTTPITTTD GENIVAVEKG VPLTQTAEGL KPIQSSYKVL
 PSGNVEVKGK DGKMKV

EF062-1 (SEQ ID NO:233)

TGATTCTTGA AGCAACAAAT GAAAGCAAAA AAACAATATA AGACATATAA AGCTAAGAAT
 CACTGGGTAA CTGTCCCTAT TCTTTTCTA AGTGTGTTAG GAGCCGTAGG ATTAGCTACT
 GATAATGTAC AAGCCGCGGA ATTAGATACG CAACCAGAAA CAACGACGGT TCAACCCAAT
 AACCCCGACC TGCAGTCAGA AAAGGAAACA CCTAAAACGG CAGTATCTGA AGAAGCAACA
 GTACAAAAAG ACACTACTTC TCAACCGACC AAAGTAGAAG AAGTAGCGCC AGAAAATAAA
 GGTACTGAAC AAAGTTCAGC TACCCCAAAT GATACCACAA ACGCGCAACA ACCAACAGTA
 GGAGCTGAAA AATCAGCACA AGAACACCA GTAGTAAGCC CTGAAACAAC CAATGAACCT
 CTAGGGCAGC CAACAGAAGT TGCACCAGCT GAAAATGAAG TGAATAAATC AACGTCCATT
 CCTAAAGAAT TTGAAACACC AGACGTTGAT AAAGCAGTTG ATGAAGTAAA AAAAGATCCA
 AACATTACCG TTGTTGAAAA ACCAGCAGAA GACTTAGGCA ACGTTTCTTC TAAAGATTTA
 GCTGCAAAAG AAAAAGAAGT AGACCAACTA CAAAAAGAAC AAGCGAAAAA GATTGCCCAA
 CAAGCAGCTG AATTAAAAGC CAAAAATGAA AAAATTGCCA AAGAAAATGC AGAAATTGCG
 GCAAAAAACA AAGCNGAAAA AGAGCGNTAN GANAAAGAAG TCGCNGAATA CAACAAGCAT
 AAGAACGAAA ACAGCTATGT CAATGAAGCG ATTAGTAAAA ACCTAGTGTT CGATCAATCT
 GTCGTGACGA AAGACACTAA AATTTCTGTCG ATTAAAGGCG GAAAATTTAT CAAAGCAACT
 GATTTTAATA AAGTAAATGC AGGGGATTC AAGATATCT TTACAAAAAT ACGGAAAGAT
 ATGGGNGGGA AAGNTACTGG CAACTTCCAG AATTCCTTTG TAAAAGAGGC AAATCTTGGG
 TCTAATGGTG GGTATGCGGT TCTTTTAGAA AAAAAATAAC CAGTGACAGT GACCTATACA
 GGACTAAACG CTAGTTATTT AGGACGTAAA ATTACAAAAG CAGAAATTTGT TTATGAACTA
 CAATCCTCAC CAAGCCAAAG TGAACCGTTA AATGCAGTAT TTTCAAACGA TCCGATTATC
 ACNGCTTTTA TTGGTACAAA CAGAGTCAAT GGTAAGGATG TTAACACAG CTTAACGATT
 AAGTTCTTTG ATGCGTCAGG TAAAGAAGTA CTACCAGATA AAGATAGTCC ATTTGCGTAT
 GCGCTGTCTT CTTTAAATTC AAGTTTAAACG AATAAAGGTG GCCATGCGGA ATTTGTTTCT
 GATTTTGGGG CNAACAATGC GTTCAAATAC ATTAATGGNT CNTATGTGAA AAAACAAGCG
 GATGGAAT TTTACTCACC GGAAGATATT GACTATGGCA CAGGACCTTC TGGATTGAAA
 AATAGTGATT GGGACGCTGT AGGTCACAAG AATGCCTACT TTGGTTTCAGG TGTAGGTCTA
 GCNAATGGNC GTATTTCTCT TTTCTTTGGT ATGACAACAA AAGGAAAAAG TAATGTGCCT
 GTATCTAGTG CGCAATGGTT TGCCTTTAGN ACTAACTTAA ATGCGCAATC AGTGAAGCCT
 ATTTTCAATT ATGGGAATCC AAAAGAACCA GAAAAAGCAA CGATTGAATT CAATNGATAC
 AAAGCCAATG TCGTTCTGT NCTTGCGCCN AATAAAGAAG TCACTGATGG NCAGAAAAAT
 NTCAATGATT TAAATGTGAA NCGTGGCGAT TCTTTACAAT ACATTGTGAC AGGGGATACG
 ACAGAACTTG CCAAAGTAGA TCCAAAAACA GTAACNAAAC AAGGGATTTC AGATACNTTT
 GATGCAGAAA AAGTGACGAT TGATTTATCC AAAGTGAAAG TTTATCAAGC AGACGCAAGT
 CTNAACGANA AAGACTNAAA AGCTGTTGCT GCAGCNATTA ATTCAGGAAN AGCTAAAGAC
 GTGACTGCTT CTTATGANCT CAATTTAGAT CAAAACACCG TCACAGCAAT GATGAAAACC
 AACGCNGACG GNTCNGTTGT TTTAGCAATG GGGTATAAAT ATTTACTTGT CTTGCCGTTT
 GTAGTGAAAA ATGTAGAAGG CGATTTTGAA AATACAGCTG TTCAGCTGAC AAANGATGGN
 GAAACGGTAA CAAATACAGT GATTAACCAT GTGCCAGGTA GTAATCCTTC CAAAGATGTA
 AAAGCAGATA AAAACGGTAC AGTTGGCAGT GTTCTCTAC ATGATAAAGA TATTCCGTTA
 CAAACAAAAA TTTATTATGA AGTGAATCT TCCGAACGTC CAGCNAACTA TGGCGGAATN
 ACNGAAGAAT GGGGCATGAA TGATGTCTTG GACACGACCC ATGATCGTTT CACAGGNAAA
 TGGCACGCTA TTACNAANTA TGACCTTAAA GTAGGGGANA AAACGTTAAA AGCAGGAACA
 GATATTTCTG CCTACATTCT TTTAGAAAAC AAAGACAATA AAGACTTGAC GTTTACNATG
 AATCAAGCAT TATTGGCNGC NTTAAATGAA GGAAGCAATA AAGTAGGCAA ACAAGCTTGG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TCTGTGTATC TGGAAGTCGA ACGGATNAAA ACAGGTGACG TAGAAAAACAC GCAAACAGAA
AACTACAACA AAGAGCTTGT NCGTTCTAAT ACNGTGGTGA CGCATACNCC TGATGATCCA
AAACCAACCA AAGCCGTTCA TAACAAGAAA GGGGAAGANA TTAANCATGG AAAAGTNGCT
CGTGGTGTATG TTCTTTCTTA TGAAATGACN TGGGACTTAA AAGGGTACGA TAAAGACTTT
GCCTTTTGATA CAGTCGATCT TGCACAGGC GTTCTTTCT TCGATGATTA CGATGAAACG
AANGTGACAC CAATCAAAGA CTTACTTCGT GTCAAAGATT CTAAAGGGGN AGACATTACG
AACCAGTTCA CGATCTCNTG GGACGATGCC AAAGGCACGG TGACNATNTC TGCCAAAGAC
CCACAAGCCT TTATTCTAGC GNATGGTGGG CAAGAATTGC GTGTAACNCT CCCTACAAAA
GTCAAAGCCG ATGTTTCTGG NGATGTTTAT AATTCAGCGG AACAAAATAC ATTTGGNCAA
CGAATTAAAA CCAATACNGT TGTCAACCAT ATTCCAAAAG TGAANCCTAA AAAAGACGTG
GTTATTAAAG TNGGTGACAA ACAAAGTCAA AATGGNGCCA CAATCAAATT AGGGGAGAAN
TTCTTCTATG AATTTACAAG TAGTGACATT CCTGCAGAA TACGCTGGNGT TGTGGAAGAA
TGGTCGATTA GCGATAAACT AGACGTCAAA CATGACAAAT TTAGTGCCCA ATGGTCTGTG
TTTGCCAATT CTAATTTTGT TTTAGCAGAC GGAACCAAAG TGAATAAAGG GGACGACATT
TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
TTTTTNGATG CGATGAATCT AAAAGAAAAC AAAAACGTTG CACACTCATG GAAAGCGTTC
ATTGGTGTAG AACGAATTGC GGCAGGAGAC GTTTACAACA CAATCGAAGA ATCTTTCAAC
AATGAGAAGA TTAAAAACNAA TACGGTAGTG ACNCATACGC CAGAAAAACC ACAACNCCA
CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAACAC CGCAAGCACC AGTAGAGCCA
TTAGTGGTAG AAAAGGCAAG TGTNGTGCCA GAATTGCCGC AAACAGGCGA AAAACAAAAT
GTCTTATTAA CGGTAGCTGG TAGTTTAGCC GCAATGCTTG GCTTAGCAGG CTTAGGCTTT
AAACGTAGAA AAGAAACAAA ATAA

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EF062-2 (SEQ ID NO:234)

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MKAKK QYKTYKAKNH WVTVPILFLS VLGAVGLATD NVQAAELDTQ PETTTVQPNN
PDLQSEKETP KTAVSEETV QKDTTSQPTK VEEVAPENKG TEQSSATPND TTNAQQPTVG
AEKSAQEQPV VSPETTNEPL GQPTVEVAPAE NEVNKSTSIP KEFETPDVDK AVDEVKDKPN
ITVVEKPAED LGNVSSKDLA AKEKEVDQLQ KEQAKKIAQQ AAELKAKNEK IAKENAEIAA
KNKAERKXX KEVAEYNKHK NENSYVNEAI SKNLVFDQSV VTKDTKISSI KGGKFIKATD
FNKVNAGDSK DFTKLKRD MGGKXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
LNASYLGRKI TKAEFVYELQ SSPSQSGTLN AVFSNDPIIT AFIGTNRVNG KDVKTRLTIK
FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGANNAFKYI NGSYVKKQAD
GKFYSPEDID YGTGPSGLKN SDWDAVGHN AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
SSAQWFAFXT NLNAQSVKPI FNYGNPKEPE KATIEFNXYK ANVVPVLVPN KEVTDGQKNX
NDLVNVRGDS LQYIVTGDIT ELAKVDPKTV TKQGIRDFTD AEKVTIDLSK VKVYQADASL
NXXDXKAVAA AINSXAKDV TASYXLNLDQ NTVTAMMKTN ADGSVVLAMG YKYLVLPLFV
VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLO
TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVKGQAWS VYLEVERXKT GDVENTQTEN
YNKELVRSNT VVHTPDPPK PTKAVHNKKG EXIXHGKVAR GDVLSYEMTW DLKGYDKDFA
FDTVDLATGV SFFDDYDETX VTPIKDLLRV KDSKGXDIIN QFTISWDDAK GTVTXSAKDP
QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQR IKTNVTVNHI PKVXPKKDVV
IKVGDKQSQN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
ANSNFVLADG TKVNGGDDIS KLFTMTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVPPTP KTPQAPVEPL
VVEKASVPE LPQTGEKQNV LLTVAGSLAA MLGLAGLGFK RRKETK

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EF062-3 (SEQ ID NO:235)

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TGATTCTTGA AGCAACAAAT GAAAGCAAAA AAACAATATA AGACATATAA AGCTAAGAAT
CACTGGGTAA CTGTCCCTAT TCTTTTCTA AGTGTGTTAG GAGCCGTAGG ATTAGCTACT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GATAATGTAC	AAGCCGCGGA	ATTAGATACG	CAACCAGAAA	CAACGACGGT	TCAACCCAAT
AACCCCGACC	TGCAGTCAGA	AAAGGAAACA	CCTAAAACGG	CAGTATCTGA	AGAAGCAACA
GTACAAAAAG	ACACTACTTC	TCAACCGACC	AAAGTAGAAG	AAGTAGCGCC	AGAAAATAAA
GGTACTGAAC	AAAGTTCAGC	TACCCCAAAT	GATACCACAA	ACGCGCAACA	ACCAACAGTA
GGAGCTGAAA	AATCAGCACA	AGAACAACCA	GTAGTAAGCC	CTGAAACAAC	CAATGAACCT
CTAGGGCAGC	CAACAGAAGT	TGCACCAGCT	GAAAAATGAAG	TGAATAAATC	AACGTCCATT
CCTAAAGAAT	TTGAAACACC	AGACGTTGAT	AAAGCAGTTG	ATGAAGTAAA	AAAAGATCCA
AACATTACCG	TTGTTGAAAA	ACCAGCAGAA	GACTTAGGCA	ACGTTTCTTC	TAAAGATTTA
GCTGCAAAAAG	AAAAAGAAGT	AGACCAACTA	CAAAAAGAAC	AAGCGAAAAA	GATTGCCCAA
CAAGCAGCTG	AATTA AAAAGC	CAAAAATGAA	AAAAATTGCCA	AAGAAAAATGC	AGAAATTGCG
GCAAAAAACA	AAGCNGAAAA	AGAGCGNTAN	GANAAAAGAA	TCGCNGAATA	CAACAAGCAT
AAGAACGAAA	ACAGCTATGT	CAATGAAGCG	ATTAGTAAAA	ACCTAGTGTT	CGATCAATCT
GTCTGTACGA	AAGACACTAA	AATTTCTGTCG	ATTAAAGGCG	GAAAAATTTAT	CAAAGCAACT
GATTTTAATA	AAGTAAATGC	AGGGGATTCA	AAAGATATCT	TTACAAAATT	ACGGAAAGAT
ATGGNGGGA	AAGNTACTGG	CAACTTCCAG	AATTCCTTTG	TAAAAGAGGC	AAATCTTGGG
TCTAATGGTG	GGTATGCGGT	TCTTTTAGAA	AAAAATAAAC	CAGTGACAGT	GACCTATACA
GGACTAAACG	CTAGTTATTT	AGGACGTAAA	ATTACAAAAG	CAGAATTTGT	TTATGAACTA
CAATCCTCAC	CAAGCCAAAG	TGGAACGTTA	AATGCAGTAT	TTTCAAACGA	TCCGATTATC
ACNGCTTTTA	TTGGTACAAA	CAGAGTCAAT	GGTAAGGATG	TTAAAACACG	CTTAACGATT
AAGTCTTTTG	ATGCGTCAGG	TAAAGAAGTA	CTACCAGATA	AAGATAGTCC	ATTTGCGTAT
GCGCTGTCTT	CTTTAAATTC	AAGTTTAACG	AATAAAGGTG	GCCATGCGGA	ATTTGTTTCT
GATTTTGGGG	CNAACAATGC	GTTCAAATAC	ATTAATGGNT	CNTATGTGAA	AAAACAAGCG
GATGGAAAAAT	TTTACTCACC	GGAAGATATT	GACTATGGCA	CAGGACCTTC	TGGATTGAAA
AATAGTGATT	GGGACGCTGT	AGGTCACAAG	AATGCC TACT	TTGGTTTCAGG	TGTAGGTTCTA
GCNAATGGNC	GTATTTCCCTT	TTCTTTTGGT	ATGACAACAA	AAGGAAAAAG	TAATGTGCCT
GTATCTAGTG	CGCAATGGTT	TGCCTTTAGN	ACTAACTTAA	ATGCGCAATC	AGTGAAGCCT
ATTTTCAATT	ATGGGAATCC	AAAAGAACCA	GAAAAAGCAA	CGATTGAATT	CAATNGATAC
AAAGCCAATG	TCGTTCCCTGT	NCTTGTGCCN	AATAAAGAAG	TCAGTGATGG	NCAGAAAAAT
NTCAATGATT	TAAATGTGAA	NCGTGGCGAT	TCTTTACAAT	ACATTGTGAC	AGGGGATACG
ACAGAACTTG	CCAAAGTAGA	TCCAAAAACA	GTAACNAAAC	AAGGGATTCTG	AGATACNTTT
GATGCAGAAA	AAGTGACGAT	TGATTTATCC	AAAGTGAAAG	TTTATCAAGC	AGACGCAAGT
CTNAACGANA	AAGACTNAAA	AGCTGTTGCT	GCAGCNATTA	ATTCAGGAAN	AGCTAAAGAC
GTGACTGCTT	CTTATGANCT	CAATTTAGAT	CAAAACACCG	TCACAGCAAT	GATGAAAACC
AACGCNGACG	GNTCNGTTGT	TTTAGCAATG	GGGTATAAAT	ATTTACTTGT	CTTGCCGTTT
GTAGTGAAAA	ATGTAGAAGG	CGATTTTGAA	AATACAGCTG	TTCAGCTGAC	AAANGATGGN
GAAACGGTAA	CAAATACAGT	GATTAACCAT	GTGCCAGGTA	GTAATCCTTC	CAAAGATGTA
AAAGCAGATA	AAAACGGTAC	AGTTGGCAGT	GTTTCTCTAC	ATGATAAAGA	TATTCCGTTA
CAAACAAAAA	TTTATTATGA	AGTGAAATCT	TCCGAACGTC	CAGCNAACTA	TGGCGGAATN
ACNGAAGAAT	GGGGCATGAA	TGATGTCTTG	GACACGACCC	ATGATCGTTT	CACAGGNAAA
TGGCACGCTA	TTACNAANTA	TGACCTTAAA	GTAGGGGANA	AAACGTTAAA	AGCAGGAACA
GATATTTCTG	CCTACATTCT	TTTAGAAAAC	AAAGACAATA	AAGACTTGAC	GTTTACNATG
AATCAAGCAT	TATTGGCNGC	NTTAAATGAA	GGAAGCAATA	AAGTAGGCAA	ACAAGCTTGG
TCTGTGTATC	TGGAAGTCGA	ACGGATNAAA	ACAGGTGACG	TAGAAAACAC	GCAAACAGAA
AACTACAACA	AAGAGCTTGT	NCGTTCTAAT	ACNGTGGTGA	CGCATACNCC	TGATGATCCA
AAACCAACCA	AAGCCGTTCA	TAACAAGAAA	GGGGAAGANA	TTAANCATGG	AAAAGTNGCT
CGTGGTGATG	TTCTTTCTTA	TGAAATGACN	TGGGACTTAA	AAGGGTACGA	TAAAGACTTT
GCCTTTGATA	CAGTCGATCT	TGCGACAGGC	GTTTCTTTCT	TGCATGATTA	CGATGAAACG
AANGTGACAC	CAATCAAAGA	CTTACTTCGT	GTCAAAGATT	CTAAAGGGGN	AGACATTACG
AACCAAGTTCA	CGATCTCNTG	GGACGATGCC	AAAGGCACGG	TGACNATNTC	TGCCAAAGAC
CCACAAGCCT	TTATTCTAGC	GNATGGTGGG	CAAGAATTGC	GTGTAACNCT	CCCTACAAAA
GTCAAAGCCG	ATGTTTCTGG	NGATGTTTAT	AATTCAGCGG	AACAAAATAC	ATTTGGNCAA
CGAATTAAAA	CCAATACNGT	TGTCAACCAT	ATTCCAAAAG	TGAANCCTAA	AAAAGACGTG
GTTATTAAAG	TNGGTGACAA	ACAAAGTCAA	AATGGNGCCA	CAATCAAATT	AGGGGAGAA
TTCTTCTATG	AATTTACAAG	TAGTGACATT	CCTGCAGAA	ACGCTGGNGT	TGTGGAAGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TGGTCGATTA	GCATAAACT	AGACGTCAAA	CATGACAAAT	TTAGTGGCCA	ATGGTCTGTG
TTTGCCAAAT	CTAATTTTGT	TTTAGCAGAC	GGAACCAAAG	TGAATAAAGG	GGACGACATT
TCGAAACTAT	TCACGATGAC	CTTTGAACAA	GGGGTAGTGA	AAATCACGGC	CAGTCAAGCC
TTTTTNGATG	CGATGAATCT	AAAAGAAAAC	AAAAACGTTG	CACACTCATG	GAAAGCGTTC
ATTGGTGTAG	AACGAATTGC	GGCAGGAGAC	GTTTACAACA	CAATCGAAGA	ATCTTTCAAC
AATGAGAAGA	TTAAAACNAA	TACGGTAGTG	ACNCATACGC	CAGAAAAACC	ACAAACNCCA
CCAGAAAAAA	CAGTGATTGT	ACCACCAACA	CCAAAAACAC	CGCAAGCACC	AGTAGAGCCA
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EF062-4 (SEQ ID NO:236)

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KNKAERKXX	KEVAEYNKHK	NENSYVNEAI	SKNLVFDQSV	VTKDTKISSI	KGGKFIKATD
FNKVNAGDSK	DIFTKLRKDM	GGKXTGNFQN	SFVKEANLGS	NGGYAVLLEK	NKPVTVTYTG
LNASYLGRKI	TKAEFVYELQ	SSPSQSGTLN	AVFSNDPIIT	AFIGTNRVNG	KDVKTRLTIK
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GKFYSPEDID	YGTGPSGLKN	SDWDAVGHN	AYFGSGVGLA	NGRISFSFGM	TTKGKSNVPV
SSAQWFAFXT	NLNAQSVKPI	FNYGPNKEPE	KATIEFNXYK	ANVVPVLVPN	KEVTDGQKNX
NDLNVXRGDS	LQYIVTGDIT	ELAKVDPKTV	TKQGIRDFTD	AEKVTIDLSK	VKVYQADASL
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VKNVEGDFEN	TAVQLTXDGE	TVTNTVINHV	PGSNPSKDVK	ADKNGTVGSV	SLHDKDIPLQ
TKIYYEVKSS	ERPANYGGXT	EEWGMNDVLD	TTHDRFTGKW	HAITXYDLKV	GXKTLKAGTD
ISAYILLENK	DNKDLTFTMN	QALLAALNEG	SNKVGKQAWS	VYLEVERXKT	GDVENTQTEN
YNKELVRSNT	VVTHTPDDPK	PTKAVHNKKG	EXIXHGKVAR	GDVLSYEMTW	DLKGYDKDFA
FDTVLDLATGV	SFFDDYDETX	VTPIKDLLRV	KDSKGXDITN	QFTISWDDAK	GTVTXSAKDP
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EF063-1 (SEQ ID NO:237)

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GTACAAAAAG	ACACTACTTC	TCAACCGACC	AAAGTAGAAG	AAGTAGCGCC	AGAAAAATAA
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CCTAAAGAAT	TTGAAACACC	AGACGTTGAT	AAAGCAGTTG	ATGAAGTAAA	AAAAGATCCA
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GATTTTAATA	AAGTAAATGC	AGGGGATTCA	AAAGATATCT	TTACAAAAAT	ACGGAAAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CCACAAGCCT	TTATTCTAGC	GNATGGTGGG	CAAGAATTGC	GTGTAACNCT	CCCTACAAAA
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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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FNKVNAGDSK DIFTKLRLKDM GGKXTGNFQN SFVKEANLGS NNGYAVLLEK NKPVTVTYTG
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VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLQ
TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GDVLSYEMTW DLKGYDKDFA
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QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQR IKTNTVVNHI PKVXPKKDVV
IKVGDKQSQN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
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GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVVPPTP KTPQAPVEPL
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EF063-3 (SEQ ID NO:239)

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ATTTTCAATT ATGGGAATCC AAAAGAACCA GAAAAAGCAA CGATTGAATT CAATNGATAC

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAAGCCAATG TCGTTCCTGT NCTTGTGCCN AATAAAGAAG TCACTGATGG NCAGAAAAAT
 NTCAATGATT TAAATGTGAA NCGTGGCGAT TCTTTTACAAT ACATTGTGAC AGGGGATACG
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EF063-4 (SEQ ID NO:240)

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EF064-1 (SEQ ID NO:241)

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GATGCAGAAA	AAGTGACGAT	TGATTTATCC	AAAGTGAAAG	TTTATCAAGC	AGACGCAAGT
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EF064-2 (SEQ ID NO:242)

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 KNKAEKERXX KEVAEYNKHK NENSYVNEAI SKNLVFDQSV VTKDTKISSI KGGKFIAKTD
 FNKVNAGDSK DIFTKLRLKDM GGKXTGNFQN SFVKEANLGS NGGYAVLLEK NKPVTVTYTG
 LNASYLGRKI TKAEFVYELQ SSPSQSGTLN AVFSNDPIIT AFIGTNRVNG KDVKTRLTIK
 FFDASGKEVL PDKDSPFAYA LSSLNSSLTN KGGHAEFVSD FGANNAFKYI NGSYVKKQAD
 GKFYSPEDID YGTGPSGLKN SDWDAVGHNK AYFGSGVGLA NGRISFSFGM TTKGKSNVPV
 SSAQWFAXXT NLNAQSVKPI FNYGNPKEPE KATIEFNXYK ANVVPVLVPN KEVTDGQKNX
 NDLNVXRGDS LQYIVTGDIT ELAKVDPKTV TKQGIRDFTD AEKVITIDLSK VKVYQADASL
 NXKDXKAVAA AINSXAKDV TASYXLNLDQ NTVTAMMKTN ADGSVVLAMG YKYLVLVLPFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGVS SLHDKDIPLQ
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GDVLSYEMTW DLKGYDKDFA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

FDTVDLATGV SFFDDYDETX VTPIKDLLRV KDSKXGDITN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQR IKTNNTVNNHI PKVXPBKDVV
 IKVGDQKQSN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVKNKGDDIS KLFTMTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVVPPTP KTPQAPVEPL
 VVEKASVVPE LPQTGEKQNV LLTVAGSLAA MLGLAGLGFK RRKETK

EF064-3 (SEQ ID NO:243)

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 CTNAACGANA AAGACTNAAA AGCTGTTGCT GCAGCNATTA ATTCAGGAAN AGCTAAAGAC
 GTGACTGCTT CTTATGANCT CAATTTAGAT CAAAACACCG TCACAGCAAT GATGAAAACC
 AACGCNGACG GNTCNGTTGT TTTAGCAATG GGGTATAAAT ATTTACTTGT CTTGCCGTTT
 GTAGTGAAAA ATGTAGAAGG CGATTTTGAA AATACAGCTG TTCAGCTGAC AAANGATGGN
 GAAACGGTAA CAAATACAGT GATTAACCAT GTGCCAGCTA GTAATCCTTC CAAAGATGTA
 AAAGCAGATA AAAACGGTAC AGTTGGCAGT GTTTCCTCTAC ATGATAAAGA TATTCCGTTA
 CAAACAAAAA TTTATTATGA AGTGAAATCT TCCGAACGTC CAGCNAACTA TGGCGGAATN
 ACNGAAGAAT GGGGCATGAA TGATGTCTTG GACACGACCC ATGATCGTTT CACAGGNAAA
 TGGCACGCTA TTACNAANTA TGACCTTAAA GTAGGGGANA AAACGTTAAA AGCAGGAACA
 GATATTTCTG CCTACATTCT TTTAGAAAAA AAAGACAATA AAGACTTGAC GTTTACNATG
 AATCAAGCAT TATTGGCNGC NTTAAATGAA GGAAGCAATA AAGTAGGCAA ACAAGCTTGG
 TCTGTGTATC TGGAAGTCGA ACGGATNAAA ACAGGTGACG TAGAAAAACAC GCAAACAGAA
 AACTACAACA AAGAGCTTGT NCGTCTTAAT ACNGTGGTGA CGCATACNCC TGATGATCCA
 AAACCAACCA AAGCCGTTCA TAACAAGAAA GGGGAAGANA TTAANCATGG AAAAGTNGCT
 CGTGGTGATG TTCTTTCTTA TGAAATGACN TGGGACTTAA AAGGGTACGA TAAAGACTTT
 GCCTTTGATA CAGTCGATCT TGCGACAGGC GTTTCCTTCT TCGATGATTA CGATGAAACG
 AANGTGACAC CAATCAAAGA CTTACTTCGT GTCAAAGATT CTAAAGGGGN AGACATTACG
 AACCAGTTCA CGATCTCNTG GGACGATGCC AAAGGCACGG TGACNATNTC TGCCAAAGAC
 CCACAAGCCT TTATTCTAGC GNATGGTGGG CAAGAATTGC GTGTAACNCT CCCTACAAAA
 GTCAAAGCCG ATGTTTCTGG NGATGTTTAT AATTCAGCGG AACAAAATAC ATTTGGNCAA
 CGAATTAAAA CCAATACNGT TGTCAACCAT ATTCCAAAAA TGAANCCTAA AAAAGACGTG
 GTTATTAAAA TNGGTGACAA ACAAAGTCAA AATGGNGCCA CAATCAAATT AGGGGAGAAN
 TTCTTCTATG AATTTACAAG TAGTGACATT CCTGCAGAAT ACCTGCGNGT TGTGGAAGAA
 TGGTCGATTA GCGATAAACT AGACGTCAAA CATGACAAAT TTAGTGCCCA ATGGTCTGTG
 TTTGCCAATT CTAATTTTGT TTTAGCAGAC GGAACCAAAG TGAATAAAGG GGACGACATT
 TCGAAACTAT TCACGATGAC CTTTGAACAA GGGGTAGTGA AAATCACGGC CAGTCAAGCC
 TTTTTNGATG CGATGAATCT AAAAGAAAAA AAAAACGTTG CACACTCATG GAAAGCGTTC
 ATTGGTGTAG AACGAATTGC GGCAGGAGAC GTTTACAACA CAATCGAAGA ATCTTTCAAC
 AATGAGAAGA TTAAACNAA TACGGTAGTG ACNCATACGC CAGAAAAACC ACAAACNCCA
 CCAGAAAAAA CAGTGATTGT ACCACCAACA CCAAAAACAC CGCAAGCACC AGTAGAGCCA
 TTAGTGGTAG AAAAGGCAAG TGTNGTGCCA GAATTGCCGC AAACAGGCGA AAAACAAAAT
 GTCTTATTAA CGGTAGCTGG TAGTTTAGCC GCAATGCTTG GCTTAGCAGG CTTAGGCTTT
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EF064-4 (SEQ ID NO:244)

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 NXKDXKAVAA AINSXKXKDV TASYXLNLDQ NTVTAMMKTN ADGSVVLAMG YKYLVLVLPFV
 VKNVEGDFEN TAVQLTXDGE TVTNTVINHV PGSNPSKDVK ADKNGTVGSV SLHDKDIPLQ
 TKIYYEVKSS ERPANYGGXT EEWGMNDVLD TTHDRFTGKW HAITXYDLKV GXKTLKAGTD
 ISAYILLENK DNKDLTFTMN QALLAALNEG SNKVGKQAWS VYLEVERXKT GDVENTQTEN
 YNKELVRSNT VVTHTPDDPK PTKAVHNKKG EXIXHGKVAR GDVLSYEMTW DLKGYDKDFA
 FDTVDLATGV SFFDDYDETX VTPIKDLLRV KDSKXGDITN QFTISWDDAK GTVTXSAKDP
 QAFILAXGGQ ELRVTLPTKV KADVSGDVYN SAEQNTFGQR IKTNNTVNNHI PKVXPBKDVV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IKVGDQSQSN GATIKLGEXF FYEFTSSDIP AEYAGVVEEW SISDKLDVKH DKFSGQWSVF
 ANSNFVLADG TKVNBKDDIS KLFTMTFEQG VVKITASQAF XDAMNLKENK NVAHSWKAFI
 GVERIAAGDV YNTIEESFNN EKIKTNTVVT HTPEKPQTPP EKTIVIVPPTP KTPQAPVEPL
 VVEKASV

EF065-1 (SEQ ID NO:245)

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 ATGGTGATTG TCGCTGGAAC AGTTGTGGGA AATTTTCAGTC CCACATTGGC TTTCAGCTGAA
 GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CCGTGAAAGT GAAAGACGAC
 AGTCTGGCTG ATTGTAAACG GATATTGGAA GGACAAGCTA CTTTCCCAGT TCAAGCGGGT
 GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
 TTTCCACATG TAAGACAAGC GATTGATGAA GTGGTTCAAG GCTTATCTGA TCAAGACCGC
 GTGATGCTGG CTTTCATATCG CGGCGGAAAA CAATTTATGT TTCCTGATGG AAAGACAAAA
 ATTAATTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA
 AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACC GCCCA
 GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
 ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGCAT
 AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
 TCAGTGGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTAGC GTTAAACCAA
 GAAATTAATA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
 AGTTTCAGTGA ATTCATACTT TGATAAATAT AAAACAGAAAG TGGGTCCTTT TGTAAACCAA
 GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
 TTTACAACCC AATTAATAACA AATTGTCAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
 GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
 GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATT T CAGCAACTAG TACAGAAGGT
 TACGTAGGAA ACATCACGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
 ACCCTTGTA GTAGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
 ACGATTCCCTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
 ACAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
 TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
 GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACTTT TGAATGAAC
 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTACATACG ATACAATGAC TATCACCCT
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 CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATTC CAACAAACCA
 ACCGTAAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAACAGC TTTCGGTAAC
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
 ACTGATGTAA AAGTCACAGA TGAAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
 CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAAACAAG CNGACAGCTA TGACTATTTA
 AGTGGTCATA CGTACACAAT GACCATTACT ACTAAAATCA AAGCTAGCGC AACGGACGAA
 GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
 AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
 GAAGATCCAA CGATTACAAA AGATATCGAA GGCCAAGAAC ATTTAGATTT AACCACCGT
 GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTCGGTA ACGAAACAAG CACATGGACC
 CAAGCCAGCA TGGTGGATGA CATTAATAAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
 GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
 ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
 ATGACTATTA CCACTAAAAA TAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
 GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAACTTTG GCAACGAAGG TGACGTGTTG
 CATTTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
 ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCATTTACC AATGACTAAT
 ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
 TTTGGCATAA CAAAAAATAA AAAAAGAAAA AATTAG

EF065-2 (SEQ ID NO:246)

MF KKATKLLSTM VIVAGTVVGN FSPTLALAE AVKAGDTEGM TNTVKVKDDS
 LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
 MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
 LKLALDYNQ THGDLTNRKT YLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPVVKQE
 LQQGSSTPED FITSQSIDD FTTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
 NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
 IPKNDNAHAC DVTPEPTIT KDIENQEHL LTNREDSFDW HVKTAFGNET STWTQASMVD
 DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLSE HTYTMTITTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHNSNKPT VTPPPVDPNI AKDVEGQEHL
 DLNTRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSYDYLSE GHYTMITIT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHNSNKPT TVTPPAPTPE DPTITKDIEG QEHLDLNTRD QEFKWNVKTA FGNETSTWTQ
 ASMVDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLPKPKP LTPTNHQAPT NPVNFGKSAS KGIHLPMNT TVNPLYMIAG LIVLIVAISF
 GITKNKKRKN

EF065-3 (SEQ ID NO:247)

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 GTGATGCTGG CTTTATATCG CGGCGGAAAA CAATTTATGT TTCCTGATGG AAAGACAAAA
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 GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
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 ACCCTTGTA GATGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
 ACGATTCCTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
 ACAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
 TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
 GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AGTAACACAA GAAATAACA AAGTAACTTT TGAAATGAAC
 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTACATACG ATACAATGAC TATCACCAC
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCCAACCAAG	CCGACTTAAA	CTTTGGCAAT	GAAGGTGACG	TGTTACATTC	CAACAAACCA
ACCGTAACAC	CACCGCCAGT	TGATCCAAAT	ATTGCTAAAG	ACGTAGAAGG	ACAAGAACAT
TTAGATTTAA	CCAACCGCGA	TCAAGAAATTT	AAATGGAACG	TCAAAACAGC	TTTCGGTAAC
GAAACAAGCA	CTTGGACCCA	AGCCAGCATG	GTAGATGACA	TTAATAAAGT	GTTAGACATC
ACTGATGTAA	AAGTCACAGA	TGAAAAATGGT	AAAGATGTTA	CAGCTAACGG	CAAAGTAACA
CAAGAAAATA	ACAAAGTAAC	TTTTGAAATG	AACAANCAAG	CNGACAGCTA	TGACTATTTA
AGTGGTCATA	CGTACACAAT	GACCATTACT	ACTAAAATCA	AAGCTAGCGC	AACGGACGAA
GAATTAGCAC	CTTATATTGA	ACAAGGTGGC	ATTCCCAACC	AAGCCGACTT	GAACCTTGGC
AACGAAGGTG	ACGTGTTGCA	TTCCAACAAA	CCAACCGTAA	CACCACCTGC	ACCAACGCCA
GAAGATCCAA	CGATTACAAA	AGATATCGAA	GGCCAAGAAC	ATTTAGATTT	AACCAACCGT
GACCAAGAAT	TTAAATGGAA	CGTCAAAACA	GCTTTCGGTA	ACGAAACAAG	CACATGGACC
CAAGCCAGCA	TGGTGGATGA	CATTAATAAA	GTGTTAGACA	TCACAGACGT	GAAAGTTNCT
GANGAAAATG	GCAAAGATGT	TACAGATAAT	GGCATAGTAA	CACAAGAAAA	TAACAAAGTA
ACTTTTACTA	TGAACAAAAA	AGATGACAGC	TACTCTTACT	TAGCTGGTCA	TACATACACA
ATGACTATTA	CCACTAAAAT	TAAACTGAC	GCAACGGATG	AAGAATTAGC	GCCTTATATT
GAACAAGGCG	GGATTCCCAA	CCAAGCCGAC	TTAAACTTTG	GCAACGAAGG	TGACGTGTTG
CATTCCAACA	AGCCAACCGT	AACACCGCCT	GCACCAACGC	CAGAAGACCC	AAAAAAACCT
GAACCTAAAC	AACCGCTAAA	ACCGAAAAAA	CCGTTGACGC	CTACAAATCA	TCAAGCACCA
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EF065-4 (SEQ ID NO:248)

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LADCKRILEG	QATFPVQAGE	TEPVDLVVVE	DASGSFSDNF	PHVRQAIDEV	VQGLSDQDRV
MLASYRGGKQ	FMFPDGKTKI	NSADYDMNVR	VNTQLTYDKS	QFVSGFGDVR	TYGGTPTAPG
LKLALDTYNQ	THGDLTNRKT	YFLLVTDGVA	NTRLDGYLHK	TNTNDSINEY	PDPRHPLQVS
VEYSNDYQGA	AAEVLALNQE	ITNQGYEMIN	AYWESVESLS	SVNSYFDKYK	TEVGPFVKQE
LQQGSSTPED	FITSQSIDDF	TTQLKQIVKD	RLAQSTPATA	SLTIANQFDI	QSATATDDAG
NDVPVQINGQ	TISATSTEGY	VGNITIHIEV	KENTAIDAAT	LVSSGTMNQG	TIAKEFPEAT
IPKNDNAHAC	DVTPEDPTIT	KDIENQEHL	LTNREDSFDW	HVKTAFGNET	STWTQASMVD
DINKVLDIID	VKVTDENGKD	VTANGTVTQD	NNKVTFEMNK	QADSYDYLSG	HTYTMITITK
IKTDATDEEL	APYIEQGGIP	NQADLNFQNE	GDVLHSNKPT	VTPPPVDPNI	AKDVEGQEHL
DLTNRDQEFK	WNVKTAFGNE	TSTWTQASMV	DDINKVLDIT	DVKVTDENGK	DVTANGKVTQ
ENNKVTFEMN	XQADSYDYLS	GHTYTMITIT	KIKASATDEE	LAPYIEQGGI	PNQADLNFQNG
EGDVLHSNKP	TVTPPAPTPE	DPTITKDIEG	QEHLDLTNRD	QEFKWNVKTA	FGNETSTWTQ
ASMVDDINKV	LDITDVKVXX	ENGKDVTDNG	IVTQENNKVT	FTMNKKDDSY	SYLAGHTYTM
TITTKIKTDA	TDEELAPYIE	QGGIPNQADL	NFGNEGDVLH	SNKPTVTPPA	PTPEDPKKPE
PKQPLPKPKP	LTPTNHQAPT	NPVNFGKSAS	KGIH		

EF066-1 (SEQ ID NO:249)

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GAAGCGGTTA	AAGCAGGAGA	TACAGAAGGA	ATGACCAATA	CGGTGAAAGT	GAAAGACGAC
AGTCTGGCTG	ATTGTAAACG	GATATTGGAA	GGACAAGCTA	CTTTCCAGT	TCAAGCGGGT
GAAACGGAAC	CAGTCGATTT	AGTAGTTGTT	GAAGATGCTA	GTGGTAGTTT	TTCAGATAAT
TTTCCACATG	TAAGACAAGC	GATTGATGAA	GTGGTTCAAG	GCTTATCTGA	TCAAGACCGC
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ATTAATTCAG	CTGATTATGA	TATGAATGTG	CGCGTCAATA	CGCAATTGAC	TTATGATAAA
AGCCAATTTG	TCTCTGGTTT	TGGAGACGTT	CGGACGTATG	GTGGTACGCC	AACCGCCCCA
GGATTGAAAC	TCGCTTTAGA	TACGTACAAT	CAAACACACG	GAGATTTAAC	GAATCGAAAA
ACGTATTTCC	TATTAGTGAC	AGATGGGGTC	GCTAATACAC	GTTTAGATGG	TTACTTGCAT
AAGACCAATA	CCAATGATTC	AATCAATGAA	TATCCAGATC	CAAGACATCC	TCITTCAAGTC
TCAGTGGAAT	ATAGTAATGA	CTACCAAGGT	GCAGCAGCAG	AAGTTTTAGC	GTTAAACCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
 AGTTCAGTGA ATTCATACTT TGATAAATAT AAAACAGAAG TGGGTCCTTT TGTAACACAA
 GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
 TTTACAACCC AATTAACACA AATTGTCAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
 GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
 GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATTT CAGCAACTAG TACAGAAGGT
 TACGTAGGAA ACATCACGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
 ACCCTTGTA GTAGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
 ACGATTCCCTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
 AAAAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
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 CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATTC CAACAAACCA
 ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAACAGC TTTCCGTTAC
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
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 CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAAACAAG CNGACAGCTA TGACTATTTA
 AGTGGTCATA CGTACACAAT GACCATTAAT ACTAAAATCA AAGCTAGCGC AACGGACGAA
 GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
 AACGAAGGTG ACGTGTGTGA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
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 GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTCGGTA ACGAAACAAG CACATGGACC
 CAAGCCAGCA TGGTGGATGA CATTAAATAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
 GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
 ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
 ATGACTATT AACTTAAAT TAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
 GAACAAGGCG CGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTG
 CATTCACACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
 GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
 ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCATTTACC AATGACTAAT
 ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
 TTTGGCATAA CAAAAAATAA AAAAAGAAAA AATTAG

EF066-2 (SEQ ID NO:250)

MF KKATKLLSTM VIVAGTVVGN FSPTLALAE AVKAGDTEGM TNTVKVKDDS
 LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
 MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
 LKLALDTYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFPVKQE
 LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
 NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
 IPKNDNAHAC DVTPEPTIT KDIENQEHL LTNREDSFDW HVKTAFGNET STWTQASMVD
 DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLSE HTYTMTITTK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHNSNKPT VTPPPVDPNI AKDVEGQEH
 DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSYDYLSE GHTYTMTITTK KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHNSNKP TVTPAPTPE DPTITKDIEG QEHLDTNRD QEFKWNVKTA FGNETSTWTQ
 ASMVDINKV LDITDVKVXX ENKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PKQPLKPKKP LTPTNHQAPT NPVNFGKSAS KGIHLPMNTN TVNPLYMIAG LIVLIVAISF
GITKNKKRKN

EF066-3 (SEQ ID NO:251)

GGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CGGTGAAAGT GAAAGACGAC
AGTCTGGCTG ATTGTAAACG GATATTGGAA GGACAAGCTA CTTTCCCAGT TCAAGCGGGT
GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
TTTCCACATG TAAGACAAGC GATTGATGAA GTGGTTCAAG GCTTATCTGA TCAAGACCGC
GTGATGCTGG CTTCATATCG CGGCGGAAAA CAATTTATGT TTCCTGATGG AAAGACAAAA
ATTAATTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA
AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACCGCCCCA
GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGCAT
AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
TCAGTGGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTAGC GTTAAACCAA
GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
AGTTCAGTGA ATTCATACTT TGATAAATAT AAAACAGAAG TGGGTCCTTT TGTAACAACAA
GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
TTTACAACCC AATTAAAACA AATTGTCAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATT T CAGCAACTAG TACAGAAGGT
TACGTAGGAA ACATCACGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
ACCCTTGTA GTAGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
ACGATTCCCTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
ACAAAAGATA TCGAAAATCA AGAACAATTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCA

EF066-4 (SEQ ID NO:252)

AVKAGDTEGM TNTVKVKDDS
LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
LKLALDTYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPVVKQE
LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
IPKNDNAHAC DVTPEPTIT KDIENTEHL DLTNREDSFDW HVKTAFGNET STWTQASMVD
DINKVLDIID VKVT

EF067-1 (SEQ ID NO:253)

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GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CGGTGAAAGT GAAAGACGAC
AGTCTGGCTG ATTGTAAACG GATATTGGAA GGACAAGCTA CTTTCCCAGT TCAAGCGGGT
GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
TTTCCACATG TAAGACAAGC GATTGATGAA GTGGTTCAAG GCTTATCTGA TCAAGACCGC
GTGATGCTGG CTTCATATCG CGGCGGAAAA CAATTTATGT TTCCTGATGG AAAGACAAAA
ATTAATTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA
AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACCGCCCCA
GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTGCAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

AAGACCAATA CCAATGATTTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
TCAGTGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTAGC GTTAAACCAA
GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
AGTTTCAGTGA ATTACACTTT TGATAAATAT AAAACAGAAG TGGGTCCTTT TGTAACAACA
GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
TTTACAACCC AATTAAAAACA AATTGTCAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATTT CAGCAACTAG TACAGAAGGT
TACGTAGGAA ACATCACGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
ACCCTTGTAA GTAGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
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ACAAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACCTT TGAAATGAAC
AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTCATACGT ATACAATGAC TATCACCACCT
AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATTC CAACAAACCA
ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAACAGC TTTCCGGTAAC
GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
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CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAANCAAG CNGACAGCTA TGACTATTTA
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GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
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CAAGCCAGCA TGGTGGATGA CATTAAATAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
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ATGACTATTA CCACTAAAAT TAAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCATTTACC AATGACTAAT
ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
TTTGGCATAA CAAAAAATAA AAAAAGAAAA AATTAG

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EF067-2 (SEQ ID NO:254)

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MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
LKLALDTYNQ THGDLTNRKT YLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGFVVKQE
LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
IPKNDNAHAC DVTPEDPITIT KDIENQEHLD LTNREDSFDW HVKTAFGNET STWTQASMVD
DINKVLDIID VKVTDENGKD VTANGTVTQE NNVKVFEMNK QADSYDYLSE HTYTMTITTK
IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHSNKPT VTPPPVDPNI AKDVEGQEHLE
DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIIT DVKVTDENGK DVTANGKVTO
ENNVKVFEMN XQADSYDYLSE GHTYTMTITT KIKASATDEE LAPYIEQGGI PNQADLNFGN
EGDVLHSNKP TVTPPAPTPE DPTITKDIEG QEHLDTNDRD QEFKWNVKA FGNSTSTWTQ

```


TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNFGKSAS KGIHLPMNT TVNPLYMIAG LIVLIVAISF
 GITKNKKRKN

EF067-3 (SEQ ID NO:255)

GCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACTTT TGAAATGAAC
 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTACATACGT ATACAATGAC TATCACCACCT
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
 CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATTC CAACAAACCA
 ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAACAGC TTTCGGTAAC
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
 ACTGATGTAA AAGTCACAGA TGAAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
 CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAAACAAG CNGACAGCTA TGACTATTTA
 AGTGGTCATA CGTACACAAT GACCATTACT ACTAAATCA AAGCTAGCGC AACGGACGAA
 GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
 AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
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 CAAGCCAGCA TGGTGGATGA CATTAATAAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
 GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
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 GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
 CATTCACAAC AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
 GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
 ACGAACCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TT

EF067-4 (SEQ ID NO:256)

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 DLNDRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENGK DVTANGKV
 ENNKVTFEMN XQADSYDYLGS HTYTMITTK KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHSNKP TVTPPAPTPE DPTITKDIEG QEHLDLNDRD QEFKWNVKTA FGNETSTWTQ
 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNFGKSAS KGIH

EF068-1 (SEQ ID NO:257)

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 CGCAAGATGC TTAATTTAGC AATATCAAGT GGTATTATTAT TTACGTCATT AGCAATCCCT
 GTAAGTATAG CTGTTACCTC TGGCACAATC AGTGCATCAG CAGCGGTCTT GGATATCGAA
 CTATTATCAA ATGTTACGTC AAATAATGAC AGTGGCACTT CAACGAGTAA TCGTTGGACA
 GCCGCAACC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCCTCCTGA GTTAAGAGGA
 AATGTAGCTG CAGCAGGCAG CGCAGCAATC AATACCAATG TCACGATTGA TCTTTCAAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTTACTTTTT	TGACTGCCGT	TTTGAATGCA	GCCAATGATT	TAACCAATGT	GATTACTCAA
ATTACCAGTG	GGGCGTTAGG	GAATTTAACT	GGTGTGATA	TTGATTTGAC	GGAAGTGAAT
CGTCAATTGG	AATTAGTTAA	TAACATTGAA	AACTTAGGTG	CTGCTTCATT	TACAGCTCCG
GAAACGTTAG	CAGCTGACGG	CTCATACATT	AGTGCACCGA	TTAGTGATGG	TTTAGGGTTA
GTTTTAGCCC	AAAATGTTTC	AAACATCTTA	CAAGATTTGA	ATGCGGCAGT	TCAAGCTTTG
GAGGCAAAAG	GTACCAGTAT	CCCAAGTAAT	CTTGTCGCCG	CAGCTATAAA	TGCAGCCTTG
CTTCCTGTCA	AAGGCACGGT	AAACGTGGCT	GTTTCAGGTG	CTTTGCCTTT	ATTAGCGGTT
GGTGGTTTCA	GCGTAAATGA	GTTAGTGGAT	GCTTCTTTAC	TAGGCACAAC	CACGGTTACT
TTACCAACTA	CCGTTTCAAC	ACCTCAAAAT	TTATCCAATA	ATTTAGATGC	TCGTTTTGTA
GGAACAGTCG	TTCAAAACAG	TCTTTTAGAC	GTTAATTTAT	TAGCAACAGC	AGACGGTGTA
TCCAACATTT	ATTTTGCTGC	AGGCACTACT	AGTGAAGTAA	CCGCACCAAC	AATCACAGGA
GTAACAGGTA	ATTCAACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
GTTGAAATCC	GAAATGCAGG	AGGCACCGTA	ATAGGCACAG	GTACCGCTGA	TGGGACAGGA
GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA	GCAGGCGCCA	ATGAAACGTT	AACCGCCGTA
GCGAAAAACG	CCAGCGGNAC	AGAAAGNACG	CCAACAACGT	TCCAAACNCC	AGCGGATGAA
GCAACCGTAA	CCGCACCAAC	AATCACAGGA	GTGACAGGTA	ATTCAACGGC	AGGTTACGAA
GTTAAAGGAA	CTGCCGATGC	CAATGCCACG	GTTGAAATCC	GAAATGCAGG	AGGCACCGTA
ATAGGCACAG	GTACCGCTGA	TGGGACAGGA	GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA
GCAGGTGCCA	ATGAAACGTT	AACCGCCGTA	GCGAAAAACG	CCAGCGGCAC	AGAAAGTACG
CCAACAACGT	TCCAAACACC	AGCGGATGAA	GCAACCGTAA	CCGCACCAAC	AATCACAGGA
GTGACAGGTA	ATTCAACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
GTTGAGATCC	GAAATGCAGG	AGGTGCCGTG	ATAGGTACAG	GTACTGCTGA	TGGGACAGGG
GCATTTACAG	TTACCATTC	CGCAGGTGAA	GCAGGTGCGA	ATGAAACGTT	AACCGCCGTA
GCGAAAAACG	CCAGCGGTAC	AGAAAGTACG	CCAACAACGT	TCCAAACGCC	AGCGGATCCT
AATACGCCCG	TGGCGACGCC	AATTGTTGAG	ACTGTAACAG	GTAGTACAAC	AAAAGGCTAT
GAGGTCAAAG	GGACTGCTGA	AGTTGGCACC	ACCATTGAGG	TTCGCGATGC	AGCTGGCACC
GTCCTTGTTA	CTGCAACAAC	TGGAACGTAC	GGAAAATATA	CAGTGACTTT	AGATTTCAGGA
ACAGCAACAG	CAAAATCAAAC	GCTGAGCGTT	GTAGCGAAAA	ACGCTAGTGG	CACGGAAGAT
CAACCAGCAA	CGGCGACAAC	ACCAGCTGAT	GTCACGTCAC	CAACAGTTGA	TAACAGTACA
GGCAACTCTG	GTTTCGGTTA	TGAAATTACA	GGAACAGCAG	ACCCTAACAC	AACAATCGAA
GTTCTGTGATC	CATCTGGGGC	AGTCATTGGT	ACAGGTACCT	CTGATGCGAA	TGGTGATTTT
ACTGTAACGC	TACCAACGGG	AACGACCAAT	CCTGGGGATA	CGTTAACAGT	GATTGGAAAG
GATAACGCGG	GAAATGAAAG	TCAACCGACT	GAAGTCCTTG	TTCCTGCTGA	TGCCACGGTT
ACAGCACCAA	CTGTAACAGG	AGTAACAGGT	AATTCAGTTG	CTGGTTATCA	GGTGACAGGC
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GGGACTGCCG	ATGGGACTGG	TTCTTTTGCT	GTGAACCTTC	CAGCTGGGAC	GGCAAATGCG
AATGAAACAT	TGACAGCGTT	AGCCAAAGAT	CCTGCTGGCA	ATACAAGTAC	ACCGACAACC
TTCCAAACAC	CAGCAGATGA	AGTAGTGGCA	CCGCCAAGTG	TCGACAAAGT	TACTGGGAAT
ACAACACAAG	GATATCAAGT	GACAGGTACC	GCTGAACTTG	GCACCACCAT	TGAAGTTCGT
GCAACAGACG	GAACAGTTTT	AGGCACCGCA	ACAACCTGGAC	CGACTGGCCA	ATATACTGTG
ACGTTAGCTT	CAGGAAAAGC	AACAGCTAAA	CAAACAGTGA	ATGTAGTTGC	TAAAAATGAT
ACTGGACTTG	AGAGTCAACC	AACTACAGCT	ATGACACCCG	CTGATGTTAC	CACACCAACA
ATTGGTGACA	TTACTGGAGA	TTCACAACT	GGTTATGAAA	TCACTGGGAC	GGCGGACCC
AATACCACCA	TTGAAGTACG	GAACCCAGAT	GGAACAATTA	TTGGTACAAC	GACAACGGAT
GATCAAGGAA	ACTTTACTGT	GGACCTTCCA	GCGGGAGCCG	CTAATCCTGG	TGATACATTA
ACAGTTGTTG	GAAAAGACGG	TGACGGCAAT	GAAAGTCAAC	CAACGGAAGT	GACGGTCCCT
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TATCAAGTAA	CCGGCACGGC	AGAGCCAAAT	GTCACCATTG	AGATTCACAA	TGAAGCAGGT
TTAGTTATTG	CTACGGGAAC	GACTGATGGT	GCTGGCGCAT	TTACAATCAC	TCTTCCGACG
GGCACAGCAA	CAGCTAACGA	AGCCTTAACT	GCCATTGCGA	AAGATGCTGC	TGGGAAAGAA
AGTAATCCGA	CTGCTTTCAA	AACACCTGCT	GATCCAGATG	CACCAGTCGC	GACACCTACT
GTTGACAAAA	TCACTGGTAG	CACGACAAAC	GGCTATCAAG	TAGTAGGAGC	AGCAGAAGTT
GGTACAACAG	TTGAGGTGCG	TGACGCCGAT	GGCACAGTCC	TTGGCATGGC	AACTACTGGA
ACTGATGGCA	AATACACAGT	GACTTTAGAG	CCAGGGAAGG	CCTCAGCTAA	CGAAACAATA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACTGTCGTAG	CGAAAAATGC	AACAGGAAAA	GAAAGTCAGC	CAGCTACAGC	AACTACACCA
GTCGACTTAG	CCACACCAAC	CATTGATTCT	ATTACCGGAA	ATTCTAGTAA	AGGTTACGAA
ATCACTGGAA	CGGCGGAGCC	AAAAACCACT	ATTGATGTCC	GTGACGCAGA	CGGAACCATC
ATTGCTGCTA	CAACTGCTAA	CGAAACCGGC	CAATATACGG	TGACTCTACC	AGCTGGCGTA
GTGACACCAG	GAGAAACGAT	TACGATTATT	AGCAAAGATG	GCGCAGGTAA	TGAAAAGTCAA
CCAGCTACAG	CCGTTATTCC	AGCGGATGTT	GTTTTAGCGG	CGCCAACTAT	TACGAAGGTT
GAAGGAAACA	AAGCCAATGG	CTATACAGTC	ACTGGAAGTG	CTGATCCAAA	TGTCACGGTT
CAATTTTACA	ATAGCAGTGA	ACAATTATTG	GCAAGTGGCA	ATACAACTAC	TGGAGGTACC
TTCTCCGTTT	ATATTGCAGC	AGGGTTAGCA	ACAGAAAAAG	AAACGTTAAC	CGCACTAACC
ACAGATACAC	AAGGAAATGT	GAGTCCTAAA	ACCACATTTA	TGACGCCAGC	CGATATTACG
GGAGAACCAG	AGATTAAAT	TGCGGCACCA	ACTGTTTCTT	CAGTTTTAGG	AACGTCTAAA
GCCGGCTACC	TCATCAAAGG	AACAGCTGAA	CCAAACCGAA	TCATTCAAAT	TAGTAACCGA
CTATTAAGAA	GTGTGATTGC	TGTAGGTGCC	ACCGATGCTG	AAGGCAACTT	CGCTATCCAA
TTAACAGCGG	GACAAGCGAC	TGCTCAACAA	AGTTTACTTG	CGACAGCTAC	CGATGGCGCA
GGACATTACA	GTACGGCTAC	AACCTTCATG	ACGCCAGCCG	ACCCAACGAA	TCCTGGAGGA
GGCAATGGTA	ACACTGGCGG	AAATAACGGC	AATACAGGCG	GCAATACAGG	AAACAATGGC
GCAACTGGCG	GGAATAATGG	GAATGGTTCA	AACACAGGTT	CAAATCCAAA	TGGAGGTTCT
GGTTTAGGCA	CAACAGGTTT	TGGCTTAGGT	TCCTAGGCA	ATGGCCTCGG	TACAAATGGT
AGTGGCTACC	ACCCTAAACT	AAGTACCATC	AGTTATGGCA	CTGGAAATCA	CGGGAAAAACA
GGCTACTTAC	CTAGCACAGG	TGAAAAAGAG	TCTTCAGCCG	TGACAACAAG	TTTGTGTTGGC
GCCTTTGTGC	CACTCCTTGC	GAGCATGGGA	ATCATCAAAC	GCAAACGTAA	AAACTAG

EF068-2 (SEQ ID NO:258)

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SIAVTSGTIS	ASAAYLDIEL	LSNVTSNNDS	GTSTSNRWTA	ANQNQPVNFT	VSGGALADAS
AVFSGQKQAV	LVPPELRGN	VAAAGSAAIN	TNVTIDLSKV	TFLTAVLNAA	NDLTNVITQI
TSGALGNLTG	VDIDLTEVNR	QLELVNNIEN	LGAASFTAPE	TLAADGSYIS	APISDGLGLV
LAQNVSNILQ	DLNAAVQALE	AKGTSIPSNL	VAAAINAALL	PVKGTVNVAV	SGALPLLAVG
GSQVNELVDA	SLLGTTTVTL	PTTVSTPQNL	SNNLDARFVG	TVVQTDLLDV	NLLATADGVS
NIYFAAGTTS	EVTAPTITGV	TGNSTAGYEV	KGTADANATV	EIRNAGGTVI	GTGTADGTGA
FTVTVPAGEA	GANETLTAVA	KNASGTESTP	TTFQTPADEA	TVTAPTITGV	TGNSTAGYEV
KGTADANATV	EIRNAGGTVI	GTGTADGTGA	FTVTVPAGEA	GANETLTAVA	KNASGTESTP
TTFQTPADEA	TVTAPTITGV	TGNSTAGYEV	KGTADANATV	EIRNAGGTVI	GTGTADGTGA
FTVTVPAGEA	GANETLTAVA	KNASGTESTP	TTFQTPADEA	TVTAPTITGV	TGNSTAGYEV
VKGTAIEVGT	IEVRDAAGTV	LGTATTGTG	KYTVTLDSGT	ATANQTLVSV	AKNASGTESQ
PATATTPADV	TAPTVDNITG	NSGSGYEITG	TADPNTTIEV	RDPSGAVIGT	GTSDANGDFT
VTLPTGTTNP	GDTLTVIGKD	NAGNESQPT	VLVPADATVT	APTVTGVTGN	SVAGYQVTGT
ADPNATIEIR	DADGNVIATG	TADGTGSFAV	NLPAGTANAN	ETLTALAKDP	AGNTSTPTTF
QTPADEVVAP	PSVDKVTGNT	TQGYQVTGTA	ELGTTIEVRA	TDGTVLGTAT	TGPTGQYTVT
LASGKATAKQ	TVNVVAKNDT	GLSQPTTAM	TPADVTTPTI	GDITGDSTTG	YEITGTADPN
TTIEVRNPDG	TIIGTTTTDD	QGNFTVDLPA	GAANPGDTLT	VVGKDGDNNE	SQPTIEVTVPE
DATVAAPTPT	TVTGTATATG	QVTGTAEPNV	TIEIHNEAGL	VIATGTTDGA	GAFITLPTG
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TTVEVRDADG	TVLGMATTGT	DGKYTVTLEP	GKASANETIT	VVAKNATGKE	SQPATATTPV
DLATPTIDSI	TGNSSKGYEI	TGTAEPKTTI	DVRDADGTII	AATTANETGQ	YTVTLFAGVV
TPGETITIIIS	KDGAGNESQP	ATAVIPADV	LAAPTITKVE	GNKANGYTVT	GTADPNVTVQ
FYNSSQQLLA	SGNTTTGGTF	SVHIAAGLAT	EKETLTALTT	DTQGNVSPKT	TFMTPADITG
EPEIKIAAPT	VSSVLGTSKA	GYLIKGTAE	NRIIQISNRL	LRSVIAVGAT	DAEGNFIAQL
TAGQATAQQS	LLATATDGAG	HYSTATTFMT	PADPTNPGGG	NGNTGGNNGN	TGGNTGNNGA
TGGNNGNGSN	TGSNPNNGSG	LGTGSGGLGS	LGNGLGTTNGS	GYHPKLSTIS	YGTGNHGKGT
YLPSTGEKES	SAVTTSLFGA	FVALLASMG	IKRKRKN		

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF068-3 (SEQ ID NO:259)

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 CTATTATCAA ATGTTACGTC AAATAATGAC AGTGGCACTT CAACGAGTAA TCGTTGGACA
 GCCGCAAACC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCCTCCTGA GTTAAGAGGA
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 ATAGGCACAG GTACCGCTGA TGGGACAGGA GCGTTTACAG TTACCGTTCC CGCAGGTGAA
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 CCAACAACGT TCCAAACACC AGCGGATGAA GCAACCGTAA CCGCACCAAC AATCACAGGA
 GTGACAGGTA ATTCAACAGC AGGTACGAA GTTAAAGGAA CTGCCGATGC CAATGCCACG
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 GCATTTACAG TTACCATTC CGCAGGTGAA GCAGGTGCGA ATGAAACGTT AACC GCCGTA
 GCGAAAAACG CCAGCGGTAC AGAAAGTACG CCAACAACGT TCCAAACGCC

EF068-4 (SEQ ID NO:260)

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 AVFSGQKQAV LVVPPPELRGN VAAAGSAAIN TNVTIDLSKV TFLTAVLNAA NDLTNVTIQI
 TSGALGNLTG VDIDLTEVNR QLELVNNIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
 LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTNVNAV SGALPLLAVG
 GSGVNELVDA SLLGTTTVTL PTTVSTPQNL SNNLDARFVG TVVQTDLLDV NLLATADGVS
 NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
 FTVTVPAGEA GANETLTAVA KNASGTEXTPT TTFQTP

EF069-1 (SEQ ID NO:261)

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 CGCAAGATGC TTAATTTAGC AATATCAAGT GGTATTATTAT TTACGTCAAT AGCAATCCCT
 GTAAGTATAG CTGTTACCTC TGGCACAATC AGTGCATCAG CAGCGGTCTT GGATATCGAA
 CTATTATCAA ATGTTACGTC AAATAATGAC AGTGGCACTT CAACGAGTAA TCGTTGGACA
 GCCGCAAACC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
 TCCGCTGTGT TTAGTGGACA AAAACAAGCG GTGTTAGTGG TTCCTCCTGA GTTAAGAGGA
 AATGTAGCTG CAGCAGGCAG CGCAGCAATC AATACCAATG TCACGATTGA TCTTTCAAAA
 GTTACTTTTT TGACTGCCGT TTTGAATGCA GCCAATGATT TAACCAATGT GATTACTCAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATTACCACTG	GGGCGTTAGG	GAATTTAACT	GGTGTTGATA	TTGATTTGAC	GGAAGTGAAT
CGTCAATTGG	AATTAGTTAA	TAACATTGAA	AACTTAGGTG	CTGCTTCATT	TACAGCTCCG
GAAACGTTAG	CAGCTGACGG	CTCATACATT	AGTGCACCGA	TTAGTGATGG	TTTAGGGTTA
GTTTTAGCCC	AAAATGTTTC	AAACATCTTA	CAAGATTTGA	ATGCGGCAGT	TCAAGCTTTG
GAGGCAAAAG	GTACCAGTAT	CCCAAGTAAT	CTTGTCGCCG	CAGCTATAAA	TGCAGCCTTG
CTTCCTGTCA	AAGGCACGGT	AAACGTGGCT	GTTTCAGGTG	CTTTGCCTTT	ATTAGCGGTT
GGTGGTTTCA	GCGTAAATGA	GTTAGTGGAT	GCTTCTTTAC	TAGGCACAAC	CACGGTTACT
TTACCAACTA	CCGTTTCAAC	ACCTCAAAAT	TTATCCAATA	ATTTAGATGC	TCGTTTTGTA
GGAACAGTCG	TTCAAACAGA	TCTTTTAGAC	GTTAATTTAT	TAGCAACAGC	AGACGGTGTA
TCCAACATTT	ATTTTGCTGC	AGGCACTACT	AGTGAAGTAA	CCGCACCAAC	AATCACAGGA
GTAACAGGTA	ATTCAACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
GTTGAAATCC	GAAATGCAGG	AGGCACCGTA	ATAGGCACAG	GTACCGCTGA	TGGGACAGGA
GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA	GCAGGCGCCA	ATGAAACGTT	AACCGCCGTA
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GCAACCGTAA	CCGCACCAAC	AATCACAGGA	GTGACAGGTA	ATTCAACGGC	AGGTTACGAA
GTTAAAGGAA	CTGCCGATGC	CAATGCCACG	GTTGAAATCC	GAAATGCAGG	AGGCACCGTA
ATAGGCACAG	GTACCGCTGA	TGGGACAGGA	GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA
GCAGGTGCCA	ATGAAACGTT	AACCGCCGTA	GCGAAAAACG	CCAGCGGCAC	AGAAAGTACG
CCAACAACGT	TCCAAACACC	AGCGGATGAA	GCAACCGTAA	CCGCACCAAC	AATCACAGGA
GTGACAGGTA	ATTCAACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
GTTGAGATCC	GAAATGCAGG	AGGTGCCGTG	ATAGGTACAG	GTACTGCTGA	TGGGACAGGG
GCATTTACAG	TTACCATTCC	CGCAGGTGAA	GCAGGTGCGA	ATGAAACGTT	AACCGCCGTA
GCGAAAAACG	CCAGCGGTAC	AGAAAGTACG	CCAACAACGT	TCCAAACGCC	AGCGGATCCT
AATACGCCCC	TGGCGACGCC	AATTTGTTGAG	ACTGTAACAG	GTAGTACAAC	AAAAGGCTAT
GAGGTCAAAG	GGACTGCTGA	AGTTGGCACC	ACCATTGAGG	TTCCGCGATG	AGCTGGCACC
GTCCTTGGTA	CTGCAACAAC	TGGAACGTGAC	GGAAAAATATA	CAGTGACTTT	AGATTCAGGA
ACAGCAACAG	CAAATCAAAC	GCTGAGCGTT	GTAGCGAAAA	ACGCTAGTGG	CACGGAAAGT
CAACCAGCAA	CGGCGACAAC	ACCAGCTGAT	GTCACTGCAC	CAACAGTTGA	TAACATCACA
GGCAACTCTG	GTTTCGGGTTA	TGAAATTACA	GGAACAGCAG	ACCCTAACAC	AACAATCGAA
GTTTCGTGATC	CATCTGGGGC	AGTCATTGGT	ACAGGTACCT	CTGATGCGAA	TGGTGATTTT
ACTGTAACCG	TACCAACGGG	AACGACCAAT	CCTGGGGATA	CGTTAACAGT	GATTGGAAAG
GATAACGCGG	GAAATGAAAG	TCAACCGACT	GAAGTCCTTG	TTCTGCTGTA	TGCCACGGTT
ACAGCAACAA	CTGTAACAGG	AGTAACAGGT	AATTCAGTTG	CTGGTTATCA	GGTGACAGGC
ACCGCTGATC	CGAATGCTAC	CATCGAAATT	CGTGATGCAG	ATGGGAACGT	GATTGCAACA
GGGACTGCCG	ATGGGACTGG	TTCTTTTGCT	GTGAACCTTC	CAGCTGGGAC	GGCAAATGCG
AATGAAACAT	TGACAGCGTT	AGCCAAAGAT	CCTGCTGGCA	ATACAAGTAC	ACCGACAACC
TTCCAAACAC	CAGCAGATGA	AGTAGTGGCA	CCGCCAAGTG	TCGACAAAGT	TACTGGGAAT
ACAACACAAG	GATATCAAGT	GACAGGTACC	GCTGAACTTG	GCACCACCAT	TGAAGTTCGT
GCAACAGACG	GAACAGTTTT	AGGCACCGCA	ACAACCTGGAC	CGACTGGCCA	ATATACTGTG
ACGTTAGCTT	CAGGAAAAGC	AACAGCTAAA	CAAAACAGTGA	ATGTAGTTGC	TAAAAATGAT
ACTGGACTTG	AGAGTCAACC	AACACAGCT	ATGACACCCG	CTGATGTTAC	CACACCAACA
ATTGGTGACA	TTACTGGAGA	TTCAACAAC	GGTTATGAAA	TCACTGGGAC	GGCGGACCC
AATACCACCA	TTGAAGTACG	GAACCCAGAT	GGAACAATTA	TTGGTACAAC	GACAACGGAT
GATCAAGGAA	ACTTTACTGT	GGACCTTCCA	GCGGGAGCCG	CTAATCCTGG	TGATACATTA
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GAAGATGCAA	CCGTAGCAGC	ACCAACTGTG	ACGACTGTTA	CAGGAACAAC	TGCCACTGGG
TATCAAGTAA	CCGGCACGGC	AGAGCCAAAT	GTCAACATTG	AGATTACAAA	TGAAGCAGGT
TTAGTTATTG	CTACGGGAAC	GACTGATGGT	GCTGGCGCAT	TTACAATCAC	TCTTCCGACG
GGCACAGCAA	CAGCTAACGA	AGCCTTAAC	GCCATTGCGA	AAGATGCTGC	TGGGAAAGAA
AGTAATCCGA	CTGCTTTCAA	AACACCTGCT	GATCCAGATG	CACCAAGTCG	GACACCTACT
GTTGACAAAA	TCACTGGTAG	CACGACAAAC	GGCTATCAAG	TAGTAGGAGC	AGCAGAAGTT
GGTACAACAG	TTGAGGTGCG	TGACGCCGAT	GGCACAGTCC	TTGGCATGGC	AACTACTGGA
ACTGATGGCA	AATACACAGT	GACTTTAGAG	CCAGGGAAGG	CCTCAGCTAA	CGAAACAATA
ACTGTCGTAG	CGAAAAATGC	AACAGGAAAA	GAAAGTCAGC	CAGCTACAGC	AACACACCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GTCGACTTAG CCACACCAAC CATTGATTCT ATTACCGGAA ATTCTAGTAA AGGTTACGAA
ATCACTGGAA CGGCGGAGCC AAAAACCCTT ATTGATGTCC GTGACGCAGA CGGAACCATC
ATTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGA CTCTACC AGCTGGCGTA
GTGACACCAG GAGAAACGAT TACGATTATT AGCAAAGATG GCGCAGGTAA TGAAAGTCAA
CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTTTAGCGG CGCCAACCTAT TACGAAGGTT
GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAACTG CTGATCCAAA TGTCACGGTT
CAATTTTACA ATAGCAGTGA ACAATTATTG GCAAGTGGCA ATACAACCTAC TGGAGGTACC
TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAC CGCCTAACCT
ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAGC CGATATTACG
GGAGAACCAG AGATTAAAAT TGCGGCACCA ACTGTTTCTT CAGTTTATAGG AACGTCTAAA
GCCGGCTACC TCATCAAAGG AACAGCTGAA CCAAACCGAA TCATTCAAAT TAGTAACCGA
CTATTAAGAA GTGTGATTGC TGTAGGTGCC ACCGATGCTG AAGGCAACTT CGCTATCCAA
TTAACAGCGG GACAAGCGAC TGCTCAACAA AGTTTACTTG CGACAGCTAC CGATGGCGCA
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GCAACTGGCG GGAATAATGG GAATGGTTCA AACACAGGTT CAAATCCAAA TGGAGGTTCT
GGTTTAGGCA CAACAGGTTT TGGCTTAGGT TCACTAGGCA ATGGCCTCGG TACAAATGGT
AGTGGCTACC ACCCTAAACT AAGTACCATC AGTTATGGCA CTGGAAATCA CGGGAAAACA
GGCTACTTAC CTAGCACAGG TGAAAAAGAG TCTTCAGCCG TGACAACAAG TTTGTTTGGC
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EF069-2 (SEQ ID NO:262)

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M KKKIVEDFNR KSQHKWTKR KMLNLAISSG LLFTSLAIPV
SIAVTSGTIS ASAAVLDEL LSNVTSNNDG GTSTSNRWT AANQNQPVNFT VSGGALADAS
AVFSGQKQAV LVVPELRGN VAAAGSAAIN TNVTIDLSKV TFLTAVLNAA NDLTNVITQI
TSGALGNLTG VDIDLTEVNR QLELVNNIEN LGAASTAPE TLAADGSYIS APISDGLGLV
LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTVNVAV SGALPLAVG
GSGVAGELVDA SLLGTTTTL PTTVSTPQNL SNNLDARFVG TVVQTDLLDV NLLATADGVS
NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
FTVTVPAGEA GANETLTAVA KNASGTEXTP TTFQTPADEA TVTAPTITGV TGNSTAGYEV
KGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA KNASGTESTP
TTFQTPADEA TVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGAVI GTGTADGTGA
FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
VKGTAEVGTI IEVRDAAGTV LGTATTGTDG KYTVTLDSGT ATANQTLSSV AKNASGTESQ
PATATTPADV TAPTVDNITG NSGSGYEITG TADPNTTIEV RDPGAVIGT GTSDANGDFT
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LASGKATAKQ TVNVVAKNDT GLESQPTTAM TPADVTTPTI GDITGDSTTG YEITGTADPN
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TTVEVRDADG TVLGMATTGT DGKYTVTLEP GKASANETIT VVAKNATGKE SQPATATTPV
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TPGETITIIIS KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGYTVT GTADPNVTQV
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TGGNNGNGSN TGSNPNGGSG LGTTGSGLGS LGNGLGTNGS GYHPKLSTIS YGTGNHGKGTG
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EF069-3 (SEQ ID NO:263)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 GAGGTCAAAG GGACTGCTGA AGTTGGCACC ACCATTGAGG TTCGCGATGC AGCTGGCAGC
 GTCCTTGGTA CTGCAACAAC TGGAACGTAC GGAAAATATA CAGTGACTTT AGATTTCAGGA
 ACAGCAACAG CAAATCAAAC GCTGAGCGTT GTAGCGAAAA ACGCTAGTGG CACGGAAAAGT
 CAACCAGCAA CGGCGACAAC ACCAGCTGAT GTCAGTGCAC CAACAGTTGA TAACATCACA
 GGCAACTCTG GTTCGGGTTA TGAAATTACA GGAACAGCAG ACCCTAACAC AACAATCGAA
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 ACTGGACTTG AGAGTCAACC AACTACAGCT ATGACACCCG CTGATGTTAC CACACCAACA
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EF069-4 (SEQ ID NO:264)

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 PATATTPADV TAPTVDNITG NSGSGYEITG TADPNTTIEV RDPGAVIGT GTSANGDFT
 VTLPTGTTNP GDTLTVIGKD NAGNESQPTL VLVPADATVT APTVTGVTGN SVAGYQVTGT
 ADPNATIEIR DADGNVIATG TADGTGSFAV NLPAGTANAN ETLTALAKDP AGNTSTPTTF
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 LASGKATAKQ TVNVVAKNDT GLESQPTTAM TPADVTTPTI GDITGDSTTG YEITGTADPN
 TTIEVRNPDG TIIGTTTTDD QGNFTVDLPA GAANPGDTLT VVGKGDGNE SQPTEVTVP
 DATVAAPTPTV TVTGT

EF070-1 (SEQ ID NO:265)

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 GTAAGTATAG CTGTTACCTC TGGCACAATC AGTGCATCAG CAGCGGTCCT GGATATCGAA
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 GCCGCAAACC AAAATCAACC AGTTAATTTT ACGGTTTCTG GTGGCGCTTT AGCAGATGCT
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 GTTACTTTTT TGAAGTCCGT TTTGAATGCA GCCAATGATT TAACCAATGT GATTACTCAA
 ATTACCAGTG GGGCGTTAGG GAATTTAACT GGTGTTGATA TTGATTTGAC GGAAGTGAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CGTCAATTGG	AATTAGTTAA	TAACATTGAA	AACTTAGGTG	CTGCTTCATT	TACAGCTCCG
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GTTTTAGCCC	AAAAATGTTT	AAACATCTTA	CAAGATTTGA	ATGCGGCAGT	TCAAGCTTTG
GAGGCAAAAG	GTACCAGTAT	CCCAAGTAAT	CTTGTCGCCG	CAGCTATAAA	TGCAGCCTTG
CTTCCTGTCA	AAGGCACGGT	AAACGTGGCT	GTTTCAGGTG	CTTTGCCTTT	ATTAGCGGTT
GGTGGTTTCAG	GCGTAAATGA	GTTAGTGGAT	GCTTCTTTAC	TAGGCACAAC	CACGGTTACT
TTACCAACTA	CCGTTTCAAC	ACCTCAAAAT	TTATCCAATA	ATTTAGATGC	TCGTTTTGTA
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TCCAACATTT	ATTTTGCTGC	AGGCACTACT	AGTGAAGTAA	CCGCACCAAC	AATCACAGGA
GTAACAGGTA	ATTCAACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
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GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA	GCAGGCGCCA	ATGAAACGTT	AACCGCCGTA
GCGAAAAACG	CCAGCGGNAC	AGAAAGNACG	CCAACAACGT	TCCAAACNCC	AGCGGATGAA
GCAACCGTAA	CCGCACCAAC	AATCACAGGA	GTGACAGGTA	ATTCAACGGC	AGGTTACGAA
GTTAAAGGAA	CTGCCGATGC	CAATGCCACG	GTTGAAATCC	GAAATGCAGG	AGGCACCGTA
ATAGGCACAG	GTACCGCTGA	TGGGACAGGA	GCGTTTACAG	TTACCGTTCC	CGCAGGTGAA
GCAGGTGCCA	ATGAAACGTT	AACCGCCGTA	GCGAAAAACG	CCAGCGGCAC	AGAAAGTACG
CCAACAACGT	TCCAAACACC	AGCGGATGAA	GCAACCGTAA	CCGCACCAAC	AATCACAGGA
GTGACAGGTA	ATTCAACAGC	AGGTTACGAA	GTTAAAGGAA	CTGCCGATGC	CAATGCCACG
GTTGAGATCC	GAAATGCAGG	AGGTGCCGTG	ATAGGTACAG	GTACTGCTGA	TGGGACAGGG
GCATTTACAG	TTACCATTC	CGCAGGTGAA	GCAGGTGCGA	ATGAAACGTT	AACCGCCGTA
GCGAAAAACG	CCAGCGGTAC	AGAAAGTACG	CCAACAACGT	TCCAAACGCC	AGCGGATCCT
AATACGCCCC	TGGCGACGCC	AATTGTTGAG	ACTGTAACAG	GTAGTACAAC	AAAAGGCTAT
GAGGTCAAAG	GGACTGCTGA	AGTTGGCACC	ACCATTGAGG	TTCGCGATGC	AGCTGGCACC
GTCTTTGGTA	CTGCAACAAC	TGGAACAGG	GGAAAATATA	CAGTACTTTT	AGATTACAGGA
ACAGCAACAG	CAAATCAAAC	GCTGAGCGTT	GTAGCGAAAA	ACGCTAGTGG	CACGGAAAGT
CAACCAGCAA	CGGCGACAAC	ACCAGCTGAT	GTCACGAC	CAACAGTTGA	TAACATCACA
GGCAACTCTG	GTTCCGGGTTA	TGAAATTACA	GGAACAGCAG	ACCCTAACAC	AACAATCGAA
GTTTCGTGATC	CATCTGGGGC	AGTCATTGGT	ACAGGTACCT	CTGATGCGAA	TGGTGATTTT
ACTGTAAACG	TACCAACGGG	AACGACCAAT	CCTGGGGATA	CGTTAACAGT	GATTGGAAAG
GATAACGCGG	GAAATGAAAG	TCAACCGACT	GAAGTCCTTG	TTCTTGCTGA	TGCCACGGTT
ACAGCACCAA	CTGTAACAGG	AGTAACAGGT	AATTCAGTTG	CTGGTTATCA	GGTGACAGGC
ACCGCTGATC	CGAATGCTAC	CATCGAAAT	CGTGATGCAG	ATGGGAACGT	GATTGCAACA
GGGACTGCCG	ATGGGACTGG	TTCTTTTGCT	GTGAACCTTC	CAGCTGGGAC	GGCAAAATGCG
AATGAAACAT	TGACAGCGTT	AGCCAAAGAT	CCTGCTGGCA	ATACAAGTAC	ACCGACAACC
TTCCAAACAC	CAGCAGATGA	AGTAGTGGCA	CCGCCAAGTG	TCGACAAAGT	TACTGGGAAT
ACAACACAAG	GATATCAAGT	GACAGGTACC	GCTGAACTTG	GCACCACCAT	TGAAGTTTCGT
GCAACAGACG	GAACAGTTTT	AGGCACCGCA	ACAACCTGGAC	CGACTGGCCA	ATATACTGTG
ACGTTAGCTT	CAGGAAAAGC	AACAGCTAAA	CAAACAGTGA	ATGTAGTTGC	TAAAAATGAT
ACTGGACTTG	AGAGTCAACC	AACACAGCT	ATGACACCCG	CTGATGTTAC	CACACCAACA
ATTGGTGACA	TTACTGGAGA	TTCAACAAC	GTTTATGAAA	TCACTGGGAC	GGCGGACCCT
AATACCACCA	TTGAAGTACG	GAACCCAGAT	GGAACAATTA	TTGGTACAAC	GACAACGGAT
GATCAAGGAA	ACTTTACTGT	GGACCTTCCA	GCGGGAGCCG	CTAATCCTGG	TGATACATTA
ACAGTTGTTG	GAAAAGACGG	TGACGGCAAT	GAAAGTCAAC	CAACGGAAGT	GACGGTCCCT
GAAGATGCAA	CCGTAGCAGC	ACCAACTGTG	ACGACTGTTA	CAGGAACAAC	TGCCACTGGG
TATCAAGTAA	CCGGCACGGC	AGAGCCAAAT	GTCACCATTG	AGATTACCAA	TGAAGCAGGT
TTAGTTATTG	CTACGGGAAC	GACTGATGGT	GCTGGCGCAT	TTACAATCAC	TCTTCCGACG
GGCACAGCAA	CAGCTAACGA	AGCCTTAACT	GCCATTGCGA	AAGATGCTGC	TGGGAAAGAA
AGTAATCCGA	CTGCTTTCAA	AACACCTGCT	GATCCAGATG	CACCAGTCGC	GACACCTACT
GTTGACAAAA	TCACTGGTAG	CACGACAAAC	GGCTATCAAG	TAGTAGGAGC	AGCAGAAAGT
GGTACAACAG	TTGAGGTGCG	TGACGCCGAT	GGCACAGTCC	TTGGCATGGC	AACTACTGGA
ACTGATGGCA	AATACACAGT	GACTTTAGAG	CCAGGGAAGG	CCTCAGCTAA	CGAAACAATA
ACTGTCGTAG	CGAAAAATGC	AACAGGAAAA	GAAAGTCAGC	CAGCTACAGC	AACACACCA
GTCGACTTAG	CCACACCAAC	CATTGATTCT	ATTACCGGAA	ATTCTAGTAA	AGGTTACGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ATCACTGGAA CGGCGGAGCC AAAAACCACCT ATTGATGTCC GTGACGCAGA CGGAACCATC
ATTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGACTCTACC AGCTGGCGTA
GTGACACCAG GAGAAACGAT TACGATTATT AGCAAAGATG GCGCAGGTAA TGAAAGTCAA
CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTTTAGCGG CGCCAACAT TACGAAGGTT
GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAAC TGATCCAAA TGTCACGGTT
CAATTTTACA ATAGCAGTGA ACAATTATTG GCAAGTGGCA ATACAAC TGGAGGTACC
TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAC CGCACTAACC
ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAGC CGATATTACG
GGAGAACCAG AGATTAAAAT TCGGCACCA ACTGTTTCTT CAGTTT TAGG AACGTCTAAA
GCCGGCTACC TCATCAAAGG AACAGCTGAA CCAAACCGAA TCATTCAAAT TAGTAACCGA
CTATTAAGAA GTGTGATTGC TGTAGGTGCC ACCGATGCTG AAGGCAACTT CGCTATCCAA
TTAACAGCGG GACAAGCGAC TGCTCAACAA AGTTTACTTG CGACAGCTAC CGATGGCGCA
GGACATTACA GTACGGCTAC AACCTTCATG ACGCCAGCCG ACCCAACGAA TCCTGGAGGA
GGCAATGGTA AACTGGCGG AAATAACGGC AATACAGCGG GCAATACAGG AAACAATGGC
GCAACTGGCG GGAATAATGG GAATGGTTCA AACACAGGTT CAAATCCAAA TGGAGGTTCT
GGTTTAGGCA CAACAGGTTT TGGCTTAGGT TCACTAGGCA ATGGCCTCGG TACAAATGGT
AGTGGCTACC ACCCTAACT AAGTACCATC AGTTATGGCA CTGGAATCA CGGGAAAACA
GGCTACTTAC CTAGCACAGG TGAAAAAGAG TCTTCAGCCG TGACAACAAG TTTGTTTGGC
GCCTTTGTGC CACTCCTTGC GAGCATGGGA ATCATCAAAC GCAAACGTAA AAAC TAG

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EF070-2 (SEQ ID NO:266)

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SIAVTSGTIS ASAAVLDEL LSNVTSNDS GTSTSNRWT AANQNPVNFT VSGGALADAS
AVFSGQKQAV LVVPPELRGN VAAAGSAAIN TNVTIDLSKV TFLTAVLNAA NDLTNVITQI
TSGALGNLTG VDIDLTEVNR QLELVNMIEN LGAASFTAPE TLAADGSYIS APISDGLGLV
LAQNVSNILQ DLNAAVQALE AKGTSIPSNL VAAAINAALL PVKGTVNVAV SGALPLLA VG
GSGVNELVDA SLLGTTTVTL PTTVSTPQNL SNNLDARFVG TVVQTDLLDV NLLATADGVS
NIYFAAGTTS EVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGTVI GTGTADGTGA
FTVTVPAGEA GANETLTAVA KNASGTEXT PTFQTPADEA TVTAPTITGV TGNSTAGYEV
KGTADANATV EIRNAGGTVI GTGTADGTGA FTVTVPAGEA GANETLTAVA KNASGTESTP
TTFQTPADEA TVTAPTITGV TGNSTAGYEV KGTADANATV EIRNAGGAVI GTGTADGTGA
FTVTVPAGEA GANETLTAVA KNASGTESTP TTFQTPADPN TPVATPIVET VTGSTTKGYE
VKGTAEVGTI IEVRDAAGTV LGTATTGTDG KYTVTLDSGT ATANQTL SVV AKNASGTESQ
PATATTPADV TAPTVDNITG NSGSGYEITG TADPNTTIEV RDPGAVIGT GTSDANGDFT
VTLPTGTTNP GDTLTVIGKD NAGNESQPT EVLVPADATVT APTVTGVTGN SVAGYQVTGT
ADPNATIEIR DADGNVIATG TADGTGSFAV NLPAGTANAN ETLTALAKDP AGNTSTPTTF
QTPADEVVAP PSVDKVTGNT TQGYQVTGTA ELGTTIEVRA TDGTVLGTAT TGPTGQYTVT
LASGKATAKQ TVNVVAKNDT GLESOPTTAM TPADVTTPTI GDI TGDSTTG YEITGTADPN
TTIEVRNPDG TIIGTTTTDD QGNFTVDLPA GAANPGDTLT VVGKDG DGNE SQPTEVTVPE
DATVAAPT VT TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTTDGA GAFTITLPTG
TATANEALTA IAKDAAGKES NPTAFKTPAD PDAPVATPTV DKITGSTTNG YQVVGAAEVG
TTVEVRDADG TVLGMATTGT DGKYTVTLEP GKASANETIT VVAKNATGKE SQPATATTPV
DLATPTIDSI TGNSSKGYEI TGTAEPKTTI DVRDADGTII AATTANETGQ YTVTL PAGVV
TPGETITIIIS KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGYTVT GTADPNVTVQ
FYNSSEQLLA SGNTTTGGTF SVHIAAGLAT EKETLTALT DTQGNVSPKT TFMT PADITG
EPEIKIAAPT VSSVLGTSKA GYLIKGTAE NRRIQISNRL LRSVIAVGAT DAEGNFAIQL
TAGQATAQQS LLATATDGAG HYSTATTFMT PADPTNPGGG NGNTGGNNGN TGGNTGNNGA
TGGNNGNGSN TGSNPNGGSG LGTTGSGLS LGNGLGTNGS GYHPKLSTIS YGTGNHKGKTG
YLPSTGEKES SAVTTSFLGA FVALLASMG I KRKRKN

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EF070-3 (SEQ ID NO:267)

CGG TGACGGCAAT GAAAGTCAAC CAACGGAAGT GACGGTCCCT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GAAGATGCAA CCGTAGCAGC ACCAACTGTG ACGACTGTTA CAGGAACAAC TGCCACTGGG
TATCAAGTAA CCGGCACGGC AGAGCCAAAT GTCACCATTG AGATTCACAA TGAAGCAGGT
TTAGTTATTC CTACGGGAAC GACTGATGGT GCTGGCGCAT TTACAATCAC TCTTCCGACG
GGCACAGCAA CAGCTAACGA AGCCTTAACT GCCATTGCGA AAGATGCTGC TGGGAAAGAA
AGTAATCCGA CTGCTTTCAA AACACCTGCT GATCCAGATG CACCAGTCGC GACACCTACT
GTTGACAAAA TCACTGGTAG CACGACAAAC GGCTATCAAG TAGTAGGAGC AGCAGAAGTT
GGTACAACAG TTGAGGTGCG TGACGCCGAT GGCACAGTCC TTGGCATGGC AACTACTGGA
ACTGATGGCA AATACACAGT GACTTTAGAG CCAGGGAAGG CCTCAGCTAA CGAAACAATA
ACTGTCGTAG CGAAAAATGC AACAGGAAAA GAAAGTCAGC CAGCTACAGC AACTACACCA
GTCGACTTAG CCACACCAAC CATTGATTCT ATTACCGAA ATTCTAGTAA AGGTTACGAA
ATCACTGGAA CGGCGGAGCC AAAAACCCTT ATTGATGTCC GTGACGCAGA CGGAACCATC
ATTGCTGCTA CAACTGCTAA CGAAACCGGC CAATATACGG TGACTCTACC AGCTGGCGTA
GTGACACCAG GAGAAACGAT TACGATTATT AGCAAAGATG GCGCAGGTAA TGAAAGTCAA
CCAGCTACAG CCGTTATTCC AGCGGATGTT GTTTTAGCGG CGCCAACTAT TACGAAGGTT
GAAGGAAACA AAGCCAATGG CTATACAGTC ACTGGAACTG CTGATCCAAA TGTCACGGTT
CAATTTTACA ATAGCAGTGA ACAATTATTG GCAAGTGGCA ATACAACTAC TGGAGGTACC
TTCTCCGTTT ATATTGCAGC AGGGTTAGCA ACAGAAAAAG AAACGTTAAC CGCCTAACC
ACAGATACAC AAGGAAATGT GAGTCCTAAA ACCACATTTA TGACGCCAGC CGATATTACG
GGAGAACCAG AGATTAAAT TGCGGCACCA ACTGTTTCTT CAGTTTTAGG AACGCTAAA
GCCGGCTACC TCATCAAAGG AACAGCTGAA CCAAACCGAA TCATTCAAAT TAGTAACCGA
CTATTAAGAA GTGTGATTGC TGTAGGTGCC ACCGATGCTG AAGGCAACTT CGCTATCCAA
TTAACAGCGG GACAAGCGAC TGCTCAACAA AGTTTACTTG CGACAGCTAC CGATGGCGCA
GGACATTACA GTACGGCTAC AACCTTCATG ACGCCAGCCG ACCCAACGAA TCCTGGAGGA
GGCAATGGTA ACACTGGCGG AAATAACGGC AATACAGGCG GCAATACAGG AAACAATGGC
GCAACTGGCG GGAATAATGG GAATGGTTCA AACACAGGTT CAAATCCAAA TGGAGGTTCT
GGTTTAGGCA CAACAGGTTT TGGCTTAGGT TCACTAGGCA ATGGCCTCGG TACAAATGGT
AGTGGCTACC ACCCTAAACT AAGTACCATC AGTTATGGCA CTGGAAATCA CGGGAACA
GGCTACT

EF70-4 (SEQ ID NO:268)

DGDGNE SQPTEVTVPE

DATVAAPT VT TVTGTTATGY QVTGTAEPNV TIEIHNEAGL VIATGTTDGA GAFTITLPTG
TATANEALTA IAKDAAGKES NPTAFKTPAD PDAPVATPTV DKITGSTTNG YQVVGAAEVG
TTVEVRDADG TVLGMATTGT DGKYTVTLEP GKASANETIT VVAKNATGKE SQPATATTPV
DLATPTIDSI TGNSSKGYEI TGTAEPKTTI DVRDADGTII AATTANETGQ YTVTLTPAGVV
TPGETITII KDGAGNESQP ATAVIPADV LAAPTITKVE GNKANGYTVT GTADPNVTVQ
FYNSSQELLA SGNTTTGGTF SVHIAAGLAT EKETLTALTT DTQGNVSPKT TFMTPADITG
EPEIKIAAPT VSSVLGTSKA GYLIKGTAE NRIIQISNRL LRSVIAVGAT DAEGNFAIQL
TAGQATAQQS LLATATDGAG HYSTATTFTT PADPTNPGGG NGNTGGNNGN TGGNTGNNGA
TGGNNGNSN TGSNPNGGSG LGTTGSGLS LGNGLGTNGS GYHPKLSTIS YGTGNHGKTG
YL

EF071-1 (SEQ ID NO:269)

TAAGTAGAAG TGTCGGGAC AAACGTAGAA CTTTCGCTGA TTGCCGAAGA AATTACTTCT
GTCCCGCCAT TTATCTGCAG GTTTAAGCCG TGGAAGGGAA GTTATTTTGA CTTTCCTTTC
ATGGCTTTTT TAAGAAAGGA GCATGCTATG TTTAAAAAAT TAATGATTCA ACTTGCTTTA
GTGATTGGTT TAAGTTTAAC GATTCCGATG ACGGCTTNCG CTTACACCAT CGAAGCGGAT
CCAATCAACT TTACTTATTT TCCCGGCTCT GCAAGCAATG AATTAATTGT TTTACATGAA
TCTGGAAACG AGCGGAACCT AGGACCACAC AGTTTAGACA ATGAAGTGGC CTATATGAAA
CGAAATTGGT CAAATGCTTA TGTCTCATAT TTTGTCGGAT CTGGTGGACG AGTGAACAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTAGCTCCTG CTGGCCAAAT TCAATATGGC GCAGGTTCTT TAGCTAATCA AAAAGCCTAT
 GCGCAAATCG AATTGGCTCG AACGAATAAT GCGGCGACAT TTAAAAAAGA TTATGCTGCC
 TATGTTAATT TGGCCCGTGA TTTGGCTCAG AACATTGGTG CTGATTTTTTC TCTGGACGAT
 GGAACAGGTT ATGGCATAGT CACTCATGAT TGGATTACAA AAAATTGGTG GGGAGATCAT
 ACAGATCCTT ATGGTTATTT AGCGCGTGGG GGATTAGTAA AGCGCATTGG CACNAGATTT
 ACAACGGGCG TTTCNGNAAC AGGTGAGACT GGTCATTATT CAGCCAGGTA A

EF071-2 (SEQ ID NO:270)

MF KKLMIQLALV

IGLSLTIPMT AXAYTIEADP INFYTFPGSA SNEIIVLHES GNERNLGPHS LDNEVAYMKR
 NWSNAYVSYF VSGGRVKQL APAGQIQYGA GSLANQKAYA QIELARTNNA ATFKKDYAAY
 VNLARDLAQN IGADFSLDDG TGYGIVTHDW ITKNWWGDHT DPYGYLARGG LVKRIGTRFT
 TGVSTGETG HYSAR

EF071-3 (SEQ ID NO:271)

G TTTAAAAAAT TAATGATTCA ACTTGCTTTA

GTGATTGGTT TAAGTTTAAC GATTCCGATG ACGGCTTNCG CTTACACCAT CGAAGCGGAT
 CCAATCAACT TTAATTATTT TCCCGGCTCT GCAAGCAATG AATTAATTGT TTTACATGAA
 TCTGGAAACG AGCGGAACCT AGGACCACAC AGTTTAGACA ATGAAGTGGC CTATATGAAA
 CGAAATTGGT CAAATGCTTA TGTCTCATAT TTTGTCGGAT CTGGTGGACG AGTGAAACAA
 TTAGCTCCTG CTGGCCAAAT TCAATATGGC GCAGGTTCTT TAGCTAATCA AAAAGCCTAT
 GCGCAAATCG AATTGGCTCG AACGAATAAT GCGGCGACAT TTAAAAAAGA TTATGCTGCC
 TATGTTAATT TGGCCCGTGA TTTGGCTCAG AACATTGGTG CTGATTTTTTC TCTGGACGAT
 GGAACAGGTT ATGGCATAGT CACTCATGAT TGGATTACAA AAAATTGGTG GGGAGATCAT
 ACAGATCCTT ATGGTTATTT AGCGCGTGGG GGATTAGTAA AGCGCATTGG CACNAGATTT
 ACAACGGGCG TTTCNGNAAC AGGTGAGACT GGTCATTATT CAGCCAGGT

EF071-4 (SEQ ID NO:272)

F KKLMIQLALV

IGLSLTIPMT AXAYTIEADP INFYTFPGSA SNEIIVLHES GNERNLGPHS LDNEVAYMKR
 NWSNAYVSYF VSGGRVKQL APAGQIQYGA GSLANQKAYA QIELARTNNA ATFKKDYAAY
 VNLARDLAQN IGADFSLDDG TGYGIVTHDW ITKNWWGDHT DPYGYLARGG LVKRIGTRFT
 TGVSTGETG HYSAR

EF072-1 (SEQ ID NO:273)

TAATCAATGA AAAACGCACG TTGGTTAAGT ATTTGCGTCA TGCTACTCGC TCTTTTCGGG
 TTTTCACAGC AAGCATTAGC AGAGGCATCG CAAGCAAGCG TTCAAGTTAC GTTGACACAAA
 TTATTGTTCC CTGATGGTCA ATTACCAGAA CAGCAGCAAA ACACAGGGGA AGAGGGAACG
 CTGCTTCAAA ATTATCGGGG CTAAATGAC GTCATTATC AAGTCTATGA TGTGACGGAT
 CCGTTTTATC AGCTTCGTTT TGAAGGAAAA ACGGTCCAAG AGGCACAGCG TCAATTAGCA
 GAAACCGGTG CAACAAATAG AAAACCGATC GCAGAAGATA AAACACAGAC AATAAATGGA
 GAAGATGGAG TGGTTTCCTTT TTCATTAGCT AGCAAAGATT CGCAGCAACG AGATAAAGCC
 TATTTATTTG TTGAAGCGGA AGCACCAGAA GTGGTAAAGG AAAAAGCTAG CAACCTAGTA
 GTGATTTTGC CTGTTCAAGA TCCACAAGGG CAATCGTTAA CGCATATTCA TTTATATCCA
 AAAAATGAAG AAAATGCCTA TGAATTACCA CCACTTGAAA AAACGGTACT CGATAAGCAA
 CAAGGCTTTA ATCAAGGAGA GCACATTAAC TATCAGTTAA CGACTCAGAT TCCAGCGAAT
 ATTTTAGGAT ATCAGGAATT CCGTTTGTC GATAAGGCGG ATACAACGTT GACACTTTTA
 CCAGAATCAA TTGAGGTAAA AGTGGCTGGA AAAACAGTTA CTACAGGTTA CACTGTGACG
 ACGCAAAAGC ATGGATTTAC GCTTGATTTT TCAATTAAAG ACTTACAAAA CTTTGCAAAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAAACAATGA CTGTGTCGTA TCAAATGCGT TTAGAAAAGA CCGCTGAACC TGACACTGCG
 ATTAACAACG AAGGACAATT AGTCACGGAC AAACATACCT TGACTAAAAG AGCCACAGTT
 CGTACAGGCG GCAAGTCTTT TGTCAAAGTT GATAGTGAAA ATGCGAAAAT CACCTTGCCA
 GAGGCTGTTT TTATCGTCAA AAATCAAGCG GGGGAATACC TCAATGAAAC AGCAAACGGG
 TATCGTTGGC AAAAAAGAAA AGCATTAGCT AAAAAATTCA CGTCTAATCA AGCCGGTGAA
 TTTTCAGTTA AAGGNNTTAA AAGATGGCCA GTACTTCTTG GAAGAAATCT CTGCACCAAA
 AGGTTATCTT CTGAATCAAA CAGAAATTCC TTTTACGGTG GGAAAAAATT CTTATGCAAC
 GAACGGACAA CGAACAGCAC CGTTACATGT AATCAATAA

EF072-2 (SEQ ID NO:274)

MKNARWLSI CVMLLALFGF SQQALAEASQ ASVQVTLHKL LFPDQQLPEQ QQNTGEEGTL
 LQNYRGLNDV TYQVYDVTDP FYQLRSEGKT VQEAQRQLAE TGATNRKPIA EDKTQTINGE
 DGVVSFSLAS KDSQQRDKAY LFVEAEAEV VKEKASNLVV ILPVQDPQGG SLTHIHLYPK
 NEENAYDLPP LEKTVLDKQQ GFNQGEHINY QLTTQIPANI LGYQEFRLSD KADTTLTLLP
 ESIEVKVAGK TVTTGYTLTT QKHGFTLDFS IKDLQNFANQ TMTVSYQMRL EKTAEPDTAI
 NNEGQLVTDK HTLTKRATVR TGGKSFVKVD SENAKITLPE AVFIVKNQAG EYLNETANGY
 RWQKEKALAK KFTSNQAGEF SVKGXKRWPV LLGRNLCTKR LSSESNRNSF YGGKKFLCNE
 RTTNSTVTCN Q

EF072-3 (SEQ ID NO:275)

ATTACCAGAA CAGCAGCAAA ACACAGGGGA AGAGGGAACG
 CTGCTTCAAA ATTATCGGGG CTAAATGAC GTCACTTATC AAGTCTATGA TGTGACGGAT
 CCGTTTTATC AGCTTCGTTT TGAAGGAAAA ACGGTCCAAG AGGCACAGCG TCAATTAGCA
 GAAACCGGTG CAACAAATAG AAAACCGATC GCAGAAGATA AAACACAGAC AATAAATGGA
 GAAGATGGAG TGGTTTCTTT TTCATTAGCT AGCAAAGATT CGCAGCAACG AGATAAAGCC
 TATTTATTTT TTGAAGCGGA AGCACCAGAA GTGGTAAAGG AAAAAGCTAG CAACCTAGTA
 GTGATTTTGC CTGTTCAAGA TCCACAAGGG CAATCGTTAA CGCATATTCA TTTATATCCA
 AAAAATGAAG AAAATGCCTA TGACTTACCA CCACTTGAAA AAACGGTACT CGATAAGCAA
 CAAGGCTTTA ATCAAGGAGA GCACATTAAC TATCAGTTAA CGACTCAGAT TCCAGCGAAT
 ATTTTAGGAT ATCAGGAATT CCGTTTGTCA GATAAGGCGG ATACAACGTT GACACTTTTA
 CCAGAATCAA TTGAGGTAAA AGTGGCTGGA AAAACAGTTA CTACAGGTTA CACACTGACG
 ACGCAAAAGC ATGGATTTAC GCTTGATTTT TCAATTAAAG ACTTACAAAA CTTTGCAAAT
 CAAACAATGA CTGTGTCGTA TCAAATGCGT TTAGAAAAGA CCGCTGAACC TGACACTGCG
 ATTAACAACG AAGGACAATT AGTCACGGAC AAACATACCT TGACTAAAAG AGCCACAGTT
 CGTACAGGCG GCAAGTCTTT TGTCAAAGTT GATAGTGAAA ATGCGAAAAT CACCTTGCCA
 GAGGCTGTTT TTATCGTCAA AAATCAAGCG GGGGAATACC TCAATGAAAC AGCAAACGGG
 TATCGTTGGC AAAAAAGAAA AGCATTAGCT AAAAAATTCA CGTCTAATCA AGCCGGTGAA
 TTTTCAGTTA AAGGNNTTAA AAGATGGCCA GTACTTCTTG GAAGAAATCT CTGCACCAAA
 AGGTTATCTT CTGAATCAAA CAGAAATTCC TTTTACGGTG GGAAAAAATT CTTATGCAAC
 GAACGGACAA CGAACAGCAC CGTTACATGT A

EF072-4 (SEQ ID NO:276)

QLPEQ QQNTGEEGTL
 LQNYRGLNDV TYQVYDVTDP FYQLRSEGKT VQEAQRQLAE TGATNRKPIA EDKTQTINGE
 DGVVSFSLAS KDSQQRDKAY LFVEAEAEV VKEKASNLVV ILPVQDPQGG SLTHIHLYPK
 NEENAYDLPP LEKTVLDKQQ GFNQGEHINY QLTTQIPANI LGYQEFRLSD KADTTLTLLP
 ESIEVKVAGK TVTTGYTLTT QKHGFTLDFS IKDLQNFANQ TMTVSYQMRL EKTAEPDTAI
 NNEGQLVTDK HTLTKRATVR TGGKSFVKVD SENAKITLPE AVFIVKNQAG EYLNETANGY
 RWQKEKALAK KFTSNQAGEF SVKGXKRWPV LLGRNLCTKR LSSESNRNSF YGGKKFLCNE
 RTTNSTVTC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF073-1 (SEQ ID NO:277)

TAAATGAACA AATTAAATAC AAAATTACTG ATTGGCTATA TTCTTTTAGG AGCCTTAATC
 ATTGCTGTCT CTAGAGAATA TGGCTTCTTC GCTTTTGTGA TTCTGGTAGG CTTTTTAGTA
 TTCGTTCTCT ATCGAAAAA GAAAAATGCC GCCGACAAA GCGATCAAAT GCCTTACTTA
 ACGAAAGATA AAGAAGCCCA TTATCGTGAG TTGGGGTTAT CTCCACAAGA AATTGATTTT
 TTCAGAAGTA CAATGAGCAC AGCCAAAAA CAAATCATAC AATTGCAAGA AAACATGAAT
 CGTTCAACTA AATTACGGGC GATTGACTTA CGTAATGATA CTACGAAGGT TTCTAAAGCT
 CTGTTTAAAG AGTTAGTGAA AGAACCTAAA AAGTTACACT TAGCCAATCA CTTTCTCTAT
 ACACATTTAC CAAATATCGT TGACTTAACA AGTAAACATT TAGAAATCGA ACAACACGAA
 GTAAAAAACA AACAAACGTA TGAAAAATTA GAAGAAAGCG CACAAATCAT TGACCAATTG
 TCAAAATTAG TTAATAATGA TTATGAGGAA ATCGTTTCCG ATGACTTAGA CGATTTAGAT
 GTCGAAATGT CGATCGCTAA AAGCAGCTTG TCGCAAAAAG CTGCAACTGA GGAATCACCT
 CAAGTAAACG AAGACCAGCA ATAA

EF073-2 (SEQ ID NO:278)

MNKLNTKLLI GYILLGALII AVAREYGFFA FVILVGFLVF VLYRKKKNAA DKSDQMPYLT
 KDKEAHYREL GLSPQEIDFF RSTMSTAKKQ IIQLQENMNR STKLRAIDLR NDTTKVSKAL
 FKELVKEPKK LHLANHFLYT HLPNIVDLTS KHLEIEQHEV KNKQTYEKL ESEAQIIDQLS
 KLVKNDYEEI VSDDLDDL DV EMSIAKSSLS QKAATEESPQ VNEDQQ

EF073-3 (SEQ ID NO:279)

CT ATCGAAAAA GAAAAATGCC GCCGACAAA GCGATCAAAT GCCTTACTTA
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 TTCAGAAGTA CAATGAGCAC AGCCAAAAA CAAATCATAC AATTGCAAGA AAACATGAAT
 CGTTCAACTA AATTACGGGC GATTGACTTA CGTAATGATA CTACGAAGGT TTCTAAAGCT
 CTGTTTAAAG AGTTAGTGAA AGAACCTAAA AAGTTACACT TAGCCAATCA CTTTCTCTAT
 ACACATTTAC CAAATATCGT TGACTTAACA AGTAAACATT TAGAAATCGA ACAACACGAA
 GTAAAAAACA AACAAACGTA TGAAAAATTA GAAGAAAGCG CACAAATCAT TGACCAATTG
 TCAAAATTAG TTAATAATGA TTATGAGGAA ATCGTTTCCG ATGACTTAGA CGATTTAGAT
 GTCGAAATGT CGATCGCTAA AAGCAGCTTG TCGCAAAAAG CTGCAACTGA GGAATCACCT
 CAAGTAAACG AAGACCAGCA AT

EF073-4 (SEQ ID NO:280)

YRKKKNAA DKSDQMPYLT
 KDKEAHYREL GLSPQEIDFF RSTMSTAKKQ IIQLQENMNR STKLRAIDLR NDTTKVSKAL
 FKELVKEPKK LHLANHFLYT HLPNIVDLTS KHLEIEQHEV KNKQTYEKL ESEAQIIDQLS
 KLVKNDYEEI VSDDLDDL DV EMSIAKSSLS QKAATEESPQ VNEDQQ

EF074-1 (SEQ ID NO:281)

TAAAGGAGTT CTCAAAAAAT GAAGCTAAAA AAAATAATTC CTGCTTTTCC CCTTCTTTCA
 ACCGTTGCAG TTGGCTTGTG GTTAACGCCT ACTCAAGCTT CTGCAGATGC TGCGGATACG
 ATGGTAGATA TCTCTGGCAA AAAAGTGTTG GTTGGATATT GGCATAACTG GGCCTCAAAA
 GGACGCGATG GTTACAAACA AGGAACATCA GCATCACTAA ACCTTTTCAGA AGTAAATCAA
 GCCTACAATG TCGTACCGGT TTCCTTCATG AAAAGCGATG GCACGACACG GATTCTTACG
 TTCAAGCCTT ATAACCAAAC GGACACTGCC TTCCGACAAG AAGTCGCACA ATTAAATAGT
 CAAGGTCGCG CAGTTTTATT GGCCTTGGT GGAGCAGATG CACATATTCA ATTAGTCAAA
 GGCGATGAAC AAGCCTTTGC GAATGAAATC ATTCTGCAAG TGGAAACATA CGGCTTTGAT
 GGTTTAGACA TCGACTTAGA GCAATTGGCG ATTACTGCTG GCGACAACCA AACCCTCATC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCTGCTACGT TGAAAATAGT CAAAGACCAT TATCGAGCAC AAGGAAAAAA TTTCATCATT
 ACGATGGCAC CAGAATTCCC TTATTTAAAA CCTGGTGCCG CTTATGAAAC ATACATTACT
 TCCCTAAATG GTTATTATGA TTACATTGCC CCACAATTAT ATAACCAAGG CGGCGACGGT
 GTCTGGGTTG ATGAAGTTAT GACTTGGGTT GCTCAAAGCA ACGATGCTCT AAAATACGAG
 TTCCTCTATN ATATT

EF074-2 (SEQ ID NO:282)

MKLKK IIPAFPLLST VAVGLWLTPT QASADAADTM VDISGKKVLV GYWHNWASKG
 RDGYKQGTSA SLNLSEVNQA YNVVPVSFMK SDGTTRIPTF KPYNQTD TAF RQEVAQLNSQ
 GRAVLLALGG ADAHIQLVKG DEQAFANEII RQVETYGFDG LDIDLEQLAI TAGDNQTVIP
 ATLKIVKDHY RAQGKNFIIT MAPEFPYLKP GAAYETYITS LNGYYDYIAP QLYNQGGDGV
 WVDEVMTWVA QSNDAKLYEF LYXI

EF074-3 (SEQ ID NO:283)

TGC TGCGGATACG
 ATGGTAGATA TCTCTGGCAA AAAAGTGTG GTTGGATATT GGCATAACTG GGCTCAAAA
 GGACGCGATG GTTACAAACA AGGAACATCA GCATCACTAA ACCTTTCAGA AGTAAATCAA
 GCCTACAATG TCGTACCGGT TTCCTTCATG AAAAGCGATG GCACGACACG GATTCCCTACG
 TTCAAGCCTT ATAACCAAAC GGACACTGCC TTCCGACAAG AAGTCGCACA ATTAAATAGT
 CAAGGTCGCG CAGTTTTTATT GGCACCTGGT GGAGCAGATG CACATATTCA ATTAGTCAAA
 GGCGATGAAC AAGCCTTTGC GAATGAAATC ATTCTGCAAG TGGAAACATA CGGCTTTGAT
 GGTTTAGACA TCGACTTAGA GCAATTGGCG ATTACTGCTG GCGACAACCA AACCGTCATC
 CCTGCTACGT TGAAAATAGT CAAAGACCAT TATCGAGCAC AAGGAAAAAA TTTCATCATT
 ACGATGGCAC CAGAATTCCC TTATTTAAAA CCTGGTGCCG CTTATGAAAC ATACATTACT
 TCCCTAAATG GTTATTATGA TTACATTGCC CCACAATTAT ATAACCAAGG CGGCGACGGT
 GTCTGGGTTG ATGAAGTTAT GACTTGGGTT GCTCAAAGCA ACGATGCTCT AAAATACGAG
 TTCCTCT

EF074-4 (SEQ ID NO:284)

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 RDGYKQGTSA SLNLSEVNQA YNVVPVSFMK SDGTTRIPTF KPYNQTD TAF RQEVAQLNSQ
 GRAVLLALGG ADAHIQLVKG DEQAFANEII RQVETYGFDG LDIDLEQLAI TAGDNQTVIP
 ATLKIVKDHY RAQGKNFIIT MAPEFPYLKP GAAYETYITS LNGYYDYIAP QLYNQGGDGV
 WVDEVMTWVA QSNDAKLYEF LY

EF075-1 (SEQ ID NO:285)

TAACCTATAA GAAAAAATC ACAACCTGTG ATAAATTATT GGAGGNAAAA TATGTCAAAA
 GGAAGAAAA TTTTGTCCAT TATCNTTGGG ATTATCTTGG NTCTATTTCT TGCAGTTGTT
 GGAATGGGAG CAAAACCTTA TTGGGATGTT TCTAAATCAA TGGATAAAAC CTATGAAACA
 GTAGAACGAT CTAAAAAAG TCAGGTCAAT TTAAACAATA AGGAGCCTTT TTCTGTTTTA
 TTATTAGGGA TTGATACAGG CGATGATGGG CGTGTGAGC AAGGTCGTTT GGATACAACA
 ATTGTTGCAA CAGTTAATCC TCGTGACAAG CAAACAACCT TAGTCAGTCT TGCTCGCGAT
 ACCTATGTTG ATATTCCAGG TCAAGGAAAA CAAGATAAAT TGAATCACGC CTATGCTTTT
 GGTGGCGCAT CTTTAGCAAT GGACACAGTT GAAAACCTATT TAAACATACC TATTAATCAT
 TATGTTTCAA TTAATATGGC TGGTTTTAAAA GAATTAGTCA ACGCGGTTGG CGGAATCGAA
 GTGAACAATA ATCTGACTTT TTCTCAAGAC GGATATGATT TTACGATTGG TAAAAATTTCA
 TTGGATGGTG AACAAGCACT CTCCTATTCA AGAATGCGTT ACGAAGACCC TAATGGTGAC
 TACGGCCGCC AAGAACGTCA AAGAAAAGTG ATTGAAGGCA TCGTCCAAAA AGTCTTAAGT
 CTTAACAGCG TAAGCAACTA TCAAGAAATT TTAACAGCTG TTTCTGATAA TATGAAGACA
 GATTTAAGTT TTGATGACAT GAAAAAATT GCCTTAGATT ATCGCAGTGC CTTTGGTAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTGAAACAAG ACCAACTTCA AGGTACTGGT TTTATGCAAG ATGGTGTTC CTATCAACGT
GTGGATGAAC AAGAATTAAC TCGTGTCCTAA CAAGAGTTGA AAAATCAATT GAATACAAAA
TAA

EF075-2 (SEQ ID NO:286)

MSKG KKIFAIIXGI ILXLFLAVVG MGAKLYWDVS KSMDKTYETV
ERSKKSQVNL NNKEPFSVLL LGIDTGDDGR VEQGRSDTTI VATVNPRDKQ TTLVSLARDT
YVDIPGQKQ DKLNHAYAFG GASLAMDTVE NYLNIPINHY VSINMAGLKE LVNAVGGIEV
NNNLTFSDG YDFTIGKISL DGEQALSYSR MRYEDPNGDY GRQERQRKVI EGIVQKVLST
NSVSNYQEIL TAVSDNMKTD LSFDDMKKIA LDYRSFAGKV KQDQLQGTGF MQDGVSYQRV
DEQELTRVQQ ELKNQLNTK

EF075-3 (SEQ ID NO:287)

ACTTTA TTGGGATGTT TCTAAATCAA TGGATAAAAC CTATGAAACA
GTAGAACGAT CTAACAAAAG TCAGGTCAAT TTAAACAATA AGGAGCCTTT TTCTGTTTTA
TTATTAGGGA TTGATACAGG CGATGATGGG CGTGTGAGC AAGGTCGTC GGATACAAAC
ATTGTTGCAA CAGTTAATCC TCGTGACAAG CAAACAACCT TAGTCAGTCT TGCTCGCGAT
ACCTATGTTG ATATTCCAGG TCAAGGAAAA CAAGATAAAT TGAATCACGC CTATGCTTTT
GGTGGCGCAT CTTTAGCAAT GGACACAGTT GAAACTATT TAAACATACC TATTAATCAT
TATGTTTCAA TTAATATGGC TGGTTTAAAA GAATTAGTCA ACGCGGTTGG CGGAATCGAA
GTGAACAATA ATCTGACTTT TTCTCAAGAC GGATATGATT TTACGATTGG TAAAATTTCA
TTGGATGGTG AACAAGCACT CTCCTATTCA AGAATGCGTT ACGAAGACCC TAATGGTGAC
TACGGCCGCC AAGAAGCTCA AAGAAAAGTG ATTGAAGGCA TCGTCCAAA AGTCTTAAGT
CTTAACAGCG TAAGCAACTA TCAAGAAATT TTAACAGCTG TTTCTGATAA TATGAAGACA
GATTTAAGTT TTGATGACAT GAAAAAATT GCCTTAGATT ATCGCAGTGC CTTTGGTAAA
GTGAAACAAG ACCAACTTCA AGGTACTGGT TTTATGCAAG ATGGTGTTC CTATCAACGT
GTGGATGAAC AAGAATTAAC TCGTGTCCTAA CAAGAGTTGA AAAATCAATT GAATACAAAA

EF075-4 (SEQ ID NO:288)

KLYWDVS KSMDKTYETV
ERSKKSQVNL NNKEPFSVLL LGIDTGDDGR VEQGRSDTTI VATVNPRDKQ TTLVSLARDT
YVDIPGQKQ DKLNHAYAFG GASLAMDTVE NYLNIPINHY VSINMAGLKE LVNAVGGIEV
NNNLTFSDG YDFTIGKISL DGEQALSYSR MRYEDPNGDY GRQERQRKVI EGIVQKVLST
NSVSNYQEIL TAVSDNMKTD LSFDDMKKIA LDYRSFAGKV KQDQLQGTGF MQDGVSYQRV
DEQELTRVQQ ELKNQLNTK

EF076-1 (SEQ ID NO:289)

TAGAAAATAA CAGAGGAGCT GAAGGAAATG AAAGCATCAA CAAAAATTGG TATCGGTTTA
AGCATTGCTG CAGTTGCAAG TGTCTCTGTT GCAGTCATCG CTTCTGAAAA AATTATTAAG
AAGGTATCTC ATGTTTCCAA TCGTTATAAA GTTAAAAAGT TTGTAGACGA TAAATTTGAT
GGAACCAAAA AATTATTATC GATTGTCGAT GATTATCCG ATGATGAATT AGATTCTGTT
TTAAATGTTG TGGATCGTGT GAAAGATGGC GGTTCAAAAT TAGCTGAATA TGGCGAAAAA
GTTAAAGACA ATACAGATTC TTTAAAAGAA CGCTTTTTCA CATTTATTGA AGATGCAATG
AAGTTAAAAA AGTGGCCTAG GCCATCTTTT TTTTATAAAA ATAATCTTTT TGTTCACAA
TAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF076-2 (SEQ ID NO:290)

MK ASTKIGIGLS IAAVASVSVA VIASEKIIKK VSHVSNRYKV KKFVDDKFDG
 NQKLLSIVDD LSDDELDSVL NVVDRVKDGG SKLAEYGEKV KDNTDSLKER FFTFIEDAMK
 LKKWPRPSFF YKNSFVST

EF076-3 (SEQ ID NO:291)

CATCG CTTCTGAAAA AATTATTAAG
 AAGGTATCTC ATGTTTCCAA TCGTTATAAA GTTAAAAAGT TTGTAGACGA TAAATTTGAT
 GGAAACCAAA AATTATTATC GATTGTCGAT GATTTATCCG ATGATGAATT AGATTCGTGT
 TTAAATGTTG TGGATCGTGT GAAAGATGGC GGTTCAAAAT TAGCTGAATA TGGCGAAAAA
 GTTAAAGACA ATACAGATTC TTTAAAAGAA CGCTTTTCA CATTATTGA AGATGCAATG
 AAGTTAAAAA AGTGGCCTAG GCCATCTTTT TTTTATAAAA ATAATTCTT

EF076-4 (SEQ ID NO:292)

VIASEKIIKK VSHVSNRYKV KKFVDDKFDG
 NQKLLSIVDD LSDDELDSVL NVVDRVKDGG SKLAEYGEKV KDNTDSLKER FFTFIEDAMK
 LKKWPRPSFF YKNS

EF077-1 (SEQ ID NO:293)

TAATGTAAAG TGAATGATGG GAGAGAAAAA GAGATGAAGC ATGTAACAAA ATTGGGGATT
 ACAATTATAA CAGGAGTTTT GGCATTATTA TTTGAATTTA TTTTACATCA GCCGAATTGG
 GCGTATGGCA TTATTTTAAT AACAGGTTCT GTAATGGCGT TAATGATGTT CTGGGAAATG
 ATTCAAACCT TACGTGAAGG AAAATATGGT GTCGATATTT TAGCGATTAC CGCTATCGTT
 GCAACCTTAG CTGTGGGAGA ATACTGGGCC AGTTTGATGA TTTTAATTAT GTTGACTGGT
 GGTGATTCAT TAGAAGACTA TGCCGCTGGA AAAGCTAACC AAGAGCTGAA GTCATTATTG
 GATAATCGC CACAAAAAGC TCATCGCTTG AATGGCGAAA ATTTAGAAGA TGTTTCTGTT
 GAGGAAATCA ATGTTGGCGA TGAATTAGTA GTAAAACCAG GGGAACTAGT TCCAGTTGAT
 GGCTTGGTAA AAACCGGGAC ATCAACAGTC GATGAATCTT CATTAACAGG AGAATCAAAA
 CCAATTGAAA AAAATCCTGG GGATGAATTA ATGTCGGGTT CCGTGAATGG TGACGGCTCT
 TTGAAAATGG TTGCTGAAAA AACTGTAGCA GACAGTCAAT ATCAAACAAT TGTGAACCTA
 GTGAAAGAAT CTGCGGCGCG TCCAGCTCAT TTTGTACGTT TAGCAGATCG CTATGCGGTA
 CCTTTTACAC TAGTTGCCA CTAATTGCA GGTGTGCTT GGTGTGTTT AAAAAGTCCG
 ACACGTTTTG CGGAAGTCTT AGTTGTGCT TCGCCGTGTC CTTTAATTCT ATCTGCCCCA
 ATTGCTTTAG TGGCAGGGAT GGGTCGTTCA AGTCGTCATG GGGTCGTTAT TAAATCGGGA
 ACGATGGTCG AAAAATTAGC TTCTGCAAAA ACGATTGCGT TTGATAAAAC AGGCACGATT
 ACGCAAGGAC AACTTTCTGT TGATCAAGTC CAACCAATCA ATGCTGGAAT AACTGCTGCT
 GAATTAGTGG GATTGGCAGC AAGCGTGGAA CAAGAATCAA GTCATATTTT AGCTAGATCA
 ATTGTTGCTT ATGCCAGAAA GCAAGATGTC CCATTAAAAA ATATTACAGA TCTAGCGGAA
 GTTTCTGGTG CTGGCGTGAA GGCATTTGTG GATGGTGCTG AGATACGGGT AGGTAAAAAG
 AATTTTGTGA CACAAGAGTC TCAAGAACT GAAAAAATTG ATAAAACGAC TATTTCATATT
 TCACGTAATG GCACATATTT AGGCCGAATT ACTTTTACAG AACTGTACG CCCAGAAGCA
 AAAGAGACTA TGGAAAAATT ACACCAATTA CATCTTCAAC GAATTTTAAT GCTGACGGGG
 GATCAAGAAT CCGTTGCAGA AACGATTGCT GCAGAAGTAG GAATTACCGA AGTACATGGG
 GAATGTTTAC CACAAGATAA ATTAACATTT CTAAGAAGAT TGCTTAAAGA AAATCATCCA
 GTCATCATGG TAGGAGATGG TGTAATATGAT GCACCTTCGC TTGCTGCTGC AGACGTAGGT
 ATTGCTATGG GTGCTCATGG AGCTACTGCG GCTAGTGAAA CTGCTGACGT TGTTATTTTA
 AAAGATGACT TAAGTAAAGT CAGCCAAGCG GTCGAAATTG CCCAAGATAC CATGAAAATT
 GCCAACAAT CTGTATTAAT CGGAATTTTT ATCTGCGTTT TACTAATGTT AATTGCTAGT
 ACCGGGATCA TTCCGGCGCT AATCGGGGCT ATGCTACAAG AAGTCGTGGA CACTGTGTCA
 ATCTTATCTG CTTTGGCGTC TCGTCGAATT GGCCAGTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF077-2 (SEQ ID NO:294)

MKHVTKLGIT IITGVLALLF EFILHQPNEWA YGIILITGSV MALMMFWEMI
 QTLREGKYGV DILAITAIVA TLAVGEYWAS LMILIMLTGG DSLEDYAAGK ANQELKSLLD
 NSPQKAHRLN GENLEDVSVE EINVGDELVV KPGELVPVDG LVKTGTSTVD ESSLTGESKP
 IEKNPGDELM SGSVNGDGS LKMAEKTVD SQYQTIVNLV KESAARPAHF VRLADRYAVP
 FTLVAYLIAG VAWFVSKSPT RFAEVLVVAS PCPLILSAPI ALVAGMGRSS RHGVVKSQT
 MVEKLASAKT IAFDKTGTIT QGQLSVDQVQ PINAGITAAE LVGLAASVEQ ESSHILARSI
 VAYARKQDVP LKNITDLAEV SGAGVKAFVD GAEIRVGKKN FVTQESQETE KIDKTTIHIS
 RNGTHYLGRT FTDTVRPEAK ETMEKLHQLH LQRILMLTGD QESVAETIAA EVGITEVHGE
 CLPQDKLTIL KELPKENHPV IMVGDGVNDA PSLAAADVGI AMGAHGATAA SETADVILK
 DDLSKVSQAV EIAQDTMKIA KQSVLIGIFI CVLLMLIAST GIIPALIGAM LQEVVDTVSI
 LSALRARRIG Q

EF077-3 (SEQ ID NO:295)

TCA GCCGAATTGG
 GCGTATGGCA TTATTTTAAT AACAGGTTCT GTAATGGCGT TAATGATGTT CTGGGAAATG
 ATTCAAACCT TACGTGAAGG AAAATATGGT GTCGATATTT TAGCGATTAC CGCTATCGTT
 GCAACCTTAG CTGTGGGAGA ATACTGGGCC AGTTTGATGA TTTTAATTAT GTTGACTGGT
 GGTGATTATCAT TAGAAGACTA TGCCGCTGGA AAAGCTAACC AAGAGCTGAA GTCATTATTG
 GATAACTCGC CACAAAAAGC TCATCGCTTG AATGGCGAAA ATTTAGAAGA TGTTTCTGTT
 GAGGAAATCA ATGTTGGCGA TGAATTAGTA GTAAACCAG GGAAGTAGT TCCAGTTGAT
 GGCTTGGTAA AAACCGGGAC ATCAACAGTC GATGAATCTT CATTACAGG AGAATCAAAA
 CCAATTGAAA AAAATCCTGG GGATGAATTA ATGTCGGGTT CCGTGAATGG TGACGGCTCT
 TTGAAAATGG TTGCTGAAAA AACTGTAGCA GACAGTCAAT ATCAAACAAT TGTGAACTTA
 GTGAAAGAAAT CTGCGGCGCG TCCAGCTCAT TTTGTACGTT TAGCAGATCG CTATGCGGTA
 CCTTTTACAC TAGTTGCCTA CCTAATTGCA GGTGTTGCTT GGTGTTGTTT AAAAAGTCCG
 ACACGTTTTG CGGAAGTCTT AGTTGTTGCT TCGCCGTGTC CTTTAATTCT ATCTGCCCCA
 ATTGCTTTAG TGGCAGGGAT GGGTCGTTCA AGTCGTCATG GGGTCGTTAT TAAATCGGGA
 ACGATGGTCG AAAAATTAGC TTCTGCAAAA ACGATTGCGT TTGATAAAAC AGGCACGATT
 ACGCAAGGAC AACTTTCTGT TGATCAAGTC CAACCAATCA ATGCTGGAAT AACTGCTGCT
 GAATTAGTGG GATTGGCAGC AAGCGTGGA CAAGAATCAA GTCATATTTT AGCTAGATCA
 ATTGTTGCTT ATGCCAGAAA GCAAGATGTC CCATTAAAAA ATATTACAGA TCTAGCGGAA
 GTTTCTGGTG CTGGCGTGAA GGCATTTGTG GATGGTGCTG AGATACGGGT AGGTAAAAAG
 AATTTTGTGA CACAAGAGTC TCAAGAACT GAAAAAATG ATAAAACGAC TATTCATATT
 TCACGTAATG GCACATATTT AGGCCGAATT ACTTTTACAG AACTGTACG CCCAGAAGCA
 AAAGAGACTA TGGAAAAATT ACACCAATTA CATCTTCAAC GAATTTTAAT GCTGACGGGG
 GATCAAGAAT CCGTTGCAGA AACGATTGCT GCAGAAAGTAG GAATTACCGA AGTACATGGG
 GAATGTTTAC CACAAGATAA ATTAACATT CTAAAAGAAT TGCTTAAAGA AAATCATCCA
 GTCATCATGG TAGGAGATGG TGTAATGAT GCACCTTCGC TTGCTGCTGC AGACGTAGGT
 ATTGCTATGG GTGCTCATGG AGCTACTGCG GCTAGTGAAG CTGCTGACGT TGTATTTTTA
 AAAGATGACT TAAGTAAAGT CAGCCAAGCG GTCGAAATTG CCCAAGATAC CATGAAATT
 GCCAAACAAT CTGTATTAAT CGGAATTTTT ATCTGCGTTT TACTAATGTT AATTGCTAGT
 ACCGGGATCA TTCCGGCGCT AATCGGGGCT ATGCTACAAG AAGTCGTGGA CACTGTGTCA
 ATCTTATCTG CTTTGCGTGC TCGTCGAATT GGCC

EF077-4 (SEQ ID NO:296)

QPNWA YGIILITGSV MALMMFWEMI
 QTLREGKYGV DILAITAIVA TLAVGEYWAS LMILIMLTGG DSLEDYAAGK ANQELKSLLD
 NSPQKAHRLN GENLEDVSVE EINVGDELVV KPGELVPVDG LVKTGTSTVD ESSLTGESKP
 IEKNPGDELM SGSVNGDGS LKMAEKTVD SQYQTIVNLV KESAARPAHF VRLADRYAVP

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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FTLVAYLIAG VAWFVSKSPT RFAEVLVVAS PCPLILSAPI ALVAGMGRSS RHGVVKSQT
MVEKLASAKT IAFDKTGTIT QGQLSVDQVQ PINAGITAAE LVGLAASVEQ ESSHILARSI
VAYARKQDVP LKNITDLAEV SGAGVKAFVD GAEIRVGKKN FVTQESQETE KIDKTTIHIS
RNGTYLGRIT FTDTVRPEAK ETMEKLHQLH LQRILMLTGD QESVAETIAA EVGITEVHGE
CLPQDKLTIL KELPKENHPV IMVG DGVNDA PSLAAADVGI AMGAHGATAA SETADVILK
DDLKSVQAV EIAQDTMKIA KQSVLIGIFI CVLLMLIAST GIIPALIGAM LQEVVDTVSI
LSALRARRIG

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EF079-1 (SEQ ID NO:297)

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CCCAGGCTCT CATGCTTTAT TTTTAAGGAG GAAGCAATGA AGTCAAAAAA GAAACGTCGT
ATCATTGATG GTTTTATGAT TCTTTTACTG ATTATTGGAA TAGGTGCATT TCGGTATCCT
TTTGTTAGCG ATGCATTAAA TAACTATCTG GATCAACAAA TTATCGCTCA TTATCAAGCA
AAAGCAAGCC AAGAAAACAC CAAAGAAATG GCTGAACTTC AAGAAAAAAT GGAAAAGAAA
AACCAAGAAT TAGCGAAAAA AGGCAGCAAT CCTGGATTAG ATCCTTTTTT TGAAACGCAA
AAAACAACGA AAAAACCAGA CAAATCCTAT TTTGAAAGTC ATACGATTGG TGTTTTAACC
ATTCCAAAAA TAAATGTCCG TTTACCAATT TTTGATAAAA CGAATGCATT GCTATTGGAA
AAAGGAAGCT CCTTGTTAGA AGGAACCTCC TATCCTACAG GTGGTACGAA TACACATGCG
GTCATTTTCA GCCATCGTGG TCTCCCTCAA GCCAAATTAT TTACAGATTT GCCAGAATTA
AAAAAAGGCG ATGAATTTTA TATCGAAGTC AATGGGAAGA CGCTTGCTTA TCAAGTAGAT
CAAATAAAAA CCGTTGAACC AACTGATACA AAAGATTTAC ACATTGAGTC TGGCCAAGAT
CTCGTCACTT TATTAACCTG CACACCGTAT ATGATAAACA GTCATCGGTT ATTAGTTCGA
GGACATCGTA TCCCATATCA ACCAGAAAAA GCAGCAGCGG GGATGAAAAA AGTGGCACAA
CAACAAAATT TACTATTATG GACATTACTT TTAATTGCCT GTGCGTTAAT TATTAGCGGC
TTCATTATCT GGTACAAGCG ACGGAAAAAG ACGACCAGAA AACCAAAGTA G

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EF079-2 (SEQ ID NO:298)

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MKSKKRRRI IDGFMILLI IGIGAFAYPF
VSDALNNYLD QQIIAHYQAK ASQENTKEMA ELQEKMEKKN QELAKKGNP GLDPFSETQK
TTKKPKDSYF ESHTIGVLT I PKINVRLPIF DKTNALLLEK GSSLLEGTSY PTGGTNTHAV
ISGHRGLPQA KLFTDLPELK KGDEFYIEVN GKTLAYQVDQ IKTVEPTDTK DLHIESGQDL
VTLLTCTPYM INSHRLLVRG HRIPYQPEKA AAGMKKVAQQ QNLLLWTL L IACALIISGF
IIWYKRKKT TRKPK

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EF079-3 (SEQ ID NO:299)

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TCCT
TTTGTTAGCG ATGCATTAAA TAACTATCTG GATCAACAAA TTATCGCTCA TTATCAAGCA
AAAGCAAGCC AAGAAAACAC CAAAGAAATG GCTGAACTTC AAGAAAAAAT GGAAAAGAAA
AACCAAGAAT TAGCGAAAAA AGGCAGCAAT CCTGGATTAG ATCCTTTTTT TGAAACGCAA
AAAACAACGA AAAAACCAGA CAAATCCTAT TTTGAAAGTC ATACGATTGG TGTTTTAACC
ATTCCAAAAA TAAATGTCCG TTTACCAATT TTTGATAAAA CGAATGCATT GCTATTGGAA
AAAGGAAGCT CCTTGTTAGA AGGAACCTCC TATCCTACAG GTGGTACGAA TACACATGCG
GTCATTTTCA GCCATCGTGG TCTCCCTCAA GCCAAATTAT TTACAGATTT GCCAGAATTA
AAAAAAGGCG ATGAATTTTA TATCGAAGTC AATGGGAAGA CGCTTGCTTA TCAAGTAGAT
CAAATAAAAA CCGTTGAACC AACTGATACA AAAGATTTAC ACATTGAGTC TGGCCAAGAT
CTCGTCACTT TATTAACCTG CACACCGTAT ATGATAAACA GTCATCGGTT ATTAGTTCGA
GGACATCGTA TCCCATATCA ACCAGAAAAA GCAGCAGCGG GGATGAAAAA AGTGGCACAA
CAACAAAATT TACTATTATG GACATTACTT TTAATTGCCT GTGCGTTAAT TATTAGCGGC
TTCATTATCT GGTACAAGCG ACGGAAAAAG ACGACCAGAA AACCAA

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EF079-4 (SEQ ID NO:300)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PF

VSDALNNYLD QQIIAHYQAK ASQENTKEMA ELQEKMEKKN QELAKKGSNP GLDPFSETQK
 TTKKPKDSYF ESHTIGVLT I PKINVRLPIF DKTNALLLEK GSSLLEGTSY PTGGTNTHAV
 ISGHRGLPQA KLFTDLPELK KGDEFYIEVN GKTLAYQVDQ IKTVEPTDTK DLHIESGQDL
 VTLLTCTPYM INSHRLLV RG HRIPTYQPEKA AAGMKKVAQ QNLLLWTL L IACALIISGF
 IIWYKRRKKT TRKP

EF080-1 (SEQ ID NO:301)

TAGTTACACT CGTTTAGGGC TAGCAACGTT AGGCATTTTC GCTGGACTCT TAGCACTCTT
 TTTATTAGGA GGTATTTTCC TATGAAAAA CGACTTTTAC CTATTTTTTT CCTAATACTT
 CTTACCTTTG GCCTTGCCCT ACCCGTTTCG GCGGCTGAAA ATTCAATTGA TGATGGCGCA
 CAATTACTGA CACCTGATCA AATCAACCAA CTAAAGCAAG AGATAACAACC TTTAGAAGAA
 AAAACAAAAG CCTCTGTCTT TATTGTAACC ACAAATAATA ATACCTATGG CGATGAACAA
 GAATATGCAG ATCATTATCT TTTAAATAAA GTTGGCAAGG ACCAAAATGC GATTCTTTTT
 CTCATTGATA TGGACTTACG GAAAATCTAC ATCTCTACTT CTGGAACAT GATTGATTAT
 ATGACAGATG CACGAATTGA TGATACCTTA GATAAAATAT GGGATAATAT GAGTCAAGGA
 AATTATTTTCG CGGCTGCTCA AACCTTTGTT CAGGAACTC AAGCATTTGT TAATAAAGGG
 GTTCCTGGGG GGCATATCG TGTGGACAGC GAAACAGGTA AAATCACTCG TTATAAAGTC
 ATTACCCCGC TGGAAATGGT AATTGCTTTT GCTGCTGCGC TGATACTCAG TTTGGTCTTC
 TTAGGCATTA ATATTTCTAA ATATCAATTA AAATTTTCAA GTTATCAATA TCCCTTTAGG
 GAAAAACAA CTTTAACTT AACCTCCCGC ACAGATCAGT TAACCAACTC TTTTCATCACT
 ACGCGTCGTA TTCCTAAAA CAATGGCGGC AGTGGCGGAA TGGGCGGTGG TGGTAGCACC
 ACCCACTCAA CTGGCGGCGG CACATTCGGT GCGGCGGTC GAAGTTTTTA G

EF080-2 (SEQ ID NO:302)

MKKR LLPIFFLILL TFGLALPVSA AENSIDDGAQ
 LLTPDQINQL KQEIQPLEEK TKASVFIVTT NNNTYGDEQE YADHYLLNKV GKDQNAIFL
 IDMDLRKIYI STSGNMIDYM TDARIDTLD KIWDNMSQGN YFAAAQTFVQ ETQAFVNGV
 PGGHYRVDSE TKGITRYKVI TPLEMVIAFA AALILSLVFL GINISKYQLK FSSYQYPFRE
 KTTLNLSRT DQLTNSFITT RRIPKNNGGS GGMGGGGSTT HSTGGGTGG GGRSF

EF080-3 (SEQ ID NO:303)

GGCTGAAA ATTCAATTGA TGATGGCGCA
 CAATTACTGA CACCTGATCA AATCAACCAA CTAAAGCAAG AGATAACAACC TTTAGAAGAA
 AAAACAAAAG CCTCTGTCTT TATTGTAACC ACAAATAATA ATACCTATGG CGATGAACAA
 GAATATGCAG ATCATTATCT TTTAAATAAA GTTGGCAAGG ACCAAAATGC GATTCTTTTT
 CTCATTGATA TGGACTTACG GAAAATCTAC ATCTCTACTT CTGGAACAT GATTGATTAT
 ATGACAGATG CACGAATTGA TGATACCTTA GATAAAATAT GGGATAATAT GAGTCAAGGA
 AATTATTTTCG CGGCTGCTCA AACCTTTGTT CAGGAACTC AAGCATTTGT TAATAAAGGG
 GTTCCTGGGG GGCATATCG TGTGGACAGC GAAACAGGTA AAATCACTCG TTATAAAGTC
 ATTACCCCGC TGGAAATGGT AATTGCTTTT GCTGCTGCGC TGATACTCAG TTTGGTCTTC
 TTAGGCATTA ATATTTCTAA ATATCAATTA AAATTTTCAA GTTATCAATA TCCCTTTAGG
 GAAAAACAA CTTTAACTT AACCTCCCGC ACAGATCAGT TAACCAACTC TTTTCATCACT
 ACGCGTCGTA TTCCTAAAA CAATGGCGGC AGTGGCGGAA TGGGCGGTGG TGGTAGCACC
 ACCCACTCAA CTGGCGGCGG CACATTCGGT GCGGCGGTC GAAGT

EF080-4 (SEQ ID NO:304)

AENSIDDGAQ
 LLTPDQINQL KQEIQPLEEK TKASVFIVTT NNNTYGDEQE YADHYLLNKV GKDQNAIFL

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IDMDLRKIYI STSGNMIDYM TDARIDDTLD KIWDNMSQGN YFAAAQTFVQ ETQAFVNKGV
 PGGHYRVDSE TGKITRYKVI TPLEMVIAFA AALILSLVFL GINISKYQLK FSSYQYPFRE
 KTTNLNLTST DQLTNSFITR RRIPKNNGS GGMGGGGSTT HSTGGGTFFG GGRS

EF081-1 (SEQ ID NO:305)

TGAATGGAAC GAAGCAATCG TAATAAAAAA TCTTCAAAAA AACCACCTTAT TCTTGGTGTT
 TCTGCCTTGG TTCTAATCGC TGCTGCCGGT GGCGGGTATT ATGCTTATAG TCAATGGCAA
 GCCAAACAAG AATTAGCCGA AGCGAAGAAA ACAGCTACTA CATTTTTTAAA CGTATTGTCA
 AAACAGGAAT TTGATAAGTT ACCGTCCGTT GTTCAAGAAG CTAGCTTAAA GAAAAATGGC
 TATGATACTA AATCTGTTGT TGAAAAATAC CAAGCAATTT ATTCAGGGAT TCAAGCAGAA
 GGAGTCAAAG CTAGTGATGT TCAAGTCAAA AAGGCGAAA ACAATCAATA CACATTTACC
 TATAAATTAT CGATGAGCAC GCCTTTAGGC GAAATGAAA ATTTGTCTTA TCAATCAAGT
 ATCGCCAAAA AAGGCGATAC CTACCAAATC GCTTGGAAGC CATCTTTAAT TTTTCCAGAT
 ATGTCAGGAA ATGATAAAAT TTCGATTCAA GTAGATAATG CCAAACGTGG AGAAATTGTC
 GATCGTAATG GTAGTGGGCT AGCAATTAAC AAAGTGTGTTG ACGAAGTGGG CGTAGTGCCT
 GGCAAACTCG GTTCTGGCGC AGAAAAACA GCCAATATCA AAGCTTTTAG TGATAAATTC
 GCGGTTTCTG TTGATGAAAT CAATCAAAAG TTAAGCCAAG GATGGGTCCA AGCAGACTCC
 TTTGTACCAA TCACAGTCGC TTCTGAACCA GTGACAGAAT TACCAACAGG GGCTGCGACA
 AAAGATACAG AGTCACGTTA TTATCCGCTG GGGGAAGCAN TCGCAATTA A

EF081-2 (SEQ ID NO:306)

MERSNRNKKS SKKPLILGVS ALVLIAAAGG GYYAYSQWQA QEELAEAKKT ATTFLNVLSK
 QEFDKLPVSV QEASLKKNY DTKSVVEKYQ AIYSGIQAEG VKASDVQVKK AKDNQYTFTY
 KLSMSTPLGE MKDLSYQSSI AKKGDYQIA WKPSLIFPDM SGNDKISIQV DNAKRGEIVD
 RNSGLAINK VFDEGVVPG KLGSGAEKTA NIKAFSDKFG VSVDEINQKL SQGWVQADSF
 VPITVASEPV TELPTGAATK DTESRYYP LG EAXRN

EF081-3 (SEQ ID NO:307)

T GGCGGGTATT ATGCTTATAG TCAATGGCAA
 GCCAAACAAG AATTAGCCGA AGCGAAGAAA ACAGCTACTA CATTTTTTAAA CGTATTGTCA
 AAACAGGAAT TTGATAAGTT ACCGTCCGTT GTTCAAGAAG CTAGCTTAAA GAAAAATGGC
 TATGATACTA AATCTGTTGT TGAAAAATAC CAAGCAATTT ATTCAGGGAT TCAAGCAGAA
 GGAGTCAAAG CTAGTGATGT TCAAGTCAAA AAGGCGAAA ACAATCAATA CACATTTACC
 TATAAATTAT CGATGAGCAC GCCTTTAGGC GAAATGAAA ATTTGTCTTA TCAATCAAGT
 ATCGCCAAAA AAGGCGATAC CTACCAAATC GCTTGGAAGC CATCTTTAAT TTTTCCAGAT
 ATGTCAGGAA ATGATAAAAT TTCGATTCAA GTAGATAATG CCAAACGTGG AGAAATTGTC
 GATCGTAATG GTAGTGGGCT AGCAATTAAC AAAGTGTGTTG ACGAAGTGGG CGTAGTGCCT
 GGCAAACTCG GTTCTGGCGC AGAAAAACA GCCAATATCA AAGCTTTTAG TGATAAATTC
 GCGGTTTCTG TTGATGAAAT CAATCAAAAG TTAAGCCAAG GATGGGTCCA AGCAGACTCC
 TTTGTACCAA TCACAGTCGC TTCTGAACCA GTGACAGAAT TACCAACAGG GGCTGCGACA
 AAAGATACAG AGTCACGTTA TTATCCGCTG GGGG

EF081-4 (SEQ ID NO:308)

G GYYAYSQWQA QEELAEAKKT ATTFLNVLSK
 QEFDKLPVSV QEASLKKNY DTKSVVEKYQ AIYSGIQAEG VKASDVQVKK AKDNQYTFTY
 KLSMSTPLGE MKDLSYQSSI AKKGDYQIA WKPSLIFPDM SGNDKISIQV DNAKRGEIVD
 RNSGLAINK VFDEGVVPG KLGSGAEKTA NIKAFSDKFG VSVDEINQKL SQGWVQADSF
 VPITVASEPV TELPTGAATK DTESRYYP LG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF082-1 (SEQ ID NO:309)

TAAAAAATGA AAAAGATCGT GCGCATTTCA AGCATTTTGT TCGTTGCTAC GCCTCTTATG
 CTTTAAATA GTTCAAAGT TGAAGCAGCT CAAGTCGCTT CTATTCAATC CAACGCTGAT
 ATTACGTTTG CTCTTGATAA TACTGTCACG CCACCTGTCA ACCCGACGAA CCCTTCTCAG
 CCTGTGACAC CTAATCCTGC TGATCCTCAT CAACCTGGTA CAGCCGGACC CCTTAGTATT
 GACTATGTTT CAAATATCCA TTTTGGATCA AAACAAATTC AAGCCGGAAC AGCGATCTAT
 TCGGCACAAC TGGATCAAGT GCAAAATAGT ACTGGCGATT TAATTAGCGT GCCAAACTAT
 GTTCAAGTAA CTGACAAACG TGGTCTAAAT CTTGGCTGGA AATTATCAGT TAAACAGAGT
 GCGCAATTTG CTACAAGTGA TTCAACACCC GCTGTTTTGG ATAATGCATC CTTGACCTTT
 TTAGCAGCAA CACCCAATTC AACACAGTTA CTTTCTTTGG CGCCATTAAC GGTCCCAGTA
 ACCTTGGATC CAACTGGTGC CGCCACTTCT CTTGTGGCGA CTGCCGCTCT TTCAACAGGA
 ATGGGCACTT GGACATTAGC TTTTGGTAGC GGANCGACCG CTGCTCAAGG CATTCAATTA
 ACTGTTCCCTG CGACAACGAA AAAAGTTGCA GCTAAACAAT ATAAAACAAC GCTTACTTGG
 ATTTTGGATG ATACACCACT TTAA

EF082-2 (SEQ ID NO:310)

MKKIVRISS ILFVATPLML LNSSKVEAAQ VASIQSNADI TFALDNTVTP PVNPTNPSQP
 VTPNPADPHQ PGTAGPLSID YVSNHFGSK QIQAGTAIYS AQLDQVQNST GDLISVPNYV
 QVTDKRG LNL GWKLSVKQSA QFATSDSTPA VLDNASLTFL AATPNSTQLL SLAPLTVPV
 LDPTGAATSP VATAALSTGM GTWTLAFGSG XTAAQGIQLT VPATTKKVAA KQYKTTLTI
 LDDTPL

EF082-3 (SEQ ID NO:311)

AGCT CAAGTCGCTT CTATTCAATC CAACGCTGAT
 ATTACGTTTG CTCTTGATAA TACTGTCACG CCACCTGTCA ACCCGACGAA CCCTTCTCAG
 CCTGTGACAC CTAATCCTGC TGATCCTCAT CAACCTGGTA CAGCCGGACC CCTTAGTATT
 GACTATGTTT CAAATATCCA TTTTGGATCA AAACAAATTC AAGCCGGAAC AGCGATCTAT
 TCGGCACAAC TGGATCAAGT GCAAAATAGT ACTGGCGATT TAATTAGCGT GCCAAACTAT
 GTTCAAGTAA CTGACAAACG TGGTCTAAAT CTTGGCTGGA AATTATCAGT TAAACAGAGT
 GCGCAATTTG CTACAAGTGA TTCAACACCC GCTGTTTTGG ATAATGCATC CTTGACCTTT
 TTAGCAGCAA CACCCAATTC AACACAGTTA CTTTCTTTGG CGCCATTAAC GGTCCCAGTA
 ACCTTGGATC CAACTGGTGC CGCCACTTCT CTTGTGGCGA CTGCCGCTCT TTCAACAGGA
 ATGGGCACTT GGACATTAGC TTTTGGTAGC GGANCGACCG CTGCTCAAGG CATTCAATTA
 ACTGTTCCCTG CGACAACGAA AAAAGTTGCA GCTAAACAAT ATAAAACAAC GCTTACTTGG
 ATTTTGGATG ATACACCACT

EF082-4 (SEQ ID NO:312)

AQ VASIQSNADI TFALDNTVTP PVNPTNPSQP
 VTPNPADPHQ PGTAGPLSID YVSNHFGSK QIQAGTAIYS AQLDQVQNST GDLISVPNYV
 QVTDKRG LNL GWKLSVKQSA QFATSDSTPA VLDNASLTFL AATPNSTQLL SLAPLTVPV
 LDPTGAATSP VATAALSTGM GTWTLAFGSG XTAAQGIQLT VPATTKKVAA KQYKTTLTI
 LDDTP

EF083-1 (SEQ ID NO:313)

TAATTTAAAA GACAAGGAGA AATAAAAAATG AAAAAGAAAA TTTTAGCAGG AGCGCTTGTC
 GCTCTGTTTT TTATGCCTAC AGCTATGTTT GCCGCAAAAG GAGACCAAGG TGTGGATTGG
 GCGATTTATC AAGGTGAACA AGGTCGCTTT GGCTATGCAC ATGATAAATT CGCTATTGCC
 CAGATTGGAG GCTACAATGC TAGCGGTATT TATGAACAAT ACACATATAA AACGCAAGTG
 GCAAGTGCTA TTGCCCCAAGG TAAACGTGCG CATACCTATA TTTGGTATGA CACTTGGGGA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AACATGGACA TTGCGAAAAC AACAAATGGAT TACTTTTTTGC CACGTATTCA AACGCCTAAA
 AATTCCATCG TTGCATTAGA TTTTGAACAT GGAGCGTTGG CTAGTGTTCC AGATGGATAT
 GGAGGATATG TAAGTTCAGA TGCCGAAAAA GCAGCAAATA CAGAGACAAT TTTGTACGGT
 ATGCGCAGAA TCAAACAGGC TGGCTATACT CCAATGTATT ACAGCTATAA GCCATTTACA
 CTAAATCATG TAAACTATCA ACAAATCATC AAAGAGTTTC CTAACCTCTT ATGGATTGCT
 GCGTATCCTA TCGATGGTGT GTCACCATAT CCATTGTATG CTTATTTCCC AAGCATGGAT
 GGTATTGGTA TTTGGCAATT CACATCCGCT TATATTGCAG GTGGTTTAGA TGGTAACGTA
 GATTTAACAG GAATTACGGA TAGTGGTTAT ACAGATACCA ATAAACCAGA AACGGATACG
 CCAGCAACAG ATGCAGGCGA AGAAATTGAA AAAATACCTA ATTCTGATGT TAAAGTTGGC
 GATACCGTCA AAGTGAAATT TAATGTAGAT GCTTGGGCAA CTGGGGAAGC TATTCCGCAA
 TGGGTAAAAG GAAACAGCTA CAAAGTGCAA GAAGTAACTG GAAGCAGAGT ATTGCTTGAA
 GGTATCTTGT CATGGATTAG CAAAGGTGAT ATTGAATTAT TGCCAGACGC AACAGTCGTC
 CCTGATAAGC AACCAGAAGC GACTCATGTG GTACAATACG GAGAAACATT ATCAAGTATT
 GCTTATCAAT ATGGAACAGA CTATCAAACG TTGGCGGCAT TAAATGGATT GGCTAATCCA
 AATCTTATTT ATCCTGGTCA AGTTTTGAAA GTCAATGGAT CGGCAACAAG TAATGTCTAC
 ACGGTTAAAT ACGGCGATAA TTTATCTAGT ATTGCAGCAA AACTTGGCAC TACTTATCAA
 GCTTTAGCTG CATTAAACGG ATTAGCAAAT CCTAACTTGA TTTATCCAGG TCAAACATTG
 AATTATTAA

EF083-2 (SEQ ID NO:314)

MK KKILAGALVA LFFMPTAMFA AKGDQGVDDA IYQGEQGRFG YAHDKFAIAQ
 IGGYNASGIY EQTYKTQVA SAIAQKRAH TYIWDYTWGN MDIAKTMDY FLPRIQTPKN
 SIVALDFEHG ALASVPDGYG GYVSSDAEKA ANTETILYGM RRIKQAGYTP MYYSYKPFLL
 NHVNYQQIHK EFPNSLWIAA YPIDGVSPYP LYAYFPSMDG IGIWQFTSAY IAGGLDGNVD
 LTGITDSGYT DTNKPETDTP ATDAGEEIEK IPNSDVKVG DTVKVKFNVD WATGEAIPQW
 VKGNSYKQVE VTGSRVLEGG ILSWISKGDI ELLPDATVVP DKQPEATHVV QYGETLSSIA
 YQYGTDYQTL AALNGLANPN LIYPGQVLKV NGSATSNVYT VKYGDNLSSI AAKLGTTYQA
 LAALNGLANP NLIYPGQTLN Y

EF083-3 (SEQ ID NO:315)

AAAAG GAGACCAAGG TGTGGATTGG
 GCGATTTATC AAGGTGAACA AGGTCGCTTT GGCTATGCAC ATGATAAAAT CGCTATTGCC
 CAGATTGGAG GCTACAATGC TAGCGGTATT TATGAACAAT ACACATATAA AACGCAAGTG
 GCAAGTGCTA TTGCCCAGG TAAACGTGCG CATACTATA TTTGGTATGA CACTTGGGGA
 AACATGGACA TTGCGAAAAC AACAAATGGAT TACTTTTTTGC CACGTATTCA AACGCCTAAA
 AATTCCATCG TTGCATTAGA TTTTGAACAT GGAGCGTTGG CTAGTGTTCC AGATGGATAT
 GGAGGATATG TAAGTTCAGA TGCCGAAAAA GCAGCAAATA CAGAGACAAT TTTGTACGGT
 ATGCGCAGAA TCAAACAGGC TGGCTATACT CCAATGTATT ACAGCTATAA GCCATTTACA
 CTAAATCATG TAAACTATCA ACAAATCATC AAAGAGTTTC CTAACCTCTT ATGGATTGCT
 GCGTATCCTA TCGATGGTGT GTCACCATAT CCATTGTATG CTTATTTCCC AAGCATGGAT
 GGTATTGGTA TTTGGCAATT CACATCCGCT TATATTGCAG GTGGTTTAGA TGGTAACGTA
 GATTTAACAG GAATTACGGA TAGTGGTTAT ACAGATACCA ATAAACCAGA AACGGATACG
 CCAGCAACAG ATGCAGGCGA AGAAATTGAA AAAATACCTA ATTCTGATGT TAAAGTTGGC
 GATACCGTCA AAGTGAAATT TAATGTAGAT GCTTGGGCAA CTGGGGAAGC TATTCCGCAA
 TGGGTAAAAG GAAACAGCTA CAAAGTGCAA GAAGTAACTG GAAGCAGAGT ATTGCTTGAA
 GGTATCTTGT CATGGATTAG CAAAGGTGAT ATTGAATTAT TGCCAGACGC AACAGTCGTC
 CCTGATAAGC AACCAGAAGC GACTCATGTG GTACAATACG GAGAAACATT ATCAAGTATT
 GCTTATCAAT ATGGAACAGA CTATCAAACG TTGGCGGCAT TAAATGGATT GGCTAATCCA
 AATCTTATTT ATCCTGGTCA AGTTTTGAAA GTCAATGGAT CGGCAACAAG TAATGTCTAC
 ACGGTTAAAT ACGGCGATAA TTTATCTAGT ATTGCAGCAA AACTTGGCAC TACTTATCAA
 GCTTTAGCTG CATTAAACGG ATTAGCAAAT CCTAACTTGA TTTATCCAGG TCAAACATTG
 AAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF083-4 (SEQ ID NO:316)

KGDQGV DWA IYQGEQGRFG YAHDKFAIAQ
 IGGYNASGIY EQYTYKTQVA SAIAQKRAH TYIWYDTWGN MDIAKTTMDY FLPRIQTPKN
 SIVALDFEHG ALASVPDGYG GYVSSDAEKA ANTETILYGM RRIKQAGYTP MYYSYKPFTL
 NHVNYQQIIK EFPNSLWIAA YPIDGVSPYP LYAYFPSMDG IGIWQFTSAY IAGGLDGNVD
 LTGITDSGYT DTNKPETDTP ATDAGEEIEK IPNSDVKVGD TVKVKFNVDA WATGEAIPQW
 VKGNSYKVQE VTGSRVLLEG ILSWISKGDI ELLPDATVVP DKQPEATHVV QYGETLSSIA
 YQYGTDYQTL AALNGLANPN LIYPGQVLKV NGSATSNVYT VKYGDNLSSI AAKLGTTYQA
 LAALNGLANP NLIYPGQTLN

EF084-1 (SEQ ID NO:317)

TAGTCAAACG TTTATTTTCT CCTTAAATCC AGAAAAATC CCGTAATTAT GGTACACTAC
 CTATTGAATT GGAGGAGAAC TATGAAGAAA TTTGATGTAA TTATTGTCGG TGCTGGGACG
 AGCGGTATGA TGGCCACGAT TCGCGCCGCC GAAGCAGGCG CTCAAGTATT ATTGATTGAA
 AAAAATCGCC GTGTTGGGAA AAAATTATTA ATGACTGGTG GCGGCCGCTG TAATGTAACC
 AATAATCGGC CCGCAGAAGA AATCATTTC A TTTATTCCTG GGAATGGAAA ATTTTATATAC
 AGCGCATTTT CACAATTTGA TAACTATGAT ATCATGAACT TTTTGAATC CAATGGTATT
 CACTTAAAAG AAGAAGATCA CGGACGCATG TTCCCTGTGA CAGATAAATC GAAGTCAATT
 GTTGATGCGC TATTTAACCG CATTACGAA TTAGGAGTCA CTGTTTGTAC AAAAACACAG
 GTCACAAAAT TACTACGAAA AGACGATCAA ATAATTGGCG TTGAAACCGA ACTGGAAAAA
 ATTTATGCAC CGTGTGTTGT ATTAACAACT GGCGGCCGCA CTTATCCTTC CACAGGAGCA
 ACTGGTGATG GCTATAAACT AGCCAAAAAA ATGGGGCATA CCATCAGCCC GCTCTACCCCT
 ACCGAATCAC CTATTATTTT TGAAGAACCT TTTATCCTGG ATAAAACGTT GCAAGGTCTC
 TCTTTACAAG ATGTTAATTT AACTGTTTGG AACC AAAAAG GAAAACCTTT AGTTAATCAT
 CAAATGGATA TGCTGTTTAC ACATTTTGGC ATTTTACGAG CTGCCGCGCT CCGCTGTCTCT
 AGTTTTATTA ACCAAGAATT AACTCGCAAC GGTAATCAAC CTGTACCGGT AGCCTTGAT
 GTGTTTCCGA CAAAATCTTT TGAAGAAGTG CCTGCCAAAC AACTAACAGA AAAGCAACGN
 CTTTCCCTTG TGGAACACT GAAAGACTTT CAGTTCAGTG TTACGAAAAC ATTGCCTTTG
 GAAAAATCTT TTGTCACAGG CCGTGGGATT TCCCTCAAAG AAGTGACCCC TAAAACAATG
 GAGAGCAAAT TAGTCAATGG TTTATTTTTT GCTGGTGAAC TTTTAGATAT TAATGGCTAT
 ACTGGAGGCT ACAATGTTAC AGCTGCATTT GTCACTGGAC ATGTTGCTGG CTCCCATGCC
 GCAGAAATTG CAGAATACAC CTATTTACCA ATTGAAGAAG TCTAA

EF084-2 (SEQ ID NO:318)

MKKF DVIIVGAGTS GMMATIAAAE AGAQVLLIEK
 NRRVGKLLM TGGGRCNVTN NRPAEEIISF IPNGKFLYS AFSQFDNYDI MNFFESNGIH
 LKEEDHGRMF PVTDKSKSIV DALFNRI NEL GVTVFTKTQV TKLLRKDDQI IGVETELEKI
 YAPCVVLTG GRTPSTGAT GDGYKLAKKM GHTISPLYPT ESPIISEEPF ILDKTLQGLS
 LQDVNLTVLN QKGKPLVNHQ MDMLFTHFGI SGPAALRCSS FINQELTRNG NQPVITVALDV
 FPTKSFEEVP AKQLTEKQRL SFVELLKDFQ FTVTKTLPLE KSFVTGGGIS LKEVTPKTIME
 SKLVNGLFFA GELLDINGYT GGYNVTA AFV TGHVAGSHAA EIAEYTYLPI EEV

EF084-3 (SEQ ID NO:319)

C GAAGCAGGCG CTCAAGTATT ATTGATTGAA
 AAAAATCGCC GTGTTGGGAA AAAATTATTA ATGACTGGTG GCGGCCGCTG TAATGTAACC
 AATAATCGGC CCGCAGAAGA AATCATTTC A TTTATTCCTG GGAATGGAAA ATTTTATATAC
 AGCGCATTTT CACAATTTGA TAACTATGAT ATCATGAACT TTTTGAATC CAATGGTATT
 CACTTAAAAG AAGAAGATCA CGGACGCATG TTCCCTGTGA CAGATAAATC GAAGTCAATT
 GTTGATGCGC TATTTAACCG CATTACGAA TTAGGAGTCA CTGTTTGTAC AAAAACACAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTCACAAAAT TACTACGAAA AGACGATCAA ATAATTGGCG TTGAAACCGA ACTGGAAAAA
 ATTTATGCAC CGTGTGTTGT ATTAACAACCT GGCGGCCGCA CTTATCCTTC CACAGGAGCA
 ACTGGTGATG GCTATAAACT AGCCAAAAAA ATGGGGCATA CCATCAGCCC GCTCTACCCT
 ACCGAATCAC CTATTATTTC TGAAGAACCT TTTATCCTGG ATAAAACGTT GCAAGGTCTC
 TCTTTACAAG ATGTTAATTT AACTGTTTTG AACCAAAAAG GAAAACCTTT AGTTAATCAT
 CAAATGGATA TGCTGTTTAC ACATTTTGGC ATTTTCAGGAC CTGCCGCGCT CCGCTGTTCT
 AGTTTTATTA ACCAAGAATT AACTCGCAAC GGTAATCAAC CTGTCACGGT AGCCTTGGAT
 GTGTTTCCGA CAAAATCTTT TGAAGAAGTG CCTGCCAAAC AACTAACAGA AAAGCAACGN
 CTTTCCTTTG TGGAACACT GAAAGACTTT CAGTTCACTG TTACGAAAAC ATTGCCTTTG
 GAAAAATCTT TTGTCACAGG CGGTGGGATT TCCCTCAAAG AAGTGACCCC TAAAACAATG
 GAGAGCAAAT TAGTCAATGG TTTATTTTTT GCTGGTGAAC TTTTAGATAT TAATGGCTAT
 ACTGGAGGCT ACAATGTTAC AGCTGCATTT GTCAGTGGAC ATGTTGCTGG CTCCCATGCC
 GCAGAAATTG CAGAATACAC CTATTTACCA ATTGAAGAAG TC

EF084-4 (SEQ ID NO:320)

E AGAQVLLIEK

NRVRGKKLLM TGGGRCNVN NRPAEEIISF IPGNGKFLYS AFSQFDNYDI MNFFESNGIH
 LKEEDHGRMF PVTDKSKSIV DALFNRI NEL GVTVFTKTQV TKLLRKDDQI IGVELELEKI
 YAPCVVLTG GRTYPSTGAT GDGYKLAKKM GHTISPLYPT ESPIISEEPF ILDKTLQGLS
 LQDVNLTVLN QKGKPLVNHQ MDMLFTHFGI SGPAALRCSS FINQELTRNG NQPVTVLADV
 FPTKSFEVP AKQLTEKQRL SFVELLKDFQ FTVTKTLPLE KSFVTGGGIS LKEVTPKIME
 SKLVNGLFFA GELLDINGYT GGYNVTAFFV TGHVAGSHAA EIAEYTYLPI EEV

EF085-1 (SEQ ID NO:321)

TAACCCATGA AATCATTTTG TCCCGCATAT GGGGATATGA CTTTGACGGT GATGGCAGCA
 CAGTCCACAC TCATATCAAA AATCTGCGGG CGAACTGCCG GAAAATATCA TCAAAACCAT
 CCGCGGTGTA GGTACCGAT TGGAGGAATC ATTATAATGG AAAGAAAAGG GATTTTCATT
 AAGGTTTTTT CCTATACGAT CATTGTCCTG TTTACTGCTTG TCGGTGTAAC GGCAACACTG
 TTTGCACAGC AATTGTGTC TTATTTTACA GCGATGGAAG CACAGCAAAC AGTAAAATCC
 TATCAGCCAT TGGTGAACT GATTGAGAAT AGCGATAGGC TTGATATGCA AGAGGTGGCA
 GGGCTGTTTC ACTACAATA CCAATCCTTT GAGTTTTATA TTGAAGATAA AGAGGGAAGC
 GTACTCTATG CCACACCGAA TGCCGATACA TCAAATAGTG TTAGGCCCCG CTTTCTTTAT
 GTGGTACATA GAGATGATAA TATTTGATT GTTGCTCAAA GCAAGGCAGG TGTGGGATTG
 CTTTATCAAG GGCTGACAAT TCGGGGAATT GTTATGATTG CGATAATGGT TGTATTTCAGC
 CTTTTATGCG CGTATATCTT TGCGCGGCAA ATGACAACGC CGATCAAAGC CTTAGCGGAC
 AGTGCGAATA AAATGGCAAA CCTGAAAGAA GTACCGCCGC CGCTGGAGCG AAAGGATGAG
 CTTGGCGCAC TGGCTCACGA CATGCATTCC ATGTATATCA GGCTGAAAGA AACCATCGCA
 AGGCTGGAGG ATGAAATCGC AAGGGAACAT GAGTTGGAGG AAACACAGCG ATATTTCTTT
 GCGGCAGCCT CTCATGAGTT AAAACGCCC ATCGCGGCTG TAAGCGTTCT GTTGGAGGGA
 ATGCTTGAAA ATATCGGTGA CTACAAAGAC CATTCTAAGT ATCTGCGCGA ATGCATCAAA
 ATGATGGACA GGCAGGGCAA AACCATTTCG GAAATACTGG AGCTTGTCAG CCTGAACGAT
 GGGAGAATCG TACCCATAGC CGAACCGCTG GACATAGGGC GCACGGTTGC CGAGCTGCTA
 CCCGATTTTC AAACCTTGGC AGAGGCAAAC AACCAGCGGT TCGTCACAGA TATTCCAGCC
 GGACAAATTG TCCTGTCCGA TCCGAAGCTG ATCCAAAAGG CGCTATCCAA TGTCATATTG
 AATGCGGTTT AGAACACGCC CCAGGGAGGT GAGGTACGGA TATGGAGTGA GCCTGGGGCT
 GAAAAATACC GTCTTTCCGT TTTGAACATG GGCGTTCACA TTGATGATAC TGCACTTTCA
 AAGCTGTTCA TCCCATTTCTA TCGCATTGAT CAGGCGCGAA GCAGCAAAAA GTGGGCGAAG
 CGGTTTGGGG CTTGCCATCG TACAAAAAAC GCTGGATGCC ATGAGCCTCC AATATGCGCT
 GGAACACACC TCAGATGGCG TTTTGTTCTG GCTGGATTTA CCGCCACAT CAACACTATA
 AATATTTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF085-2 (SEQ ID NO:322)

MERKGIFIK

VFSYTIIVLL LLVGVATLTF AQQFVSFYFRA MEAQQTIVKSY QPLVELIQNS DRLDMQEVAG
 LFHYNNQSFE FYIEDKEGSV LYATPNADTS NSVRPDLFLYV VHRDDNISIV AQSKAGVGLL
 YQGLTIRGIV MIAIMVVFSL LCAYIFARQM TTPIKALADS ANKMANLKEV PPPLERKDEL
 GALAHDMHSM YIRLKETIAR LEDEIAREHE LEETQRYFFA AASHELKTPI AAVSVLLEGM
 LENIGDYKDH SKYLRECIKM MDRQGKTISE ILELVSLNDG RIVPIAEPLD IGRTVAELLP
 DFQTLAEANN QRFVTDIPAG QIVLSDPKLI QKALSNVILN AVQNTPOGGE VRIWSEPGAE
 KYRLSVLNMG VHIDDTALSK LFIPFYRIDQ ARSSKKWAKR FGACHRTKNA GCHEPPICAG
 KHLRWRFVLA GFTAHINTIN I

EF085-3 (SEQ ID NO:323)

GC AATTTGTGTC TTATTTTCAGA GCGATGGAAG CACAGCAAAC AGTAAAATCC
 TATCAGCCAT TGGTGGAACT GATTCAGAAAT AGCGATAGGC TTGATATGCA AGAGGTGGCA
 GGGCTGTTTC ACTACAATAA CCAATCCTTT GAGTTTTATA TTGAAGATAA AGAGGGAAGC
 GTACTCTATG CCACACCGAA TGCCGATACA TCAAATAGTG TTAGGCCCGA CTTTCTTTAT
 GTGGTACATA GAGATGATAA TATTTTCGATT GTTGCTCAAA GCAAGGCAGG TGTGGGATTG
 CTTTATCAAG GGCTGACAAT TCGGGGAATT GTTATGATTG CGATAATGGT TGTATTCAGC
 CTTTATGCG CGTATATCTT TCGCGGGCAA ATGACAACGC CGATCAAAGC CTTAGCGGAC
 AGTGCGAATA AAATGGCAAA CCTGAAAGAA GTACCGCCGC CGCTGGAGCG AAAGGATGAG
 CTTGGCGCAC TGGCTCACGA CATGCATTCC ATGTATATCA GGCTGAAAGA AACCATCGCA
 AGGCTGGAGG ATGAAATCGC AAGGGAACAT GAGTTGGAGG AAACACAGCG ATATTTCTTT
 GCGGCAGCCT CTCATGAGTT AAAAACGCCC ATCGCGGCTG TAAGCGTTCT GTTGGAGGGA
 ATGCTTGAAA ATATCGGTGA CTACAAAGAC CATTCTAAGT ATCTGCGCGA ATGCATCAAA
 ATGATGGACA GGCAGGGCAA AACCATTTCG GAAATACTGG AGCTTGTCAG CCTGAACGAT
 GGGAGAATCG TACCCATAGC CGAACCGCTG GACATAGGGC GCACGGTTGC CGAGCTGCTA
 CCCGATTTTC AAACCTTGGC AGAGGCAAAC AACCAGCGGT TCGTCACAGA TATTCCAGCC
 GGACAAATTG TCCTGTCCGA TCCGAAGCTG ATCCAAAAGG CGCTATCCAA TGTCATATTG
 AATGCGGTTT AGAACACGCC CCAGGGAGGT GAGGTACGGA TATGGAGTGA GCCTGGGGCT
 GAAAAATACC GTCTTTCCGT TTTGAACATG GGCGTTTACA TTGATGATAC TGCACTTTCA
 AAGCTGTTCA TCCCATTCTA TCGCATTGAT CAGGCGCGAA GCAGCAAAAA GTGGGCGAAG
 CGGTTTGGGG CTTGCCATCG TACAAAAAAC GCTGGATGCC ATGAGCCTCC AATATGCGCT
 GGAAAAACACC TCAGATGGCG TTTTGTTCG GCTGGATTTA CCGCCACAT CAACACTATA
 AATATTT

EF085-4 (SEQ ID NO:324)

QFVSFYFRA MEAQQTIVKSY QPLVELIQNS DRLDMQEVAG
 LFHYNNQSFE FYIEDKEGSV LYATPNADTS NSVRPDLFLYV VHRDDNISIV AQSKAGVGLL
 YQGLTIRGIV MIAIMVVFSL LCAYIFARQM TTPIKALADS ANKMANLKEV PPPLERKDEL
 GALAHDMHSM YIRLKETIAR LEDEIAREHE LEETQRYFFA AASHELKTPI AAVSVLLEGM
 LENIGDYKDH SKYLRECIKM MDRQGKTISE ILELVSLNDG RIVPIAEPLD IGRTVAELLP
 DFQTLAEANN QRFVTDIPAG QIVLSDPKLI QKALSNVILN AVQNTPOGGE VRIWSEPGAE
 KYRLSVLNMG VHIDDTALSK LFIPFYRIDQ ARSSKKWAKR FGACHRTKNA GCHEPPICAG
 KHLRWRFVLA GFTAHINTIN I

EF086-1 (SEQ ID NO:325)

TAACTGGTGG GATTGGCAAA TTGGTTCCGC GCAGCGCTAA CAGATACATT GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AAATTAAATA AATTTACTGC TCCGCTGATG
 CTGTATGCAA AAGATCCAAA CATACAATGG CCAATTTATC GTGCAACAGG AGCTAACTTA
 ACAGATATTT CAATCACCGT TTTAGGTACT GGAATTTTGT TAGAAGATAA TCAACGCCTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GTACAAGTAC AAGAAGCTGT TCCGTCCGTT TTAAAAAGTG TTTCTCTCTGG TGATGGCTTA
 TATCCTGATG GTTCCTTGAT TCAACATGGT TATTTTCCGT ACAACGGCAG TTACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTCAG ACTATTTTAC AAGGTTCCGA CTGGGAGATG
 AATGACCCTA ACATTAGTAA TTTATTTAAT GTTGTGGATA AAGGTTACTT ACAATTGATG
 GTAAATGGAA AAATGCCATC GATGGTTTCT GGTAGAAGTA TTTCCAGAGC GCCAGAAACG
 AATCCTTTTA CTACAGAGTT TGAATCGGGT AAAGAAACAA TAGCTAATTT AACCTTAATT
 GCAAAATTTG CACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCACTACTA TCATTTCTTT AAAAAACCAA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCTGCCCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCCTA CAGAAAAATA ACGAATATGC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAAATTGGGA ATACGGAAAA TAAAAAGGC
 TGGCATAACG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACCTGG CAACGATCGA TCCATATCGA TTACCAGGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAAATG GTGCTTATAC AGGGAAACGC AGTCCCCAGT CATGGGTAGG TGGCTCAAAT
 AATGGACAGG TTGCCTCTAT AGGAATGTTT TTAGATAAAA GTAATGAAGG AATGAACCTA
 GTTGCTAAAA AATCTTGTTT CTTATTAGAT GGTCAAATCA TTAATTTGGG AAGTGGCATT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCCTCGATA ATCGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GGATTAGTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTCNA TGAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AGACTGTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CCATTGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCAG GACTGTATGC GTATGATCCA
 ATGTCGGTTA TTTCAGAAAA AATTGATAAC GGTGTTTATC GCTTAACTCT TGCGAATCCT
 TTACAAAATA ATGCATCCGT TTCTATTGAA TTTGATAAGG GCATTCTTGA AGTAGTCGCA
 GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATAGTGC GGGGTTAAAT
 GGCAGCTCGC GTTCAATCAT TGTAAAAACA ACTCCTGAAG TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACCGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAAACAAC AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGGCAG TGAAGCAATT GGTAAAAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTGAAAATCA TCAAAGAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAAATAGT GGGAAAAATA AAAGGAGCAA
 AAAAATGGGG GGAATAATGG ACACTTAAAT ACTAGTACAG GAGTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAG CTAGCCAAAT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGTG ATTATTGGTC TTCTAGTTAT CGCCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF086-2 (SEQ ID NO:326)

LVGLANWFRA ALTDTLILLH DDLNLTDAEK LNKFTAPLML YAKDPNIQWP IYRATGANLT
 DISITVLGTG LLEDNQRLV QVQEAVPSVL KSVSSGDGLY PDGSLIQHGY FPNYSYSGNE
 LLKGFGRIFT ILQGSWEMN DPNISNLFNV VDKGYLQLMV NGKMPSMVSG RSISRAPETN
 PFTTEFESGK ETIANLTIA KFAPENLRND IYTSIQTWLQ QSGSYHFFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMRVLQ KNNEYAVGIS MYSQRVGNYE FGNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTTVDREL ANGAYTGKRS PQSWVGSSNN
 GQVASIGMFL DKSNEGMNLV AKKSWFLLDG QIINLGSGIT GTTDASIETI LDNRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDVQI EERSGRYDI NEYFVNDKTY
 TNTFAKISKY YGKTVENGTY EYLTUVGKTN EEIAALSKNK GYTVLENTAN LQAI EAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNASVSIEF DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIVKTT PEVTKEALEK LIQEKEHQE KDYTAASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVKVP TKEVDKTNLL KIIKENEKHQ

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EKDYTASSWK VYSEALKQAO TVADQTTATQ AEVDQAEAKL RSAVKRLTLK NSGENKKEQK
 NGGNNGHLNT STGVDQGTGK QVKPSSQGGF RKASQFLPST GEKKSIALVI IGLLVIASGC
 LLVFRKSKSK K

EF086-3 (SEQ ID NO:327)

ACCAGAAAA TTTAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCATACTA TCATTTCTTT AAAAACCACAA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCTGCCCCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCCTA CAGAAAAATA ACGAATATGC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGGAAAA TAAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACCAGGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAATG GTGCTTATAC AGGGAAACGC AGTCCCCAGT CATGGGTAGG TGGCTCAAAT
 AAT

EF086-4 (SEQ ID NO:328)

PENLRND IYTSIQTWLQ QSGSYHFFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMDRVLO KNNYAVGIS MYSQRVGNIE FGNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTTVDREL ANGAYTGKRS PQSWVGGSN

EF087-1 (SEQ ID NO:329)

TAACTGGTGG GATTGGCAAA TTGGTTCCGC GCAGCGCTAA CAGATACATT GATTTTATTA
 CATGATGACC TATTGAATAC AGATGCAGAA AAATTAAATA AATTTACTGC TCCGCTGATG
 CTGTATGCAA AAGATCCAAA CATACAATGG CCAATTTATC GTGCAACAGG AGCTAACTTA
 ACAGATATTT CAATCACCCT TTTAGGTACT GGACTTTTGT TAGAAGATAA TCAACGCCTA
 GTACAAGTAC AAGAAGCTGT TCCGTCCGTT TTA AAAAGTG TTTCTCTG TGATGGCTTA
 TATCCTGATG GTTCCTTGAT TCAACATGGT TATTTTCCGT ACAACGGCAG TTACGGGAAT
 GAGTTGCTAA AAGGGTTTGG ACGAATTCAG ACTATTTTAC AAGGTTCCGA CTGGGAGATG
 AATGACCCTA ACATTAGTAA TTTATTTAAT GTTGTGGATA AAGGTTACTT ACAATTGATG
 GTAAATGGAA AAATGCCATC GATGGTTTCT GGTAGAAGTA TTTCCAGAGC GCCAGAAACG
 AATCCTTTTA CTACAGAGTT TGAATCGGGT AAAGAAACAA TAGCTAATTT AACCTTAATT
 GCAAAATTTG CACCAGAAAA TTAAAGAAAT GACATTTATA CATCTATCCA AACGTGGCTT
 CAACAAAGTG GGTCATACTA TCATTTCTTT AAAAACCACAA GAGATTTTGA AGCGTTAATT
 GACTTGAAAA ATGTAGTGAA TAGTGCGTCA CCTGCCCCAAG CGACACCAAT GCAATCTTTA
 AATGTATATG GTTCGATGGA TCGAGTCCTA CAGAAAAATA ACGAATATGC GGTGGGGATC
 AGTATGTATT CACAACGTGT CGGAAACTAT GAATTTGGGA ATACGGAAAA TAAAAAAGGC
 TGGCATAACAG CAGACGGCAT GCTTTATTTA TACAATCAAG ACTTTGCTCA GTTTGATGAA
 GGATACTGGG CAACGATCGA TCCATATCGA TTACCAGGAA CGACAGTTGA CACAAGAGAA
 TTGGCAAATG GTGCTTATAC AGGGAAACGC AGTCCCCAGT CATGGGTAGG TGGCTCAAAT
 AATGGACAGG TTGCCTCTAT AGGAATGTTT TTAGATAAAA GTAATGAAGG AATGAACCTA
 GTTGCTAAAA AATCTTGGTT CTTATTAGAT GGTCAAATCA TTAATTTGGG AAGTGGCATT
 ACTGGTACGA CAGATGCTTC GATTGAAACA ATCCTCGATA ATCGGATGAT TCATCCACAG
 GAAGTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GGATTAGTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CTAATTCNA TGAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AGACTGTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CCATTGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCAG GACTGTATGC GTATGATCCA
 ATGTCGGTTA TTTCAGAAAA AATTGATAAC GGTGTTTATC GCTTAACTCT TGCGAATCCT
 TTACAAAATA ATGCATCCGT TTCTATTGAA TTTGATAAGG GCATTCCTGA AGTAGTCGCA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCGGACCCAG AAATTTCTGT TGACCAAAAT ATTATCACTT TAAATAGTGC GGGGTTAAAT
 GGCAGCTCGC GTTCAATCAT TGTTAAACA ACTCCTGAAG TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACCGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAAACAAC AGCAACGCAA
 GCAGAAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGGCAG TGAAGCAATT GGTAAGAGTG
 CCAACTAAAG AAGTAGATAA AACCAACTTG TTGAAAATCA TCAAAGAAAA CGAGAAACAC
 CAAGAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTTCG CAGTGAAGCG ATTAACATTG AAAAATAGTG GAGTTGATCA AACTGGTACG
 AAAAATGGGG GGAATAATGG ACACTTAAAT ACTAGTACAG GAGTTGATCA AACTGGTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAAG CTAGCCAATT TTTACCGAGC
 ACAGGAGAAA AGAAATCGAT CGCGCTTGTG ATTATTGGTC TTCTAGTTAT CGCCAGTGGG
 TGTCTTTTAG TTTTTCGTAA AAGTAAATCG AAGAAGTAA

EF087-2 (SEQ ID NO:330)

LVGLANWFRA ALTDTLILLH DDLNLTDAEK LNKFTAPLML YAKDPNIQWP IYRATGANLT
 DISITVLGTG LLEDNQRLV QVQEA VPSVL KSVSSGDGLY PDGSLIQHGY FPYNGSYGNE
 LLKGFGRIGT ILQGS DWEMN DPNISNLFNV VDKGYLQLMV NGKMPSMVSG RSISRAPETN
 PFTTEFESGK ETIANLTLIA KFAPENLRND IYTSIQTWLQ QSGSYHFFK KPRDFEALID
 LKNVNSASP AQATPMQSLN VYGSMDRVLQ KNNEYAVGIS MYSQRVGNYE FGNTENKKGW
 HTADGMLYLY NQDFAQFDEG YWATIDPYRL PGTVDREL ANGAYTGKRS PQSWVGSSNN
 GQVASIGMFL DKSNEGMNLV AKKSWFLLDG QIINLGSGIT GTTDASIETI LDNRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDVQI EERSGRYDI NEYFVNDKTY
 TNTFAKISKY YGKTVENGTY EYLTVVGKTN EEIAALSKNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNASVSIEF DKGILEVVA
 DPEISVDQNI ITLNSAGLNG SSRSIIVKTT PEVTKEALEK LIQEKEHQE KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVKVP TKEVDKTNLL KIIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSVKRLTLK NSGENKKEQK
 NGGNNGHLNT STGVDQGTGK QVKPSSQGGF RKASQFLPST GEKKSIALVI IGLLVIASGC
 LLVFRKSKSK K

EF087-3 (SEQ ID NO:331)

A ATCGGATGAT TCATCCACAG
 GAACTGAAGC TTAACCAAGG TTCAGACAAA GATAATTCTT GGATTAGTTT AAGCGCAGCG
 ANTCCATTGA ATAACATTGG CTATGTTTTT CCTAATTCNA TGAATACGCT TGATGTTCAA
 ATAGAAGAAC GCTCTGGTCG CTACGGAGAT ATTAACGAAT ACTTTGTTAA TGATAAAACC
 TATACAAATA CATTTGCTAA AATTAGTAAA AATTATGGCA AGACTGTTGA AAATGGTACT
 TACGAATATT TAACAGTGGT TGGGAAAACG AATGAAGAAA TCGCAGCTCT TTCTAAAAAC
 AAAGGCTATA CTGTTCTAGA AAATACAGCA AACTTACAAG CCATTGAAGC AGGTAATTAT
 GTCATGATGA ATACATGGAA TAATGACCAA GAAATTGCAG GACTGTATGC GTATGATCCA
 ATGTCGGTTA TTTTCAGAAAA AATTGATAAC GGTGTTTATC GCTTAACTCT TGCGAATCCT
 TTACAAAATA ATGCATCC

EF087-4 (SEQ ID NO:332)

NRMIHPQE
 VKLNQGSDDK NSWISLSAAX PLNNIGYVFP NSMNTLDVQI EERSGRYDI NEYFVNDKTY
 TNTFAKISKY YGKTVENGTY EYLTVVGKTN EEIAALSKNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNAS

EF088-1 (SEQ ID NO:333)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TAAGTGGTGG	GATTGGCAAA	TTGGTTCCGC	GCAGCGCTAA	CAGATACATT	GATTTTATTA
CATGATGACC	TATTGAATAC	AGATGCAGAA	AAATTAAATA	AATTTACTGC	TCCGCTGATG
CTGTATGCAA	AAGATCCAAA	CATACAATGG	CCAATTTATC	GTGCAACAGG	AGCTAACTTA
ACAGATATTT	CAATCACCGT	TTTAGGTACT	GGACTTTTGT	TAGAAGATAA	TCAACGCCTA
GTACAAGTAC	AAGAAGCTGT	TCCGTCCGTT	TTAAAAAGTG	TTTCCTCTGG	TGATGGCTTA
TATCCTGATG	GTTCCTTGAT	TCAACATGGT	TATTTTCCGT	ACAACGGCAG	TTACGGGAAT
GAGTTGCTAA	AAGGGTTTGG	ACGAATTCAG	ACTATTTTAC	AAGGTTCCGA	CTGGGAGATG
AATGACCCTA	ACATTAGTAA	TTTATTTAAT	GTTGTGGATA	AAGGTTACTT	ACAATTGATG
GTAAATGGAA	AAATGCCATC	GATGGTTTCT	GGTAGAAGTA	TTTCCAGAGC	GCCAGAAACG
AATCCTTTTA	CTACAGAGTT	TGAATCGGGT	AAAGAAACAA	TAGCTAATTT	AACCTTAATT
GCAAAATTTG	CACCAGAAAA	TTTAAGAAAT	GACATTTATA	CATCTATCCA	AACGTGGCTT
CAACAAAGTG	GGTCATACTA	TCATTTCTTT	AAAAAACCAA	GAGATTTTGA	AGCGTTAATT
GACTTGAAAA	ATGTAGTGAA	TAGTGCCTCA	CCTGCCCAAG	CGACACCAAT	GCAATCTTTA
AATGTATATG	GTTCGATGGA	TCGAGTCCTA	CAGAAAAATA	ACGAATATGC	GGTGGGGATC
AGTATGTATT	CACAACGTGT	CGGAACTAT	GAATTTGGGA	ATACGAAAAA	TAAAAAAGGC
TGGCATAACG	CAGACGGCAT	GCTTTATTTA	TACAATCAAG	ACTTTGCTCA	GTTTGATGAA
GGATACTGGG	CAACGATCGA	TCCATATCGA	TTACCAGGAA	CGACAGTTGA	CACAAGAGAA
TTGGCAAATG	GTGCTTATAC	AGGGAAACGC	AGTCCCCAGT	CATGGGTAGG	TGGCTCAAAT
AATGGACAGG	TTGCCTCTAT	AGGAATGTTT	TTAGATAAAA	GTAATGAAGG	AATGAACCTA
GTTGCTAAAA	AATCTTGGTT	CTTATTAGAT	GGTCAAATCA	TTAATTTGGG	AAGTGGCATT
ACTGGTACGA	CAGATGCCTC	GATTGAAACA	ATCCTCGATA	ATCGGATGAT	TCATCCACAG
GAAGTGAAGC	TTAACCAAGG	TTCAGACAAA	GATAATTCTT	GGATTAGTTT	AAGCGCAGCG
ANTCCATTGA	ATAACATTGG	CTATGTTTTT	CCTAATTCNA	TGAATACGCT	TGATGTTCAA
ATAGAAGAAC	GCTCTGGTCG	CTACGGAGAT	ATTAACGAAT	ACTTTGTTAA	TGATAAAACC
TATACAAATA	CATTTGCTAA	AATTAGTAAA	AATTATGGCA	AGACTGTTGA	AAATGGTACT
TACGAATATT	TAACAGTGGT	TGGGAAAACG	AATGAAGAAA	TCGCAGCTCT	TTCTAAAAAC
AAAGGCTATA	CTGTTCTAGA	AAATACAGCA	AACTTACAAG	CCATTGAAGC	AGGTAATTAT
GTCATGATGA	ATACATGGAA	TAATGACCAA	GAAATTGCAG	GAATGTATGC	GTATGATCCA
ATGTCGGTTA	TTTCAGAAAA	AATTGATAAC	GGTGTTTATC	GCTTAACCTT	TGCGAATCCT
TTACAAAATA	ATGCATCCGT	TTCTATTGAA	TTTGATAAGG	GCATTCTTGA	AGTATTCGCA
GCGGACCCAG	AAATTTCTGT	TGACCAAAAT	ATTATCACTT	TAAATAGTGC	GGGTTTAAAT
GGCAGCTCGC	GTTCAATCAT	TGTTAAAACA	ACTCCTGAAG	TAACGAAAGA	AGCGTTAGAA
AAATTAATTC	AGGAACAAAA	AGAACACCAA	GAAAAAGACT	ACACCGCAAG	CAGCTGGAAA
GTCTACAGCG	AAGCAATTGA	ACAAGCACAA	ACTGTGGCAG	ATCAAACAAC	AGCAACGCAA
GCAGAAGTAG	ACCAAGCAGA	AACAGAGTTA	CGTTCCGCAG	TGAAGCAATT	GGTAAAAGTG
CCAACTAAAG	AAGTAGATAA	AACCAACTTG	TTGAAAATCA	TCAAAGAAAA	CGAGAAAACAC
CAAGAAAAAG	ACTACACCGC	AAGCAGTTGG	AAAGTCTACA	GTGAAGCATT	GAAGCAAGCG
CAAACGTGG	CAGATCAAAC	AACAGCAACG	CAAGCAGAAG	TAGACCAAGC	AGAAGCAAAA
CTACGTTCCG	CAGTGAAGCG	ATTAACATTG	AAAAATAGTG	GGGAAAATAA	AAAGGAGCAA
AAAAATGGGG	GGAATAATGG	ACACTTAAAT	ACTAGTACAG	GAGTTGATCA	AACTGGTACG
AAACAAGTTA	AGCCATCAAG	CCAAGGTGGT	TTCAGAAAAG	CTAGCCAATT	TTTACCGAGC
ACAGGAGAAA	AGAAATCGAT	CGCGCTTGTC	ATTATTGGTC	TTCTAGTTAT	CGCCAGTGGG
TGTCCTTTAG	TTTTTCGTAA	AAGTAAATCG	AAGAAGTAA		

EF088-2 (SEQ ID NO:334)

LVGLANWFRA	ALDRTLILLH	DDLNTDAEK	LNKFTAPLML	YAKDPNIQWP	IYRATGANLT
DISITVLGTG	LLLEDNQRLV	QVQEAVPSVL	KSVSSGDGLY	PDGSLIQHGY	FPYNGSYGNE
LLKGFGRIFT	ILQGSWEMN	DPNISNLFNV	VDKGYLQLMV	NGKMPSMVSG	RSISRAPETN
PFTTEFESGK	ETIANLTLIA	KFAPENLRND	IYTSIQTWLQ	QSGSYHHFFK	KPRDFEALID
LKNVNSASP	AQATPMQSLN	VYGSMRVLQ	KNNEYAVGIS	MYSQVRVGNYE	FGNTENKKGW
HTADGMLYLY	NQDFAQFDEG	YWATIDPYRL	PGTTVDREL	ANGAYTGKRS	PQSWVGGSNN
GQVASIGMFL	DKSNEGMLNV	AKKSWFLLDG	QIINLGSGIT	GTTDASIETI	LDNRMIHPQE
VKLNQGSDDK	NSWISLSAAX	PLNNIGYVFP	NSMNTLDVQI	EERSGRYGDI	NEYFVNDKTY

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TNTFAKISK N YGKTVENGTY EYLTVVGKTN EEIAALSKNK GYTVLENTAN LQAIEAGNYV
 MMNTWNNDQE IAGLYAYDPM SVISEKIDNG VYRLTLANPL QNNASVSIEF DKGILEVVAA
 DPEISVDQNI ITLNSAGLNG SSRSIIVKTT PEVTKEALEK LIQEKEHQE KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVKVP TKEVDKTNLL KIIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSAVKRLTLK NSGENKKEQK
 NGGNNHGLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKKSIALVI IGLLVIASGC
 LLVFRKSKSK K

EF088-3 (SEQ ID NO:335)

A ACTCCTGAAG TAACGAAAGA AGCGTTAGAA
 AAATTAATTC AGGAACAAAA AGAACACCAA GAAAAAGACT ACACCGCAAG CAGCTGGAAA
 GTCTACAGCG AAGCATTGAA ACAAGCACAA ACTGTGGCAG ATCAAACAAC AGCAACGCAA
 GCAGAAAGTAG ACCAAGCAGA AACAGAGTTA CGTTCGGCAG TGAAGCAATT GGTAAGAGTG
 CCAACTAAAAG AAGTAGATAA AACCACCTTG TTGAAAATCA TCAAAGAAAA CGAGAAACAC
 CAAGAAAAAAG ACTACACCGC AAGCAGTTGG AAAGTCTACA GTGAAGCATT GAAGCAAGCG
 CAAACTGTGG CAGATCAAAC AACAGCAACG CAAGCAGAAG TAGACCAAGC AGAAGCAAAA
 CTACGTTCCG CAGTGAAGCG ATTAACATTG AAAAAATAGTG GGGAAAATAA AAAGGAGCAA
 AAAAAATGGGG GGAATAATGG AACTTTAAAT ACTAGTACAG GAGTTGATCA AACTGCTACG
 AAACAAGTTA AGCCATCAAG CCAAGGTGGT TTCAGAAAAA CTAGCCAATT TTTACCGAGC
 ACAGGAGAAA AGAAA

EF088-4 (SEQ ID NO:336)

T PEVTKEALEK LIQEKEHQE KDYTASSWKV
 YSEALKQAQT VADQTTATQA EVDQAETELR SAVKQLVKVP TKEVDKTNLL KIIKENEKHQ
 EKDYTASSWK VYSEALKQAQ TVADQTTATQ AEVDQAEAKL RSAVKRLTLK NSGENKKEQK
 NGGNNHGLNT STGVDQTGTK QVKPSSQGGF RKASQFLPST GEKK

EF089-1 (SEQ ID NO:337)

TGACAGATAC ACCTGCTAAC ACAGGAAACT AAGAACGACA GCATACACGC AAGATCGGGA
 TATAGGTCAA AAATTTTTTG GCTTATCTTT CCGTCTTTTG GTGCTTATAA TACAACAAAG
 AATGACAGAC ATAGGAGAAT GAATATGAAC AGATGGAAAG TATATGCAAC GGTAATCGCT
 TGTATGTTAT TTGGCTGGAT TGGCGTGGAG GCGCACGCTT CTGAATTTAA TTTTGC GGTC
 ACACCAACAA TTCCCGAAAA TCAAGTGGAT AAATCAAAAA CCTACTTTGA CTTAAAAATG
 GCGCCTGGTG CCAAACAAAC CGTAGAAAT CAGTTACGCA ATGATACAGA TGAAGACATT
 ACCATTGAAA ATACGGTGAA CTCAGCGACA ACAAATTTAA ATGGCGTAGT AGAATATGGC
 CAAAACGGGA TCAAACCTGA CAAAACCTTA CGTTTTAACT TAAAAGATTA TGTGGAAGCA
 CCGAAAGAAA TCATCTTGCC GAAGCATTCC CAAAAGACCT TACCTTTAAC CATTACGATG
 CCTAAAGATT CTTTTGATGG CGTGATGGCT GCGCGTATAA CACTCAAAGA GAAAAAGAAA
 GAAACAACGA CTTCTGCGGA TCAATCAAAA GGGTTAGCTA TTAATAATGA ATACTCCTAT
 GTTGTGGCTA TTATTCTTCA GCAAAATGAG ACAAAGGTTT AACCAGATTT AAAATTACTG
 GGGGTTAAAC CAGGCCAAGT CAACGCGCGA AACGTCATCA ATGTTTCTTT ACAAACCCA
 CAAGCGGCCCT ATTTAAACCA ATTACATTTA ATCAACACTG TTTCAAAGG AGGCGAAACG
 CTTTACCAAT CCGATACTGA GGATATGCAA GTGGCGCCAA ACTCTAACTT TAGTTACCCA
 ATTTCTTTAA AAGGGGAACG ATTAACGCCA GGAAAATATG TCTTGAAATC AACGGCCTAT
 GGTGTAAAAG ATGAAAAGGG CACCTATCAA GTCAAAGGCG CCAATGGTGA AGAACGGTAC
 CTGTACAAAT GGAATTTTAC AAAAGAATTT ACTATTTCTG GGGACGTCGC TAAAGAATTA
 AATGAAAAAG ACGTAACCAT TAAAGGAACC AATTGGTGGT TGTATCTACT GATTGCATTA
 ATCATCTAG CGCTGCTCTT ATTGATTTTC TTCTTGATATC GTAAAAAGAA AAAAGAGGAA
 GAACAACAAT CTGAGCAATA A

EF089-2 (SEQ ID NO:338)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

MNR WKVYATVIAC

MLFGWIGVEA HASEFNFAVT PTIPENQVDK SKTYFDLKMA PGAKQTVEIQ LRNDTDEDIT
 IENTVNSATT NLNGVVEYGQ NGIKPDKTLR FNLKDYVEAP KEIILPKHSQ KTLPLTITMP
 KDSFDGVMAG GITLKEKKKE TTTSADQSKG LAINNEYSYV VAIILQQNET KVQPDLLKLG
 VKPGQVNARN VINVSLQNPQ AAYLNQLHLI NTVSKGGETL YQSDTEDMQV APNSNFSYPI
 SLKGERLTPG KYVLKSTAYG VKDEKGTQV KGANGEERYL YKWEFTKEFT ISGDVAKELN
 EKDVTIKGTN WWLYLLIALI ILALLLLIFF LYRKKKKEEE QQSEQ

EF089-3 (SEQ ID NO:339)

T CTGAATTTAA TTTTGCGGTC

ACACCAACAA TTCCCGAAAA TCAAGTGGAT AAATCAAAAA CCTACTTTGA CTTAAAAATG
 GCGCCTGGTG CCAAACAAAC CGTAGAAATT CAGTTACGCA ATGATACAGA TGAAGACATT
 ACCATTGAAA ATACGGTGAA CTCAGCGACA ACAAATTTAA ATGGCGTAGT AGAATATGGC
 CAAAACGGGA TCAAACCTGA CAAAACCTTA CGTTTTAACT TAAAAGATTA TGTGGAAGCA
 CCGAAAGAAA TCATCTTGCC GAAGCATTCC CAAAAGACCT TACCTTTAAC CATTACGATG
 CCTAAAGATT CTTTTGATGG CGTGATGGCT GGCGGTATAA CACTCAAAGA GAAAAAGAAA
 GAAACAACGA CTTCTGCGGA TCAATCAAAA GGGTTAGCTA TTAATAATGA ATACTCCTAT
 GTTGTGGCTA TTATTCTTCA GCAAAATGAG ACAAAGGTTT AACCAGATTT AAAATTACTG
 GGGGTTAAAC CAGGCCAAGT CAACGCGCGA AACGTCATCA ATGTTTCTTT ACAAACCCA
 CAAGCGGCCT ATTTAAACCA ATTACATTTA ATCAACACTG TTTCAAAGG AGGCGAAACG
 CTTTACCAAT CCGATACTGA GGATATGCAA GTGGCGCAA ACTCTAACTT TAGTTACCCA
 ATTTCTTTAA AAGGGGAACG AT

EF089-4 (SEQ ID NO:340)

SEFNFAVT PTIPENQVDK SKTYFDLKMA PGAKQTVEIQ LRNDTDEDIT

IENTVNSATT NLNGVVEYGQ NGIKPDKTLR FNLKDYVEAP KEIILPKHSQ KTLPLTITMP
 KDSFDGVMAG GITLKEKKKE TTTSADQSKG LAINNEYSYV VAIILQQNET KVQPDLLKLG
 VKPGQVNARN VINVSLQNPQ AAYLNQLHLI NTVSKGGETL YQSDTEDMQV APNSNFSYPI
 SLKGER

EF090-1 (SEQ ID NO:341)

TAGTCTCTAA GAAATAAACC TAAATTATT GATATAAAGG ATGAACAAAT GAAAAAGAA
 GAAATGCAAA TGCGTAATAC ACGTCGTCAA AAATCAGGAA AAAATAATAA AAAGAAAGTA
 ATTATTACTT CTTTGGTTGG ACTAGCTCTG GTTGCTGGGG GCAGTTATGT TTATTTTCAA
 AGTCACTTTT TNCCAACCAC AAAAGTAAAT GGAGTTTCTG TAGGCTGGTT AAATGTAAAT
 GCTGCAGAAG AAAAATTAGC GCAAGTTAAT CAAACCGAAG AAGTTGTGGT TCAAACGGGG
 ACAAAGAAG AAAAAATTCA ACTTCCTAAA AAATACCAAT TGGATCAAAA ATTTTAAAA
 GACCATTAC ACAGTAGCAA GGTGAAGCTA CCGTTAAACG AGGCATTCAA AAAAGAACTA
 GAAGCCAAAT TAGCAACTTT GAGTTTTCCA GAGGGGAAAC CAAGCAAAA TGCGAGTATC
 CGTCGAGGCA ATGGCACTTT TGAAATTGTT CCCGAAGAAC AAGGCACAGT AGTGGACACA
 CAGCGCTTAA ACCAGCAGAT TATTGCGGAT GTTGAAGCGG GAAAAGGCAA CTATCAATAT
 AATGCCAAAG ATTTTATAA AGCCCCTGAA ATTACAAAAG AGGATCAAAC GTTAAAGGCA
 ACATTGACAA CGCTCAATAA CAAGTTAAAT AAAACAATTA CAGTTGATAT TAATGGTGAA
 AAAGTAGCCT TTGATAAAAC ACAAATTCAA AACGTGCTGA ATGATGATGG CACAATCAAC
 AAAGAAAAAC TAACTACTTG GGTGACACAA TTAGAAACAA CATATGGTTC TGCTAATCAA
 CCAGTTTTAT TTACAGATGT TCACGGCACG ACACGTCGTT TAAAAACAA CGGAAGTTAT
 GGCTGGTCTGA TTGATGGGGC CAAAACGCAA GAACTACTAG TAAACGCGCT GAATAGCCAA
 GAACAAACGA ATGCAATCAC TGCTCCGTTG GTTGGTGATA CCAAAGAAAA TAGTAAATTT
 GCCAATAATT ACATTGAAAT TGATTTAAAA GATCAAAAAA TGTATTGTTT CATTGATGGC
 AAAAAAATAG TCACCACAGA TGTCATTACT GGCAGATATA ACAAAGGAAC CGCAACAGTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGGATTCC ATACAATTTT ATATCGGACA ACCGATGTGA ATTTAGAAGG TCAAATGCTT
 GATGGTTCTC GATACAGTGT GCCAGTAAAA TATTGGATGC CGTTATTAAG TCAAGGGGGC
 GTTGTCACAC AAATCGGGAT TCATGACTCC GACCATAAAT TGGATAAGTA TGGCGATAAA
 GAAGCCTTTA AAACCGATGC TGGTAGTAAT GGCTGTATCA ATACGCCAGG AACAGAAGTT
 TCAAAAATCT TTGATGTATC CTATGACGGA ATGCCGGTAA TTATTTATGG ACATATCTAT
 GATGATGCAC CAGGTGAATT TGATAAACCT GTAGATTACG GCGAAGAAGT ATAA

EF090-2 (SEQ ID NO:342)

MRNTRRQK SGKNNKKKVI ITS LVGLALV AGGSYVYFQS
 HFXPTTKVNG VSVGWLVNVA AEEKLAQVNO TEEVVVQTGT KEEKIQLPKK YQLDQKFLKD
 HLHSSKVKLP LNEAFKKELE AKLATLSFPE GKPSKNASIR RGNGTFEIVP EEQGTVVDTQ
 RLNQIIADV EAGKGNQYN AKDFYKAPEI TKEDQTLKAT LTTLNNKLNK TITVDINGEK
 VAFDKTQIQN VLNDGDTINK EKLTTWVTQL ETTYGSANQP VLFTDVHGTT RRFKNNGSYG
 WSIDGAKTQE LLVNALNSQE QTNAITAPLV GDTKENSIA NNYIEIDLKD QKMYCFIDGK
 KIVTTDVITG RYNKGTATVP GFHTILYRTT DVNLEGQMLD GSRYSVPVKY WMPLLSQGGV
 VTQIGIHSD HKLDKYGDKE AFKTDAGSNG CINTPGTEVS KIFDVSYDGM PVIIYGHYD
 DAPGEFDKPV DYGEV

EF090-3 (SEQ ID NO:343)

CAC AAAAGTAAAT GGAGTTTCTG TAGGCTGGTT AAATGTAAAT
 GCTGCAGAAG AAAAATTAGC GCAAGTTAAT CAAACCGAAG AAGTTGTGGT TCAAACGGGG
 ACAAAGAAG AAAAAATTCA ACTTCCTAAA AAATACCAAT TGGATCAAAA ATTTTAAAAA
 GACCATTTAC ACAGTAGCAA GGTGAAGCTA CCGTTAAACG AGGCATTCAA AAAAGAACTA
 GAAGCCAAAT TAGCAACTTT GAGTTTTCCTA GAGGGGAAAC CAAGCAAAAA TGCGAGTATC
 CGTCGAGGCA ATGGCACTTT TGAAATTGTT CCCGAAGAAC AAGGCACAGT AGTGGACACA
 CAGCGCTTAA ACCAGCAGAT TATTGCGGAT GTTGAAGCGG GAAAAGGCAA CTATCAATAT
 AATGCCAAAG ATTTTATATA AGCCCCTGAA ATTACAAAAG AGGATCAAAC GTTAAAGGCA
 ACATTGACAA CGCTCAATAA CAAGTTAAAT AAAACAATTA CAGTTGATAT TAATGGTGAA
 AAAGTAGCCT TTGATAAAAC ACAAATTCOA AACGTGCTGA ATGATGATGG CACAATCAAC
 AAAGAAAAAC TAACTACTTG GGTGACACAA TTAGAAACAA CATATGGTTC TGCTAATCAA
 CCAGTTTAT TTACAGATGT TCACGGCAGC ACACGTCGTT TTA AAAACAA CGGAAGTTAT
 GGCTGGTCGA TTGATGGGGC CAAAACGCAA GAACACTAG TAAACGCGCT TAAGTAAAT
 GAACAAACGA ATGCAATCAC TGCTCCGTTG GTTGGTGATA CCAAAGAAAA TAGTAAAT
 GCCAATAATT ACATTGAAAT TGATTTAAAA GATCAAAAAA TGTATTGTTT CATTGATGGC
 AAAAAAATAG TCACCACAGA TGTCATTACT GGCAGATATA ACAAAGGAAC CGCAACAGTA
 CCAGGATTCC ATACAATTTT ATATCGGACA ACCGATGTGA ATTTAGAAGG TCAAATGCTT
 GATGGTTCTC GATACAGTGT GCCAGTAAAA TATTGGATGC CGTTATTAAG TCAAGGGGGC
 GTTGTCACAC AAATCGGGAT TCATGACTCC GACCATAAAT TGGATAAGTA TGGCGATAAA
 GAAGCCTTTA AAACCGATGC TGGTAGTAAT GGCTGTATCA ATACGCCAGG AACAGAAGTT
 TCAAAAATCT TTGATGTATC CTATGACGGA ATGCCGGTAA TTATTTATGG ACATATCTAT
 GATGATGCAC CAGGTGAATT TGATAAACCT GTAGATTACG GCGAAGAAGT AT

EF090-4 (SEQ ID NO:344)

TKVNG VSVGWLVNVA AEEKLAQVNO TEEVVVQTGT KEEKIQLPKK YQLDQKFLKD
 HLHSSKVKLP LNEAFKKELE AKLATLSFPE GKPSKNASIR RGNGTFEIVP EEQGTVVDTQ
 RLNQIIADV EAGKGNQYN AKDFYKAPEI TKEDQTLKAT LTTLNNKLNK TITVDINGEK
 VAFDKTQIQN VLNDGDTINK EKLTTWVTQL ETTYGSANQP VLFTDVHGTT RRFKNNGSYG
 WSIDGAKTQE LLVNALNSQE QTNAITAPLV GDTKENSIA NNYIEIDLKD QKMYCFIDGK
 KIVTTDVITG RYNKGTATVP GFHTILYRTT DVNLEGQMLD GSRYSVPVKY WMPLLSQGGV
 VTQIGIHSD HKLDKYGDKE AFKTDAGSNG CINTPGTEVS KIFDVSYDGM PVIIYGHYD

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

DAPGEFDKPV DYGEV

EF091-1 (SEQ ID NO:345)

TAATTGGNGG AGATTTTAT GGCTAAAAA GGCGGATTTT TCTTAGGNGC AGTAATTGGT
 GGAACAGCAG CAGCCGTTGC CGCATTATTA CTTGCACCAA AATCAGGTAA AGAATTACGT
 GATGATTTAT CAAATCAAAC AGATGATTTA AAAACAAAG CGCAAGATTA CACAGATTAT
 GCTGTTCAAA AAGGAACAGA ATTAACAGAA ATCGCAAAAC AAAAAGCCGG CGTTTTATCA
 GATCAAGCCT CTGATTTGGC AGGTTCTGTC AAAGAAAAA CAAAAGATTC ATTGGATAAA
 GCACAAGGTG TTTCTGGCGA CATGCTTGAT AACTTTAAAA AACAAACAGG TGATTTATCT
 GATCAATTTA AAAAAGCAGC TGACGATGCT CAAGATCACG CAGAAGATTT AGGTGAAATT
 GCCGAAGATG CAGCAGAAGA TATCTATATT GACGTTAAAG ATTCTGCGGC AGCGGCCAAA
 GAAACTGTTT CTGCTGGTGT CGATGAAGCA ANAGAAACCA CCAAAGATGT TCCTGAAAAA
 GCTGCAGAAG CAAAAGAAGA TGTTAAAGAT GCAGCGAAAG ACGTAAAAA AGAATTTAA
 GGTAA

EF091-2 (SEQ ID NO:346)

MAKKG GFFLGAVIGG TAAVAALLL APKSGKELRD DLSNQTDDLK NKAQDYTDYA
 VQKGTTELTEI AKQKAGVLSQ QASDLAGSVK ETKDSDLKA QGVSGDMLDN FKKQTGDLSD
 QFKKAADDAQ DHAEDLGEIA EDAAEDIYID VKDSAAAAKE TVSAGVDEAX ETTKDVPEKA
 AEAKEDVKDA AKDVKEFKG

EF091-3 (SEQ ID NO:347)

AT CAAATCAAAC AGATGATTTA AAAACAAAG CGCAAGATTA CACAGATTAT
 GCTGTTCAAA AAGGAACAGA ATTAACAGAA ATCGCAAAAC AAAAAGCCGG CGTTTTATCA
 GATCAAGCCT CTGATTTGGC AGGTTCTGTC AAAGAAAAA CAAAAGATTC ATTGGATAAA
 GCACAAGGTG TTTCTGGCGA CATGCTTGAT AACTTTAAAA AACAAACAGG TGATTTATCT
 GATCAATTTA AAAAAGCAGC TGACGATGCT CAAGATCACG CAGAAGATTT AGGTGAAATT
 GCCGAAGATG CAGCAGAAGA TATCTATATT GACGTTAAAG ATTCTGCGGC AGCGGCCAAA
 GAAACTGTTT CTGCTGGTGT CGATGAAGCA ANAGAAACCA CCAAAGATGT TCCTGAAAAA
 GCTGCAGAAG CAAAAGAAGA TGTTAAAGAT GCAGCGAAAG ACGTAAAAA AGAATTTAA
 GGTAA

EF091-4 (SEQ ID NO:348)

SNQTDDLK NKAQDYTDYA
 VQKGTTELTEI AKQKAGVLSQ QASDLAGSVK ETKDSDLKA QGVSGDMLDN FKKQTGDLSD
 QFKKAADDAQ DHAEDLGEIA EDAAEDIYID VKDSAAAAKE TVSAGVDEAX ETTKDVPEKA
 AEAKEDVKDA AKDVKEFKG

EF092-1 (SEQ ID NO:349)

TAAGGGGATG AAGAAAAAAT GGCAAAAAA ACAATTATGT TAGTTTGTTT CGCAGGAATG
 AGCACGAGTT TATTAGTAAC AAAAATGCAA AAAGCAGCAG AAGATCGTGG CATGGAAGCA
 GACATCTTTG CAGTATCGGC TTCTGAAGCA GATACAACT TGGAAAATAA AGAGGTGAAT
 GTTTTACTTT TAGGTCCACA AGTTCGTTT ATGAAAGGGC AATTGGAACA AAAATTACAA
 CCAAAGGGA TTCCTTTAGA TGTAATTAAC ATGGCAGATT ATGGCATGAT GAATGGCGAA
 AAAGTTTTAG ATCAAGCAAT CTCATTAATG GGATAA

EF092-2 (SEQ ID NO:350)

MAKKT IMLVCSAGMS TSLLVTKMQK AAEDRGMEAD IFVSAASEAD TNLENKEVNV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LLLGPQVRFM KGQFEQKLQP KGIPLDVINM ADYGMMNGEK VLDQAISLMG

EF092-3 (SEQ ID NO:351)

AG AAGATCGTGG CATGGAAGCA

GACATCTTTG CAGTATCGGC TTCTGAAGCA GATACAACT TGGAAAATAA AGAGGTGAAT
GTTTTACTTT TAGGTCCACA AGTTCGTTTC ATGAAAGGCG AATTTGAACA AAAATTACAA
CCAAAAGGGA TTCTTTTAGA TGTAATTAAC ATGGCAGATT ATGGCATGAT GAATGGCGAA
AAAGTTTTAG ATCAAGCAAT CTCATTAATG GGAT

EF092-4 (SEQ ID NO:352)

EDRGMEAD IFAVSASEAD TNLENKEVNV

LLLGPQVRFM KGQFEQKLQP KGIPLDVINM ADYGMMNGEK VLDQAISLMG

EF093-1 (SEQ ID NO:353)

TAGTTTTTTT CCGATAAAGG GAGAATTTTA ATGAGGCAAA AATATTCAGG AAAC TTATTG
TTCACGGCCA TGGCCATTGT TTATTTGATG AGTTTTCTCG CCCTTCAGTT ACTAGAAGAA
CGTCAGTTAA CACAAAAATT TACGCAAGCT ACCCAGGAAT ACTATGCAGG GAAAAGTATC
TTTCATTTAT TTCTTGCAGA TGTTAAACAA AATAGACGAA AGTTAAAAAC AGAAGAAAGG
CTCGTATACG CGCAAGTGAC CCTCGATTAT ACATACAAAA ATGAACAATT AAGAATAACT
GTTTTATTAA ACAAATCTGG TCGAAAATAC CAATATCAAG AGAGAGTTTC TCATCAAAAA
AAAGCGGAAA CAATACTGGA ATAG

EF093-2 (SEQ ID NO:354)

M RQKYSGNLLF TAMAIVYLMs FLALQLLEER QLTQKFTQAT QEYYAGKSIF
HLFLADVQN RRLKTEERL VYAQVTLDT YKNEQLRITV LLNKSGRKYQ YQERVSHQKK
AETILE

EF093-3 (SEQ ID NO:355)

CCTTCAGTT ACTAGAAGAA

CGTCAGTTAA CACAAAAATT TACGCAAGCT ACCCAGGAAT ACTATGCAGG GAAAAGTATC
TTTCATTTAT TTCTTGCAGA TGTTAAACAA AATAGACGAA AGTTAAAAAC AGAAGAAAGG
CTCGTATACG CGCAAGTGAC CCTCGATTAT ACATACAAAA ATGAACAATT AAGAATAACT
GTTTTATTAA ACAAATCTGG TCGAAAATAC CAATATCAAG AGAGAGTTTC TCATCAAAAA
AAAGCGGAAA CAATACTGG

EF093-4 (SEQ ID NO:356)

LQLLEER QLTQKFTQAT QEYYAGKSIF

HLFLADVQN RRLKTEERL VYAQVTLDT YKNEQLRITV LLNKSGRKYQ YQERVSHQKK
AETI

EF094-1 (SEQ ID NO:357)

TAAACATTTG AGACATTCAG AGGTGAATGT CTCTTTTTTA TTA CTCAAAA ACGAAAGGGG
ATTAATTATA TGAACAAAAC AACATTTAAA AATTGGTCGT TATTTGCGAC TTTGGCTCTA
TTAAGTCAAA CAATTGGCGG AACGATTGGT CCTACGATTG CTTTGGCCGA TGAAATTACT
CACCCTCAAG AGGTAACAAT TCATTATGAC GTAAGTAAAC TGTATGAAGT TGACGGAAC
TTTAGCGATG GCAGCACGCT CTCAGAACGT ACTACGTCAT TATATGCAGA ATACAATGGT
GCAAAACAAA CAGTATTTTG TATTGAACCA GGTGTTAGTA TTCCAACAGA AGTGACGCAC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

GGTTATCAGA AAAACCCCTTT GCCATCAATG TCTGATAAAG CGAAACTAGT ATCGGTTCTT
TGGGAAAAGG CTGGAACAGA TATTGATACA AATATGGTTG CACAAAAGAT GATTGGGGAA
GAAGTGAACG GTTATAAACT CCATTCCATA AAAAGATTAG GTGGTGCTTC AGTTGATATA
AAATCTATTG AAGGAAAAAT TAATAAGGCA ATTGAGGAGT ATCAAAAAAA ACCAAGTTTT
CATAATACCA CTGTAAAAAC AATTTTAGGT CAATCGACAA CTTTAATAGA TAAAAATGAA
TTAAATTTAT CTGAGTTTGA TAAAGTCGTC CAAAATACGG CGAATATAGA TTACCGTGTA
ATTGGGAATC AATTAGTGCT TACTCCAAAC TCTAATTCCA AATCAGGAAC ATTAACATTG
AAAAAATCAG CTGGTACTGG AACTCCAGTC GCTTATAAAA AAGCAGGACT TCAAACGTG
ATGGCTGGTG CGCTTGATAA GCCCAATACC TACGCTATTA AAATTAATGT GGAAACTAAG
GGTTCTTTAA AGATCAAAAA AATCGATAAA GAATCAGGTG ATATTGTACC AGAAACGGTT
TTCCATTTAG ATTTTGGGAA AGCTTTACCT TCAAAAGATG TGACAACAGA TAAAGATGGG
ATTTCTATTT TGGATGGAAT TCCCCATGGT ACAAAGGTAA CTATTACTGA AAAATCGGTG
CCAGATCCTT ATATGATTGA TACCACACCC ATGGCTGCCA CCATTAAAGC GGGCGAGACC
ATTTCCATGA CTTCGAAAAA TATGCGACAA AAAGGTCAAA TTCTTTTAGA GAAGACTGGG
GTAGAAACAG GTACTGATCT TTGGAATGAC AATTATTCTC TAGCTGGAAG TACATTGCCC
ATTCGTAAAG ACAGCCCAGC TGGTGAAATG GTCCAAGAAA TAACAACGGA TGAAAAAGGT
CGTGCGGAAA CACCAAAAGA GCTTGCTAAT GCTTTGGAAC TGGGAACCTA TTACGTGACA
GAAACTAAAT CTAGTAATGG TTTCGTGAAT ACCTTCAAAC CAACAAAAGT CGAGTTAAAA
TATGCCAATC AAACCGTGGC TCTTGTTACC AGTAACGTAA AAGGGCAAAA CCAAGAAATT
ACTGGGGAAA CCACTTTGAC AAAAGAAGAC AAAGATACCG GTAATGAGAG TCAAGGGAAA
GCTGAGTTTA AAGGAGCTGA ATATACTCTC TTTACTGCAA AAGATGGTCA AGCTGTTAAA
TGGAGTGAAG CTTTTTAAAC AGAATTAGTG AAGGGAACGA AAGCTTCTGA TGAAACAGTG
ACTTTGGCTT TAGATGAAAA GAACCAAGTT GCCGTAAAC ACCTAGCAAT TAACGAGTAT
TTCTGGCAAG AAACCAAAGC ACCTGAAGGA TATACTTTGG ATGAAACGAA GTATCCTGTA
TCCATCAAAA AAGTTGATAA TAACGAAAAA AATGCCGTAA TTACTIONG TGTACGGCA
AAAGAACAAG TTATTCGCTT TGGCTTTGAT TTCTTTAAAT TTGCTGGATC GGCTGATGGC
ACTGCCGAAA CTGGATTTAA CGACTTATCT TTAAAGTGT CGCCATTGGA AGGGACCAAN
GAAATCACAG GTGCTGAAGA TAAAGCGACC ACAGCTTGTA ACGAGCAATT AGGTTTGTGAT
GGCTATGGTA AGTTTGAAAA TCTTCTTAT GGGGATTATT TACTTGAAGA AATAGAGGCT
CCAGAGGAT TTCAAAAGAT TACACCTA GAAATCCGTT CTACATTTAA GGAAACAAA
GACGACTATG CGAAGAGTGA GTATGCTTTT ACCATTACCG AAGAAGGACA AAAACAACCA
ATTAAGATGG TGACCGTTCC TTACGAGAAA CTAACATAA ACGAGTTTTT TGTAGTCTG
AACCGTTTGA TGCTTTATGA TTTGCCCGAG AAAGAAGATA GTTTGACTTC TCTGCGACT
TGGAAAGACG GAAATAAAAA ATTGAATACC CTTGATTTTA CCGAGCTAGT TGATAAATTG
AGATATAACT TGCATGAAAT CAAAGAAGAC TGGTATGTCG TAGCTCAAGC CATTGATGTG
GAAGCCACAA AAGCTGCCCA AGAAAAAGAC GAAAAAGCCA AACCGGTGGT GATTGCCGAA
ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ACTGGAACCT GGAAAATTCT GCATAAATTA
ACCGCTGAAC AAGTTTTTGA TAAAAGCATC GTCTTGTTCA ATTATGTGTA TGAAAACAAG
GTAGCCTTTG AAGCAGGCAA TGAGCCAGTA GCGAAGGATG CTAGCTTGAA CAATCAAGCA
CAAACCGTCA ATTGTACGAT TGAACGCCAT GTTTCCATCC AAACAAAAGC CCACCTAGAA
GATGGTTCGC AAACTTTTAC TCATGGTGAC GTGATGGATA TGTTTGATGA TGTGTCGGTT
ACCATGATG TACTGGATGG CTCAAAGAA GCTTTCGAAA CAATTCTGTA TGCTTTACTA
CCAGATGGTA CGAACAAAGA AATTTGGAAA TCTGGCAAAA TTGAGCATGA AGTGAATGAT
AAAGAATTTA CCAAAACCGT ACTTGCGGAA AAAGTAGATA CCGGAAAGTA TCCAGAAGGA
ACTAAGTTTA CTTTTACGGA AATCAATTAC GAAAAAGATG GAAACGTGAA TGGAAAACAC
AATGAAGATT TGAAAGAAAA ATCTCAAACC TTAACACCAA AAGAAGTGCC AACCATACCG
AGTACGCCAA AACAACCGGA AACACCAGCT GTTCCAAGTA ATTCTCAAGA ATCTAGTCCC
ACAGTGAAGA CATTCACCGA AACTGGGGAG AAAAAATTCCA ACGTTCTACT GTTAGTTGGC
TTTATCTTGA TTTTTTCGAC TGCTGGGTAT TATTTCTGGA ATCGCCGCAA TTAA

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EF094-2 (SEQ ID NO:358)

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MKKTTFKN WSLFATLALL SQTIGGTIGP TIAFADEITH
PQEVTIHYDV SKLYEVDGTF SDGSTLSERT TSLYAEYNGA KQTVFCIEPG VSIPTEVTHG

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YQKNPLPSMS	DKAKLVSVLW	EKAGTDIDTN	MVAQKMIWEE	VNGYKLHSIK	RLGGASVDIK
SIEGKINKAI	EEYQKKPSFH	NTTVKTIILGQ	STTLIDKNEL	NLSEFDKVVQ	NTANIDYRVI
GNQLVLTPNS	NSKSGTLTLK	KSAGTGTPVA	YKKAGLQTVM	AGALDKPNTY	AIKINVETKG
SLKIKKIDKE	SGDIVPETVF	HLDFGKALPS	KDVTTDKDIG	SILDGIPHGT	KVTITEKSVP
DPYIMDTTPM	AATIKAGETI	SMTSKNMRQK	GQILLEKTGV	ETGTDLWNDN	YSLAGNTFAI
RKDSPAGEIV	QEITTDEKGR	AETPKELANA	LELGTYVTE	TKSSNGFVNT	FKPTKVELKY
ANQTVALLTS	NVKGQNQEIT	GETTLTKEDK	DTGNESQGKA	EFKGAEYTLF	TAKDGGQAVKW
SEAFKTELVK	GTKASDETVT	LALDEKNQVA	VKHLAINEYF	WQETKAPEGY	TLDETKYPVS
IKKVDNNEKN	AVITRDVTAK	EQVIRFGFDF	FKFAGSADGT	AETGFNDLSF	KVSPLEGTXE
ITGAEDKATT	ACNEQLGFDG	YGKFENLPYG	DYLLEEIEAP	EGFQKITPLE	IRSTFKENKD
DYAKSEYVFT	ITEEGQKQPI	KMVTVPYEKL	TNNEFSVSLN	RLMLYDLPEK	EDSLTSLATW
KDGNKKLNTL	DFTLVKDLR	YNLHEIKEDW	YVVAQAIDVE	ATKAAQEKDE	KAKPVVIAET
TATLANKEKT	GTWKILHKLT	AEQVLDSIV	LFNVVYENKV	AFEAGNEPVA	KDASLNNQAQ
TVNCTIERHV	SIQTKAHLED	GSQTFTHGDV	MDMFDDVSVT	HDVLDGSKEA	FETILYALLP
DGTNKEIWKS	GKIEHEVNDK	EFTKTVLAEK	VDTGKYPEGT	KFTFTEINYE	KDGNVNGKHN
EDLKEKSQTL	TPKEVPTIPS	TPKQPETPAV	PSNSQESSPT	VKTFPQTGEK	NSNVLLLVGF
ILIFSTAGYY	FWNRRN				

EF094-3 (SEQ ID NO:359)

CGA TGAAATTACT

CACCCCTCAAG	AGGTAACAAT	TCATTATGAC	GTAAGTAAAC	TGTATGAAGT	TGACGGAAGT
TTTAGCGATG	GCAGCACGCT	CTCAGAACGT	ACTACGTCAT	TATATGCAGA	ATACAATGGT
GCAAAACAAA	CAGTATTTTG	TATTGAACCA	GGTGTTAGTA	TTCCAACAGA	AGTGACGCAC
GGTTATCAGA	AAAACCCCTT	GCCATCAATG	TCTGATAAAG	CGAAACTAGT	ATCGGTTCTT
TGGGAAAAGG	CTGGAACAGA	TATTGATACA	AATATGGTTG	CACAAAAGAT	GATTTGGGAA
GAAGTGAACG	GTTATAAACT	CCATTCCATA	AAAAGATTAG	GTGGTGCTTC	AGTTGATATA
AAATCTATTG	AAGGAAAAAT	TAATAAGGCA	ATTGAGGAGT	ATCAAAAAAA	ACCAAGTTTT
CATAATACCA	CTGTAAAAAC	AATTTTAGGT	CAATCGACAA	CTTTAATAGA	TAAAAATGAA
TTAAATTTAT	CTGAGTTTGA	TAAAGTCGTC	CAAAATACGG	CGAATATAGA	TTACCGTGTA
ATTGGGAATC	AATTAGTGCT	TACTCCAAAC	TCTAATTCCA	AATCAGGAAC	ATTAACATTG
AAAAAATCAG	CTGGTACTGG	AACTCCAGTC	GCTTATAAAA	AAGCAGGACT	TCAAACGTGT
ATGGCTGGTG	CGCTTGATAA	GCCCAATACC	TACGCTATTA	AAATTAATGT	GGAAACTAAG
GGTTCCTTAA	AGATCAAAAA	AATCGATAAA	GAATCAGGTG	ATATTGTACC	AGAAACGGTT
TTCCATTTAG	ATTTTGGGAA	AGCTTTACCT	TCAAAAGATG	TGACAACAGA	TAAAGATGGG
ATTTCTATTT	TGGATGGAAT	TCCCCATGGT	ACAAAAGTAA	CTATTACTGA	AAAATCGGTG
CCAGATCCTT	ATATGATTGA	TACCACACCC	ATGGCTGCCA	CCATTAAAGC	GGGCGAGACC
ATTTCCATGA	CTTCGAAAAA	TATGCGACAA	AAAGGTCAAA	TTCTTTTAGA	GAAGACTGGG
GTAGAAACAG	GTAATGATCT	TTGGAATGAC	AATTATTCTC	TAGCTGGAAA	TACATTTGCC
ATTCGTAAAG	ACAGCCCAGC	TGGTGAAATT	GTCCAAGAAA	TAACAACGGA	TGAAAAAGGT
CGTGCGGAAA	CACCAAAAGA	GCTTGCTAAT	GCTTTGGAAC	TGGGAACCTA	TTACGTGACA
GAAACTAAAT	CTAGTAATGG	TTTCGTGAAT	ACCTTCAAAC	CAACAAAAGT	CGAGTTAAAA
TATGCCAATC	AAACCGTGGC	TCTTGTTACC	AGTAACGTAA	AAGGGCAAAA	CCAAGAAATT
ACTGGGGAAA	CCACTTTGAC	AAAAGAAGAC	AAAGATACCG	GTAATGAGAG	TCAAGGGAAA
GCTGAGTTTA	AAGGAGCTGA	ATATACTCTC	TTTACTGCAA	AAGATGGTCA	AGCTGTTAAA
TGGAGTGAAG	CTTTTAAAAAC	AGAATTAGTG	AAGGGAACGA	AAGCTTCTGA	TGAAACAG

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DEITH

PQEVTHYDV	SKLYEVDGTF	SDGSTLSERT	TSLYAEYNGA	KQTVFCIEPG	VSIPTEVTHG
YQKNPLPSMS	DKAKLVSVLW	EKAGTDIDTN	MVAQKMIWEE	VNGYKLHSIK	RLGGASVDIK
SIEGKINKAI	EEYQKKPSFH	NTTVKTIILGQ	STTLIDKNEL	NLSEFDKVVQ	NTANIDYRVI
GNQLVLTPNS	NSKSGTLTLK	KSAGTGTPVA	YKKAGLQTVM	AGALDKPNTY	AIKINVETKG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

SLKIKKIDKE SGDIVPETVF HLDFGKALPS KDVTDDKDI SILDGIPHGT KVTITEKSVP
 DPYIMDTTPM AATIKAGETI SMTSKNMRQK GQILLEKTGV ETGTDLWNDN YSLAGNTFAI
 RKDSPAGEIV QEITTTDEKGR AETPKELANA LELGTYVTE TKSSNGFVNT FKPTKVELKY
 ANQTVALVTS NVKGQNEIT GETTLTKEDK DTGNESQGA EFKGAEYTLF TAKDGQAVKW
 SEAFKTELVK GTKASDET

EF095-1 (SEQ ID NO:361)

TAAGAATTGT TGGATTGTTC TTTAGAAAGA AGGGACAATA TGAAGCGAAG TAAATGGAAA
 GAATTGATAG TAACGGGCAT CTGCCATATA TTAGTATTCC CCATACTAAT ACAGACAACCT
 GTTTTTGCAG AAACATTACC AAGTACAAAA CAAGTAAGAG AAGGAACCAA TCATTTCATTA
 ACAGCAGAAA AAGCCGAAAG TGAACAACCA CAGACAAAAGG ATAAACTACA TGATGAAGAA
 AACTGGCAT TGTCAAAAAG TGAGTTAATC GATAATGAGG CTAATGTTAC AAGTCAAACG
 ATTAGAGAAA GAATTGAGAC GCCTAACCTA ACTTATCGTT ATGGATTTAT TAATGAAGAG
 GGGCAGCCAG TAAACGCCAA TGAGATCCTT CTACAGTATC ATAGTTGGCA AGGCAATTCC
 CCAGATGGCA TAAATGTGTG GGAAGGTGAA AGTCAACCAG TGACAGCATC TACAGTGGCT
 AATTTAAAAG AAGTGGTAAT TCCAAGTGAG AAAGTAGCCG TCTATTCCGA CATGTCAACG
 GTGCTTGCAG CGAGTAATCA AACATTTTTT TTACCAAGAT ATTATACTTC TTTAAGCTTA
 TACAATAAGA AAGGGGAAAT TGATCCCAAT TATCCGCTGC CAACTATTTT CGACGCATCA
 GGAAACCAAT ATCCAACAAC AATTTTCGCAA TTTGAATTGG AAAAAATGTC TGCACAACAA
 TATAGTCAGA AAACAGGAGT AACGTTTAACT ATTAGCGAGA GTCAAAAACCT AATCGTTCCT
 TTGTACAACC AAGTGAAGGT TGATTTCATCG AATCAATCTG GGCTATTGAA TTACTTTTAAA
 TTTTCAGGGC CGGTTTATTA TCATGTTACC AATCGCAAAG TGACAGAACA TTTTGTGGAT
 ACTCAAGGGA AACCAATCCC TCCACCACCG GGGTTTAGAC AAGGAAAGCA AACACTTATT
 GAGCGTGACC CTTACACCTT TAAACAGAAA GATCTTTTGC CAAGTAGCTA TGAAATTGAC
 TCAAAAACGT ATCAATTTCA AGGATGGTAT AAAGGGAAAA CGAAACCTGA AAATTTAGAA
 AAAAGCGTAA CGCCAGTTA TGATATTACC TATGACGACA ATGATGATTT AACTGTTGTC
 TATAAGGAGA TACCTCAAAA AAATTATACA TTTGAGGATG TCAATGGTGT TGAAATTGCA
 CCACCATCTG ATTTTATTCA GGATCACCAA CAACCAATAA CTACGGATGG CTTTCGCTAT
 TTAGCTGGAA AAAAAGTACC ACAACAATAC AGCGTTAACG GTAAACTTA TTTATATCAA
 GGTGTTGATC AAGATAAAAC NAAACAAGAG AGCTTAGAAA AAACGAAGCG ACCCATAAAC
 TCCCTGTTTT TTAATGAAAT GAACGCTATT ACAGCAGTGT ATAAGGAAAT AACTGCAAAA
 GCTGAAATGC AAATAGAAGG ACTAGTCAAA GTCATGCCAA GTGGTTATAT ACAAATTTGG
 CAGATTATGC TTACAAATGT GGGAGAAGTA CCGTTAAAAA AAATAAACTT AAAGCCAGCA
 AGTGGTTGGT CACGAGGTCT AGCTCGGCCA ATCCAAGTCA CGATTTCGTGT TGGATCTGAA
 CCAAACAAAA TTGTTCTTAT TACTGATGAA AATTGGCGAG TTGGCATTAC TTTAAATACG
 GAAGTGCCTA TTGGTCAGAC AGCAACTATT ATGATGACAA CAATTGCTAC AGGTGAACCA
 GATCAAGTGT TACAAGCGGC TGTTGAAATG AATGGAAATT TTTCTGCTGT TCACGCAGCT
 GATACTGTCA GAATCCAACC TAAAAATCAA GAAATTGTGG CACCAGATGA GGAAGGTTTT
 ATCAGCACAC CAACTTTTGA TTTTGGCAAA GTCGCCATTT CTAGCAACAC GCAGCAACAT
 GGTTTAAAGC AGGCAGCAGA TTATTATGAA AATGGTCAGG AAAATCCATA TTTACGTTTG
 AAAAAATCAC AACCCAATTG GGCACAACT GCAGAACTAT CCCCCTTTGA AGGAAGAGTG
 GATCAACTAT CATCAATGAC AAAGTTATTG TTAGGAACAA CCAATGTTTC AGGTTTTATT
 CAGTACAATC AACCAACGGA AACTAAAGTT GCTCTTGGCA AAACAACCGC TATTCAATTA
 GTTGCCAACG GTGTAGCTAG CCATATTGTT GCCAATGGTC AGTTTGACGA AAGTGATGTT
 TATCAATTTG ATTTTCTTT TGATCAAATC AAATTAGAAA TTCCAGCAA TCAAGGTAGA
 AAAGATCAAA CTTATCAAGC AATGGTGACT TGAATTTAG TGACAGGCC ATAA

EF095-2 (SEQ ID NO:362)

MKRSKWKE LIVTGICHIL VFPILQTTV FAETLPSTKQ VREGTNHSLT
 AEKAESQPPQ TKDKLHDEET LALSKSELID NEANVTSQTI RERIETPNLT YRYGFINEEG
 QPVNANEILL QYHSWQGNP DGINWEGES QPVTASTVAN LKEVVIPSEK VAVYSMDSTV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

LAASNQTFFL	PRYYTSLSLY	NKKGEIDPNY	PLPTISDASG	NQYPTTISQF	ELEKMSAQOY
SQKTGVTFNI	SESQKLIVPL	YNQVKVDSSN	QSGLLNFKF	SGPVYHVTN	RKVTEHFVDT
QGKPIPPPPG	FRQKQTLIE	RDYTFKQKD	LLPSSYEIDS	KTYQFQGWYK	GKTKPENLEK
SVTPSYDITY	DDNDLTVVY	KEIPQKNYTF	EDVNGVEIAP	PSDFIQDHQQ	PITTDGFRYL
AGKKLPQQYS	VNGKTYLYQG	WYQDKTKQES	LEKTKRPINS	PVFNEMNAIT	AVYKEITAKA
EMQIEGLVKV	MPSGYIQIWQ	IMLTNVGEVP	LKKINLKPAS	GWSPGLARPI	QVTIRVGSEP
NKIVPITDEN	WRVGITLNT	VPIGQTATIM	MTTIATGEPD	QVLQAAVEMN	GNFSAVHAAD
TVRIQPKNQE	IVAPDEEGFI	STPTDFDGKV	AISSNTQQHG	LKQAADYYEN	GQENPYLRKL
KSQPNWALTA	ELSPFEGRVD	QLSSMTKLLL	GTTNVSGFIQ	YNQPTETKVA	LGKTTAIQLV
ANGVASHIVA	NGQFDESVDY	QFDFSFDQIK	LEIPANQGRK	DQTYQAMVTW	NLVTGP

EF095-3 (SEQ ID NO:363)

AAGTACAAAA	CAAGTAAGAG	AAGGAACCAA	TCATTCATTA		
ACAGCAGAAA	AAGCCGAAAG	TGAACAACCA	CAGACAAAGG	ATAAACTACA	TGATGAAGAA
ACACTGGCAT	TGTCAAAAAG	TGAGTTAATC	GATAATGAGG	CTAATGTTAC	AAGTCAAACG
ATTAGAGAAA	GAATTGAGAC	GCCTAACCTA	ACTTATCGTT	ATGGATTTAT	TAATGAAGAG
GGGCAGCCAG	TAAACGCCAA	TGAGATCCTT	CTACAGTATC	ATAGTTGGCA	AGGCAATTCC
CCAGATGGCA	TAAATGTGTG	GGAAGGTGAA	AGTCAACCAG	TGACAGCATC	TACAGTGGCT
AATTTAAAG	AAGTGGTAAT	TCCAAGTGAG	AAAGTAGCCG	TCTATTCCGA	CATGTCAACG
GTGCTTGCAG	CGAGTAATCA	AACATTTTTT	TTACCAAGAT	ATTATACTTC	TTTAAGCTTA
TACAATAAGA	AAGGGGAAAT	TGATCCCAAT	TATCCGCTGC	CAACTATTTT	CGACGCATCA
GGAAACCAAT	ATCCAACAAC	AATTTTCGCA	TTTGAATTGG	AAAAAATGTC	TGCACAACAA
TATAGTCAGA	AAACAGGAGT	AACGTTTAAC	ATTAGCGAGA	GTCAAAAAC	AATCGTTTCT
TTGTACAACC	AAGTGAAGGT	TGATTCATCG	AATCAATCTG	GGCTATTGAA	TTACTTTAAA
TTTTTCAGGGC	CGGTTTATTA	TCATGTTACC	AATCGCAAAG	TGACAGAACA	TTTTGTGGAT
ACTCAAGGGA	AACCAATCCC	TCCACCACCG	GGGTTTAGAC	AAGGAAAGCA	AACACTTATT
GAGCGTGACC	CTTACACCTT	TAAACAGAAA	GATCTTTTGC	CAAGTAGCTA	TGAAATTGAC
TCAAAAACGT	ATCAATTTCA	AGGATGGTAT	AAAGGGAAAA	CGAAACCTGA	AAATTTAGAA
AAAAGCGTAA	CGCCCAGTTA	TGATATTACC	TATGACGACA	ATGATGATTT	AACGTGTTGC
TATAAGGAGA	TACCTCAAAA	AAATTATACA	TTTGAGGATG	TCAATGGTGT	TGAAATTGCA
CCACCATCTG	ATTTTATTCA	GGATCACCAA	CAACCAATAA	CTACGGATGG	CTTTCGCTAT
TTAGCTGGAA	AAAAACTGCC	ACAACAATAC	AGCGTTAACG	GTAAAACCTA	TTTATATCAA
GGTTGGTATC	AAGATAAAAC	NAAACAAGAG	AGCTTAGAAA	AAACGAAGCG	ACCCATAAAC
TCCCCTGTTT	TTAATGAAAT	GAACGCTATT	ACAGCAGTGT	ATAAGGAAAT	AACATGCAAAA
GCTGAAATGC	AAATAGAAGG	ACTAGTCAAA	GTCATGCCAA	GTGGTTATAT	ACAAATTTGG
CAGATTATGC	TTACAAATGT	GGGAGAAGTA	CCGTTAAAAA	AAATAAACTT	AAAGCCAGCA
AGTGGTTGGT	CACCAGGTCT	AGCTCGGCCA	ATCCAAGTCA	CGATTCTGTT	TGGATCTGAA
CCAAACAAAA	TTGTTTCTAT	TACTGATGAA	AATTGGCGAG	TTGGCATTAC	TTTAAATACG
GAAGTGCCTA	TTGGTCAGAC	AGCAACTATT	ATGATGACAA	CAATTGCTAC	AGGTGAACCA
GATCAAGTGT	TACAAGCGGC	TGTTGAAATG	AATGGAAATT	TTTCTGCTGT	TCACGCAGCT
GATACTGTCA	GAATCCAACC	TAAAAATCAA	GAAATTGTGG	CACCAGATGA	GGAAGGTTTT
ATCAGCACAC	CAACTTTTGA	TTTTGGCAAA	GTCGCCATTT	CTAGCAACAC	GCAGCAACAT
GGTTTAAAGC	AGGCAGCAGA	TTATTATGAA	AATGGTCAGG	AAAATCCATA	TTTACGTTTG
AAAAAATCAC	AACCCAATTG	GGCACTAACT	GCAGAACTAT	CCCCCTTTGA	AGGAAGAGTG
GATCAACTAT	CATCAATGAC	AAAGTTATTG	TTAGGAACAA	CCAATGTTTC	AGGTTTTATT
CAGTACAATC	AACCAACGGA	AACTAAAGTT	GCTCTTGGCA	AAACAACCGC	TATTCAATTA
GTTGCCAACG	GTGTAGCTAG	CCATATTGTT	GCCAATGGTC	AGTTTGACGA	AAGTGATGTT
TATCAATTTG	ATTTTTCTTT	TGATCAAAATC	AAATTAGAAA	TTCCAGCAAA	TCAAGGTAGA
AAAGATCAAA	CTTATCAAGC	AATGGTGACT	TGGAATTTAG	TGACAGGCC	A

EF095-4 (SEQ ID NO:364)

STKQ VREGTNHSLT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AEKAESEQPQ	TKDKLHDEET	LALSKSELID	NEANVTSQTI	RERIETPNLT	YRYGFINEEG
QPVNANEILL	QYHSWQGNP	DGINVWEGES	QPVTASTVAN	LKEVVIPSEK	VAVYSDMSTV
LAASNQTFFL	PRYYTSLSLY	NKKGEIDPNY	PLPTISDASG	NQYPTTISQF	ELEKMSAQQY
SQKTGVTFNI	SESQKLIVPL	YNQVKVDSSN	QSGLLNYFKF	SGPVYYHVTN	RKVTEHFVDT
QGKPIPPPPG	FRQKQTLIE	RDPTTFKQKD	LLPSSYEIDS	KTYQFQGWYK	GKTKPENLEK
SVTPSYDITY	DDNDDLTVVY	KEIPQKNYTF	EDVNGVEIAP	PSDFIQDHQQ	PITTDGFRYL
AGKKLPQQYS	VNGKTYLYQG	WYQDKTKQES	LEKTKRPINS	PVFNEMNAIT	AVYKEITAKA
EMQIEGLVKV	MPSGYIQIWQ	IMLTNVGEVP	LKKINLKPAS	GWSPLARPI	QVTIRVGSEP
NKIVPITDEN	WRVGITLNT	VPIGQTATIM	MTTIATGEPD	QVLQAAVEMN	GNFSAVHAAD
TVRIQPKNQE	IVAPDEEGFI	STPTDFDGKV	AISSNTQQHG	LKQAADYYEN	GQENPYLRLLK
KSQPNWALTA	ELSPFEGRVD	QLSSMTKLLL	GTTNVSGFIQ	YNQPTETKVA	LGKTTAIQLV
ANGVASHIVA	NGQFDESDVY	QFDFSFDQIK	LEIPANQGRK	DQTYQAMVTW	NLVTGP

EF096-1 (SEQ ID NO:365)

TGAGGTGGCC	AAGTTAAAAT	GAAAAAATTA	CAGTCACTTT	TTATTGGAAT	TATCGCTATT
ATTGTCATCT	TGTTTTTTGG	CGTGCGCCAA	TTGGAGAAAG	CAAGTGGCAT	GGCAGGAGCA
GATACCTTGA	CCATTTACAA	TTGGGGGGAC	TATATAGATC	CGGCCTTGAT	TAAGAAATTT
GAAAAAGAAA	CAGGCTATAA	AGTCAATTAC	GAAACCTTTG	ATTCTAATGA	AGCTATGTAT
ACAAAAATTC	AGCAAGGTGG	CACAGCCTAT	GATATTGCCA	TTCCTTCTGA	ATATATGATT
CAAAAAATGA	TGAAAGCGAA	GATGCTTTTA	CCACTTGATC	ACAGCAAATT	AAAAGGCTTA
GAAAACATTG	ATGCACGCTT	TTTAGATCAA	TCCTTTGATC	CCAAAAATAA	GTTTTCCGTT
CCGTACTTCT	GGGGCACGTT	GGGGATTATT	TATAATGATA	AATTTATTGA	CGGCCGTCAG
ATCCAACATT	GGGATGATTT	ATGGCGCCCG	GAATTAAGAA	ATAATGTCAT	GCTGATTGAT
GGCGCTCGCG	AAGTGTTAGG	ATTATCTTTG	AACAGTTTAG	GCTATTTCGTT	AAACAGTAAA
AACGACCAAC	AATTACGTCA	GGCTACCGAT	AAGTTAAACC	GATTAACGAA	CAATGTCAAA
GCAATTGTTG	CCGATGAAAT	CAAAATGTAC	ATGGCTAATG	AAGAAAGTGC	AGTTGCTGTA
ACTTTCTCTG	GTGAAGCTGC	TGAAATGCTA	GAAAACAATG	AACATCTACA	TTATGTGATT
CCCAGTGAAG	GCTCTAATCT	CTGGTTTGAT	AACATTGTGA	TGCCTAAGAC	AGCCAAAAAT
AAAGAGGGTG	CCTATGCATT	TATGAACCTT	ATGTTACGAC	CAGAAAATGC	GGCACAAAAAT
GCAGAAATATA	TTGGTTATT	CACACCAAAT	AAAGAAGCTA	AAAAACTATT	ACCAAAAGAA
GTTGCCGAAG	ATAAACAATT	TTATCCAGAT	GATGAAACTA	TCAAACATTT	AGAAGTTTAC
CAAGACTTAG	GTCAGAATA	CTTAGGAATT	TATAACGATC	TGTTCTTGGA	GTTTAAGATG
TATCGGAAAT	AA				

EF096-2 (SEQ ID NO:366)

MKKLQ	SLFIGIIAII	VILFFGVRQL	EKASGMAGAD	TLTIYNWGDY	IDPALIKKFE
KETGYKVNIE	TFDSNEAMYT	KIQQGGTAYD	IAIPSEYMIQ	KMMKAKMLLP	LDHSLKLGLE
NIDARFLDQS	FDPKNKFSVP	YFWGTLGIIY	NDKFIDGRQI	QHWDDLWRPE	LKNNVMLIDG
AREVLGLSLN	SLGYSLNSKN	DQQLRQATDK	LNRLTNVKA	IVADEIKMYM	ANEEASAVVT
FSGEAAEMLE	NNEHLHYVIP	SEGSNLWFDN	IVMPKTAKNK	EGAYAFMFM	LRPENAAQNA
EYIGYSTPNK	EAKKLLPKEV	AEDKQFYPPD	ETIKHLEVYQ	DLGQEYLGIV	NDLFLEFKMY
RK					

EF096-3 (SEQ ID NO:367)

AAGTGGCAT	GGCAGGAGCA				
GATACCTTGA	CCATTTACAA	TTGGGGGGAC	TATATAGATC	CGGCCTTGAT	TAAGAAATTT
GAAAAAGAAA	CAGGCTATAA	AGTCAATTAC	GAAACCTTTG	ATTCTAATGA	AGCTATGTAT
ACAAAAATTC	AGCAAGGTGG	CACAGCCTAT	GATATTGCCA	TTCCTTCTGA	ATATATGATT
CAAAAAATGA	TGAAAGCGAA	GATGCTTTTA	CCACTTGATC	ACAGCAAATT	AAAAGGCTTA
GAAAACATTG	ATGCACGCTT	TTTAGATCAA	TCCTTTGATC	CCAAAAATAA	GTTTTCCGTT
CCGTACTTCT	GGGGCACGTT	GGGGATTATT	TATAATGATA	AATTTATTGA	CGGCCGTCAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ATCCAACATT GGGATGATTT ATGGCGCCCG GAATTAAAA ATAATGTCAT GCTGATTGAT
 GGCGCTCGCG AAGTGTTAGG ATTATCTTTG AACAGTTTAG GCTATTCGTT AAACAGTAAA
 AACGACCAAC AATTACGTCA GGCTACCGAT AAGTTAAACC GATTAAACGAA CAATGTCAAA
 GCAATTGTTG CCGATGAAAT CAAAATGTAC ATGGCTAATG AAGAAAGTGC AGTTGCTGTA
 ACTTTCTCTG GTGAAGCTGC TGAAATGCTA GAAAACAATG AACATCTACA TTATGTGATT
 CCCAGTGAAG GCTCTAATCT CTGGTTTGAT AACATTGTGA TGCCTAAGAC AGCCAAAAAT
 AAAGAGGGTG CCTATGCATT TATGAACTTT ATGTTACGAC CAGAAAATGC GGCACAAAAT
 GCAGAATATA TTGGTTATTC CACACCAAAT AAAGAAGCTA AAAAATCTAT ACCAAAAGAA
 GTTGCCGAAG ATAAACAATT TTATCCAGAT GATGAACTA TCAAACATTT AGAAGTTTAC
 CAAGACTTAG GTCAAGAATA CTTAGGAATT TATAACGATC TGTTCTTGGA GTTTAAGATG
 TATCGGAAA

EF096-4 (SEQ ID NO:368)

SGMAGAD TLTIYNWGDY IDPALIKKFE
 KETGYKVNYE TFDSNEAMYT KIQQGGTAYD IAIPSEYMIQ KMMKAKMLLP LDHSLKLGLE
 NIDARFLDQS FDPKNKFSVP YFWGTGIIY NDKFIDGRQI QHWDDLWRPE LKNNVMLIDG
 AREVLGLSLN SLGYSLNSKN DQQLRQATDK LNRLTNNVKA IVADEIKMYM ANEESAVAVT
 FSGEAAEMLE NNEHLHYVIP SEGSNLWFDN IVMPKTAKNK EGAYAFMNFM LRPENAAQNA
 EYIGYSTPNK EAKKLLPKEV AEDKQFYPDD ETIKHLEVYQ DLGQEYLGIV NDLFLEFKMY
 RK

EF097-1 (SEQ ID NO:369)

TAGAAGTATT CTAATTATCT ACATAGAGAG CGAGGGACAA GGAATATGAA GGAAAAAGAA
 ATGCATTCGC TCTTTTTTAA ACATAAGTTT GTGAAAGTAA CTCCCTATTT ACGTCGTTTT
 GGTCAATCGTT TGAGTGGGAT GATTATGCCA AATTTGAGTA TTTTATTTGC GTGGAGCTTA
 TTGTCTTTGG TGGCTGGCTA TACGACTGGG AATCTACGGC TAGCTCTTTC TGAAGTCGAA
 ACGATAATGA TTCGAGTTGT TTTACCGATT CTAATTGGTT TTACAGGCGG AAAAATGTTC
 GAGGAACAAC GTGGCGGCGT TGTGCTGCT ATTGCGACAG TGGGCGTGAT TGTTTCCACA
 GATGTTCCAC AGTTGTTTGG TGCTATGTTT ATTGGCCCTT TAGCAGGATA TACTTTCGCC
 AAAATTGAAC AAATTCTCTT ACCGAAAGTT AAAGAAGGCT ACGAGATGCT GACTAAACAC
 TTTTATGACG GAATTGTGGG AGGACTGCTG TGCTGTTTTG GTATTCTGGT GTAGACTCCG
 GCTGTTGAAA CGCTAGTTTT TTGGCTGTAT CAATTTTCTT CTTGGTTAAT TGAAGCCAAT
 CTTTACCAT TGGTTCACGT TTTCTTAGAG CCCTTAAAG TGTATTTTTT TAATAATGCG
 ATTAACCATG GCTTATTAAC GCCTCTAGGT TTAGAAGGTG CTAGTCAAAC AGGTCAGTCC
 ATTTTATTTT TATTGGAAC AAACCCTGGA CCAGGCGTGG GCGTTTTGGT TGCTTTTCTG
 CTGTTTGGGC CTGTAGGACA ACGAAAAACA GCAGGAGGTG CCACCATGAT TCAACTGATT
 GGGGGCATTG ATGAAATTTA TTTTCCGTTT GTTTTGATGG ACCCGCGCTT ATTTTATGCA
 GTAATTGCTG GAGGAATGAG TGGTACGCTT GTTTTCAA TATTTAATGT GGGTCTAAGT
 GCTCCAGCTT CGCCAGGTTT ATTTGGTTGCG ATTTTAGCCA ATGCCCCGAC TGATGCGAGG
 CTGGCGGTTT TTAGCGGAAT TTTTGTAGC TTTCTGTGCT CTTTGTCAAT AGCAAGCTTG
 TTATTAACAC GTCAACGAGG AATTGAACCA GTTTCAATGA TAAAGATGAA GGAGGAAGAC
 CAAGTGGAAC CAGTCACACC TAACATCAG CAAATTTTAT TTGTTTGTGA TGCAGGAATG
 GGCTCAAGTG CCATGGGGGC TAGTTTGCTA AGCCGACAAT TAAAAGCTGT GAACTTGGAG
 ATGCTGTGA CTTACAGTC CGTTCATCAG ATGAAGTGGC AGCCTAAGAC ATTAGTGGTC
 ATCAAGCAG AATTGAAACA GTTAGCACA AAGTACGTCC CAGAAAAGGA TATGGTGAGT
 GTTCAAAATT TTTTAGAAAT TAAATCCTAT TACCCGCAAG TTTTAGCCAA ACTGACTGCT
 TCTTCTCAAG AGCAATCTTC ACTTGTTTCA GAGTCTACTG AAACGAACTC GACAAAAACA
 ATACAGAAGC TTGTTTTTTT ATATGCCGAG AATGTTTCGAG GATCGCAAAC AATGGGAATG
 GAATTATTGC GGCAACAAGC GGCGAAACAA GGAGTCGCGA TTGAAGTATC TAAAGAGCCA
 CTGGAACAG TCTTTTTTAC CAAGGAGACA ACCTACGTAG TGACTCGTGA ACTGGCGCAA
 GCCTATCATT TAGATCTAAC GCAACAAAAT TTATACGTAG TTACTAGTTT TTTGAATAAG
 AAAGAGTATC AAGAATGGCT GGAAGGAGGA GCTGATAGAT GTTTTTAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF097-2 (SEQ ID NO:370)

MLTKNF LAGIVGGLLC CFGILVVAPA

VESASFWLYQ FSSWLEIANL LPLVHVLFEP LKVLFFNNAI NHGLLTPLGL EGASQTGQSI
 LFLLETNPGP GVGVLVAFLL FGPVGQRKTA GGATMIQLIG GIHEIYFPFV LMDPRLFLAV
 IAGMSGTLV FQIFNVGLSA PASPGSLVAI LANAPTDARL AVFSGIFVSF LCSFAIASLL
 LKRQRGIEPV SMIKMKEEDQ VETVTPNYQQ ILFVCDAGMG SSAMGASLLS RQLKAVNLEM
 PVTYQSVHQM KWQPKTLVVI QAEKQLAQK YVPEKDMVSV QNFLEIKSY YPQVLAKLTAS
 SQEQSSLGSE STETNSTKQI QKLVFLYAEN VRGSQTMGME LLRQQAQKQG VAIEVSKEPL
 ETVFFTKETT YVVTRELAQA YHLDLTQQNL YVVTSTFLNKK EYQEWLEGGA DRCF

EF097-3 (SEQ ID NO:371)

ACGAGG AATTGAACCA GTTCAATGA TAAAGATGAA GGAGGAAGAC

CAAGTGGAAA CAGTCACACC TAACTATCAG CAAATTTTAT TTGTTTGTGA TGCAGGAATG
 GGCTCAAGTG CCATGGGGGC TAGTTTGCTA AGCCGACAAT TAAAAGCTGT GAACTTGGAG
 ATGCCTGTGA CTTACCAGTC CGTTCATCAG ATGAAGTGGC AGCCTAAGAC ATTAGTGGTC
 ATTCAGCAG AATTGAAACA GTTAGCACA AAGTACGTCC CAGAAAAGGA TATGGTGAGT
 GTTCAAAATT TTTTAGAAAT TAAATCCTAT TACCCGCAAG TTTTAGCCAA ACTGACTGCT
 TCTTCTCAAG AGCAATCTTC ACTTGGTTC GAGTCTACTG AAACGAACTC GACAAAACAA
 ATACAGAAGC TTGTTTTTTT ATATGCCGAG AATGTTTCGAG GATCGCAAAC AATGGGAATG
 GAATTATTGC GGCAACAAGC GGCAGAACAA GGAGTCGCGA TTGAAGTATC TAAAGAGCCA
 CTGGAAACAG TCTTTTTTAC CAAGGAGACA ACCTACGTAG TGACTCGTGA ACTGGCGCAA
 GCCTATCATT TAGATCTAAC GCAACAAAAT TTATACGTAG TTACTAGTTT TTTGAATAAG
 AAAGAGTATC AAGAATGGCT GGAAGGAGGA GCTGATAGAT GTTTTT

EF097-4 (SEQ ID NO:372)

RGIEPV SMIKMKEEDQ VETVTPNYQQ ILFVCDAGMG SSAMGASLLS RQLKAVNLEM

PVTYQSVHQM KWQPKTLVVI QAEKQLAQK YVPEKDMVSV QNFLEIKSY YPQVLAKLTAS
 SQEQSSLGSE STETNSTKQI QKLVFLYAEN VRGSQTMGME LLRQQAQKQG VAIEVSKEPL
 ETVFFTKETT YVVTRELAQA YHLDLTQQNL YVVTSTFLNKK EYQEWLEGGA DRCF

EF098-1 (SEQ ID NO:373)

TAAATGAAAA AGACAAAAGT AATGACATTG ATGGCAACCA CAACTTTAGG CGCACTGGCA
 CTTGTACCAA TGAGTGCATT AGCAGTCGAC GGTGGTGAAT ACCAAACAAA CGGAGCGATT
 CAATTTGCAC CAAATACGAA CCCAACGAAT CCAGTTGATC CGACGAATCC AGACCCAGAT
 AAACCAATTA CACCAGTTGA TCCAACTGAT CCGACAGGGC CTAAGCCAGG GACAGCAGGT
 CCGTTATCCA TTGACTATGC ATCTAGCTTA TCTTTTGGGG AACAAACGAT TACCTCAAAA
 AATATGACCT ACTATGCAGA AACACAAAAA TACAAAGATA ACGCTGGTGC CGACCAAGAA
 GGCCCAAACCT TTGTTCAAGT CTCAGATAAT CGTGGGACTG AGACAGGTTG GACGCTAAAA
 GTAAAACAAA ATGGTCAATT CAAACTGAA GCCAACCAAG AACTAACAGC GGCCAAAGTA
 ACTTTAAGCA ACGGACGCGT GGTTTCAGCT TCACAATCTG CAAAGCCAAC GACAGCGCCA
 GCTACGATTG AATTAAACCC AACTGGGGCT GAATCAGTGG TCATGGCTGC TGGCGATAAA
 GAAGGTGCGG GTACGTACTT AATGAGCTGG GGCGATAGTG TAGATACCGC TAAAACAAGT
 ATTTTCATTAG AAGTACCTGG TTCAACCACA AAATATGCGA AAAAATACAC GACAACCTTT
 ACTTGGACTT TGACAGATAC ACCTGCTAAC ACAGGAAACT AA

EF098-2 (SEQ ID NO:374)

MKTKVMTLM ATTTLGALAL VPMSALAVDG GEYQTNGAIQ FAPNTNPTNP VDPTNPDPDK
 PITVPDPTDP TGPKPGTAGP LSIDYASSLS FGEQTITSKN MTYYAETQKY KDNAGADQEG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PNFVQVSDNR GTETGWTLKV KQNGQFKTEA NQELTAAKVT LSNGRVVSAS QSAKPTTAPA
 TIELNPTGAE SVVMAAGDKE GAGTYLMSWG DSVDTAKTSI SLEVPGSTTK YAKKYTTTFT
 WTLTDTPANT GN

EF098-3 (SEQ ID NO:375)

AGTCGAC GGTGGTGAAT ACCAAACAAA CGGAGCGATT
 CAATTTGCAC CAAATACGAA CCCAACGAAT CCAGTTGATC CGACGAATCC AGACCCAGAT
 AAACCAATTA CACCAGTTGA TCCAACGTAT CCGACAGGGC CTAAGCCAGG GACAGCAGGT
 CCGTTATCCA TTGACTATGC ATCTAGCTTA TCTTTTGGGG AACAAACGAT TACCTCAAAA
 AATATGACCT ACTATGCAGA AACACAAAAA TACAAAGATA ACGCTGGTGC CGACCAAGAA
 GGCCCAAACT TTGTTCAAGT CTCAGATAAT CGTGGGACTG AGACAGGTTG GACGCTAAAA
 GTAAAAACAA ATGGTCAATT CAAACTGAA GCCAACCAAG AACTAACAGC GGCCAAAGTA
 ACTTTAAGCA ACGGACGCGT GGTTTCAGCT TCACAATCTG CAAAGCCAAC GACAGCGCCA
 GCTACGATTG AATTAAACCC AACTGGGGCT GAATCAGTGG TCATGGCTGC TGGCGATAAA
 GAAGGTGCGG GTACGTACTT AATGAGCTGG GCGGATAGTG TAGATACCGC TAAAACAAGT
 ATTTTCATTAG AAGTACCTGG TTCAACCACA AAATATGCGA AAAAATACAC GACAACTTT
 ACTTGGACTT TGACAGATAC ACCTGCTAAC ACAGGAAACT

EF098-4 (SEQ ID NO:376)

VDG GEYQTNGAIQ FAPNTNPTNP VDPTNPDPDK
 PITPVDPTDP TGPKPGTAGP LSIDYASSLS FGEQTITSKN MTYYAETQKY KDNAGADQEG
 PNFVQVSDNR GTETGWTLKV KQNGQFKTEA NQELTAAKVT LSNGRVVSAS QSAKPTTAPA
 TIELNPTGAE SVVMAAGDKE GAGTYLMSWG DSVDTAKTSI SLEVPGSTTK YAKKYTTTFT
 WTLTDTPANT GN

EF099-1 (SEQ ID NO:377)

TGATGTTGTA GAGGGCTGAT GAAATGTTTA TCAGTCTTCT TTTTATTGAA AGGAGAGATC
 ATGAAGAAAT TAGGCAAGGT TTAAATTGTT AGTTGTTTTA TTTTATTCT TCCTTTTTTA
 TTATTTTATG GTGTATTTTC TTCTAGTGAA AGCGGAGATT CTTCCAGTT TCAGCCCGCT
 ACACCACAGG AAAAAGTAGC ATTAGAAGTT TCTAACTACG TGACGTCACA TGGCGGAACG
 TTGCAGTTTG CTTCCGCTTG GATTGGCAAT ATGGAACATG AAAGTGGATT AAATCCTGCT
 AGAATTCAAA GTGATTTATC GTTTAATTCA GCGATAGCTT TTAATCCTTC GTTAGGCGGT
 TATGGAATTG GGTTAGGACA ATGGGATTCA GGACGAAGAG TTAATTTATT AAATTTTGCA
 AAAAGTCAAA AAAAGGAATG GAAATCAGTA GCTTACAAA TGGATTTTGC GTGGAATAAG
 GATGGTTCTG ATAGTGACTT ACTTAAAAGA ATGTCTAAAT CAAAAGATGT GAATACACTT
 GCGGTAGATA TTTTGAAGCT GTGGGAACGA GCTGGAACAA AAGATGATCC CGCAGAACAA
 GTAAAAAGAA AGGCTAGTGC TAATAATTGG TATAAACGAC TTTCTACAGG TTCCATGGGC
 GGAGGTTTCA CCAATGTTGG TGGAGGAAAA ATTGATGCCT TGGAAAAAGT GATGGGGCAA
 ACTATTAATG GTGGTCAATG TTATGGCTTA TCTGCTTTTT TTGTTGAAAA ACAAGGAGGT
 CTACAAATGA TGGGTACGGG GCATATGTTT GCGAGTGAAA TTGGTAATGA TTATCCTTGG
 AGTTCAATTG GTTGGACAGT CATAAAGAAT CCAAATTATT CAGATATTAA AGCAGGAGAT
 GTCATTAAAT TTGGTCAAGG TGGTGTGGCT ACTAGTATTT ATGGGCATAC TGGTGTAGTG
 GCAAGTGTTG AAGGTAAAAA CAAGTTTACT ACTTATGAGC AAAACGCTGA ACAAGGTCAA
 ATTGTTGCTA AGTATTTTCG GACTTGGGGA TTAGATTTTC CACATGTGAC CAGCATAGTA
 AGGAAATAG

EF099-2 (SEQ ID NO:378)

MKCLS VFLLKGEIM KKLKVLIVS CFIFILPFL FLGVFSSSES GDSSQFQPAT
 PQEKVALEVS NYVTSHGGTL QFASAWIGNM EHESGLNPAR IQSDLSFN SA IAFNPSLGGY
 GIGLGQWDSG RRVNLLNFAK SQKKEWKSVA LQMDFAWNKD GSDSDLKRM SKSKDVNTLA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VDILKLWERA GTKDDPAEQV KRKASANNWY KRLSTGSMGG GSANVGGGKI DALEKVMGQT
 INGGQCYGLS AFFVEKQGGL QMMGTGHMFA SEIGNDYPWS SIGWTVIKNP NYSDIKAGDV
 INFGQGGVAT SIYGHTGVVA SVEGKNKFTT YEQNAEQGQI VAKYFRTWGL DFPHVTSIVR
 K

EF099-3 (SEQ ID NO:379)

TAGTGAA AGCGGAGATT CTTCCCAGTT TCAGCCCGCT
 ACACCACAGG AAAAAGTAGC ATTAGAAGTT TCTAACTACG TGACGTCACA TGGCGGAACG
 TTGCAGTTTG CTTCCGCTTG GATTGGCAAT ATGGAACATG AAAGTGGATT AAATCCTGCT
 AGAATTCAAA GTGATTTATC GTTTAATTCA GCGATAGCTT TTAATCCTTC GTTAGGCGGT
 TATGGAATTG GGTTAGGACA ATGGGATTCA GGACGAAGAG TTAATTTATT AAATTTTGCA
 AAAAGTCAAA AAAAGGAATG GAAATCAGTA GCTTTACAAA TGGATTTTGC GTGGAATAAG
 GATGGTTCTG ATAGTGACTT ACTTAAAAGA ATGTCTAAAT CAAAAGATGT GAATACACTT
 GCGGTAGATA TTTTGAAGCT GTGGGAACGA GCTGGAACAA AAGATGATCC CGCAGAACAA
 GTAAAAAGAA AGGCTAGTGC TAATAATTGG TATAAACGAC TTTCTACAGG TTCCATGGGC
 GGAGGTTTCA CCAATGTTGG TGGAGGAAAA ATTGATGCCT TGGAAAAAGT GATGGGGCAA
 ACTATTAATG GTGGTCAATG TTATGGCTTA TCTGCTTTTT TTGTTGAAAA ACAAGGAGGT
 CTACAAATGA TGGGTACGGG GCATATGTTT GCGAGTGAAA TTGGTAATGA TTATCCTTGG
 AGTTCAATTG GTTGGACAGT CATAAAGAAT CCAAATTATT CAGATATTAA AGCAGGAGAT
 GTCATTAATT TTGGTCAAGG TGGTGTGGCT ACTAGTATTT ATGGGCATAC TGGTGTAGTG
 GCAAGTGTG AAGGTAAAAA CAAGTTTACT ACTTATGAGC AAAACGCTGA ACAAGGTCAA
 ATTGTTGCTA AGTATTTTCG GACTTGGGGA TTAGATTTTC CACATGTGAC CAGCATAGTA
 AGGAAAT

EF099-4 (SEQ ID NO:380)

SES GDSSQFQPAT
 PQEKVALEVS NYVTSHGGTL QFASAWIGNM EHESGLNPAR IQSDLFNSA IAFNPSLGGY
 GIGLGQWDSG RRVNLLNFAK SQKKEWKSVA LQMDFAWNKD GSDSDLKRM SKSKDVNTLA
 VDILKLWERA GTKDDPAEQV KRKASANNWY KRLSTGSMGG GSANVGGGKI DALEKVMGQT
 INGGQCYGLS AFFVEKQGGL QMMGTGHMFA SEIGNDYPWS SIGWTVIKNP NYSDIKAGDV
 INFGQGGVAT SIYGHTGVVA SVEGKNKFTT YEQNAEQGQI VAKYFRTWGL DFPHVTSIVR
 K

EF100-1 (SEQ ID NO:381)

TANTTATGGC AATATGGAAG GAGTTTTATA ATGAAAAAGA AACAAAAATA CGCAGGGTTT
 ACATTATTAG AAATGTTGAT TGTCTTATTG ATTATTTCCG TATTGATTTT ACTTTTGTGTC
 CCTAACTTAG CGAAACATAA AGAAACAGTT GATAAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCAGTTAG ATAAATATAC AGCAGAAAAG
 CAATGA

EF100-2 (SEQ ID NO:382)

MKKKQKYAGF TLLEMLIVLL IISVLILLFV PNLAKHKETV DKKGNEAIVK
 IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLDKYTAEK Q

EF100-3 (SEQ ID NO:383)

TAA AGAAACAGTT GATAAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCAGTTAG ATAAATATAC AGCAGAAAAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CAAT

EF100-4 (SEQ ID NO:384)

KETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLDKYTAEK Q

EF100-1 (SEQ ID NO:385)

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 ACATTATTAG AAATGTTGAT TGTCTTATTG ATTATTTCCG TATTGATTTT ACTTTTGTGTC
 CCTAACTTAG CGAAACATAA AGAAACAGTT GATAAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCAGTTAG ATAAATATAC AGCAGAAAAAG
 CAATGA

EF100-2 (SEQ ID NO:386)

MKKKQKYAGF TLLEMLIVLL IISVLILLFV PNLAKHKETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLDKYTAEK Q

EF100-3 (SEQ ID NO:387)

TAA AGAAACAGTT GATAAAAAAG GCAATGAAGC AATCGTAAAA
 ATTGTAGAAT CACAAATCGA GCTCTACACA CTAGAAAAAA ATAAGACGCC TTCCTTAAAT
 GAATTAGTCA ACGAAGGCTA CATTACTAAA GAGCAGTTAG ATAAATATAC AGCAGAAAAAG
 CAAT

EF100-4 (SEQ ID NO:388)

KETV DKKGNEAIVK

IVESQIELYT LEKNKTPSLN ELVNEGYITK EQLDKYTAEK Q

EF101-1 (SEQ ID NO:389)

TGAGGAGATG AAACGAAGAA AATGAAGAAG AAAACGATAA TTATATTGGG GGCAGTTGCG
 GTAATTGCGG TTGGGGGCAT CGTAACTGTG AATGCGTTAA ATAAAAATGC ACAACAAGTA
 GCTGTCAAGC AAGCGCCTAA AGATGACTGG GGAATTGACT ATTTTGACGT TCCCGACTTG
 CAACAAATTT ATATTAACGG TGTCATCCAA CCGGAACAAA TGGAAGCCTT TCGCGTGAT
 CAAAAAATAA CAAAGGATCC AGAGATTAAG GTGAAAAACG GCGATGTCGT AGATGCAGGC
 ACAGAATTAT TTACTTATGA AGATGAGGCG GTCACAAAAG AAATTGAGGC ACAACAAAAT
 AGCTTAGCCA AATTAGAAAC GAAGCGGGCG AATATCTATA ATAAGTGGAA TCGGGCCATT
 GATAAATTTA ATAAACTAA AGAAGAAGAC CGCACGATGT CTGGTGATGA TTTAAATGAA
 CAATATCAAA CAGAAGTCGA TGCAGTAGAT GAAGAGATTA CCTTCACCAA TGAAACCTTA
 GCGGATTTAG GAGCGAAGCA ATATATTTC ACAAAGGCTA ATTTCAAAGG TCGTGTATCA
 ATTCCAGAAG TAAAAGATGC CAATTCACCG ATTTTACGGT TAAC TTCAGA AGATCTTTAT
 TTAGCTGGAA AAGTGAATGA AAAGGACTTG ACTAAAATTA GTGTTGGGCA AAAAGCTAAA
 CTAACCTCTG TTTCCAACAA TGTGGTTGTG GATGGCTCAA TTTCTTACAT CGATGATAAT
 CCTCCTGAAG GCAACAGCGA TGCCGCGAGT GGCAATCCAG AGGGCGGCAC AACGATGTCT
 AGTTATAGCG TCAAAATTGC GTTGCCAAT TTAGACAAAG TCAAAAATGG CTACCATATG
 CAAGCAACCA TTGATTTAGG CGATTTAGGG GCGATTGAGT TACCGAAAAA AGCGATTCAA
 AAAGAGGGTG AACAGGCCTA CGTTT TAGTG AATGATTTTG GAACCATCAT TCGTCGTGAT
 GTCCAAGTCG GGCAAGAAAA TGGCGACAAA ATGGCGATTG AATCTGGCTT AGAATCAGCC
 GACCGAGTGG TTATTTCTTC AAAAAACCA GTAAAAGTCG GTGATATTGT TGAATCAGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCAGCGATTG CTTCTGATGA ATCAGCAACC AACGAATCAA TGACAGATGC GTCGAAATAG

EF101-2 (SEQ ID NO:390)

MKKK TIIILGAVAV IAVGGIVTVN ALNKNAQQVA VKQAPKDDWG IDYFDVDPDLQ
 QIYINGVIQP EQMEAFARDQ KITKDPEIKV KNGDVVDAGT ELFTYEDEAV TKEIEAQONS
 LAKLETKRAN IYNKWNRAID KFNKTKEEDR TMSGDDLNEQ YQTEVDAVDE EITFTNETLA
 DLGAKQYIST KANFKGRVSI PEVKDANSPI LRLTSEDLYL AGKVNEKDLT KISVGQKAKL
 TSVSNVVDV GSISYIDNP PEGNSDAASG NPEGGTTMSS YSVKIALANL DKVKNGYHMQ
 ATIDLGLGA IELPKKAIQK EGEQAYVLVN DFGTIIRRDV QVGQENGDKM AIESGLESAD
 RVVISSKKPV KVGDIVESDA AIASDESATN ESMTDASK

EF101-3 (SEQ ID NO:391)

TAAAAATGC ACAACAAGTA
 GCTGTCAAGC AAGCGCCTAA AGATGACTGG GGAATTGACT ATTTTGACGT TCCCGACTTG
 CAACAAATTT ATATTAACGG TGTCATCCAA CCGGAACAAA TGGAAGCCTT TGCGCGTGAT
 CAAAAAATAA CAAAGGATCC AGAGATTAAG GTGAAAAACG GCGATGTCGT AGATGCAGGC
 ACAGAATTAT TTAATTATGA AGATGAGGCG GTCACAAAAG AAATTGAGGC ACAACAAAAT
 AGCTTAGCCA AATTAGAAAC GAAGCGGGCG AATATCTATA ATAAGTGGA TCGGGCCATT
 GATAAATTTA ATAAAACTAA AGAAGAAGAC CGCACGATGT CTGGTGATGA TTTAAATGAA
 CAATATCAAA CAGAAGTCGA TGCAGTAGAT GAAGAGATTA CCTTCACCAA TGAAACCTTA
 GCGGATTTAG GAGCGAAGCA ATATATTTCC ACAAAGGCTA ATTTCAAAGG TCGTGATCA
 ATTCCAGAAG TAAAAGATGC CAATTCACCG ATTTTACGGT TAACTTCAGA AGATCTTTAT
 TTAGCTGGAA AAGTGAATGA AAAGGACTTG ACTAAAATTA GTGTGGGCA AAAAGCTAAA
 CTAACCTCTG TTTCCAACAA TGTGGTTGTG GATGGCTCAA TTTCTTACAT CGATGATAAT
 CCTCTGAAG GCAACAGCGA TGCCGCGAGT GGCAATCCAG AGGGCGGCAC AACGATGTCT
 AGTTATAGCG TCAAAATTGC GTTGGCCAAT TTAGACAAAG TCAAAAATGG CTACCATATG
 CAAGCAACCA TTGATTTAGG CGATTTAGGG GCGATTGAGT TACCGAAAAA AGCGATTCAA
 AAAGAGGGTG AACAGGCCTA CGTTTGTAGT AATGATTTTG GAACCATCAT TCGTCGTGAT
 GTCCAAGTCG GGCAAGAAAA TGGCGACAAA ATGGCGATTG AATCTGGCTT AGAATCAGCC
 GACCGAGTGG TTATTTCTTC AAAAAACCA GTAAAAGTCG GTGATATTGT TGAATCAGAT
 GCAGCGATTG CTTCTGATGA ATCAGCAACC AACGAATCAA TGACAGATGC GTCGAAAT

EF101-4 (SEQ ID NO:392)

KNAQQVA VKQAPKDDWG IDYFDVDPDLQ
 QIYINGVIQP EQMEAFARDQ KITKDPEIKV KNGDVVDAGT ELFTYEDEAV TKEIEAQONS
 LAKLETKRAN IYNKWNRAID KFNKTKEEDR TMSGDDLNEQ YQTEVDAVDE EITFTNETLA
 DLGAKQYIST KANFKGRVSI PEVKDANSPI LRLTSEDLYL AGKVNEKDLT KISVGQKAKL
 TSVSNVVDV GSISYIDNP PEGNSDAASG NPEGGTTMSS YSVKIALANL DKVKNGYHMQ
 ATIDLGLGA IELPKKAIQK EGEQAYVLVN DFGTIIRRDV QVGQENGDKM AIESGLESAD
 RVVISSKKPV KVGDIVESDA AIASDESATN ESMTDASK

EF102-1 (SEQ ID NO:393)

TAAACATTTG AGACATTGAG AGGTGAATGT CTCTTTTTTA TTAATCAAAA ACGAAAGGGG
 ATTAATTATA TGAAAAAAC AACATTTAAA AATTGGTCGT TATTTGCGAC TTTGGCTCTA
 TTAAGTCAAA CAATTGGCGG AACGATTGGT CCTACGATTG CTTTTGCCGA TGAAATTAAT
 CACCTCAAG AGGTAACAAT TCATTATGAC GTAAGTAAAC TGTATGAAGT TGACCGAACT
 TTTAGCGATG GCAGCAGCT CTCAGAACGT ACTACGTCAT TATATGCAGA ATACAATGGT
 GCAAAACAAA CAGTATTTTG TATTGAACCA GGTGTTAGTA TTCCAACAGA AGTGACGCAC
 GGTATACAGA AAAACCTTT GCCATCAATG TCTGATAAAG CGAAACTAGT ATCGGTTCTT
 TGGGAAAAGG CTGGAACAGA TATTGATACA AATATGGTTG CACAAAAGAT GATTTGGGAA
 GAAGTGAACG GTTATAAACT CCATTCATA AAAAGATTAG GTGGTGCTTC AGTTGATATA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AAATCTATTG AAGGAAAAAT TAATAAGGCA ATTGAGGAGT ATCAAAAAAA ACCAAGTTTT
CATAATACCA CTGTAAAAAC AATTTTAGGT CAATCGACAA CTTTAAATAGA TAAAAATGAA
TTAAATTTAT CTGAGTTTGA TAAAGTCGTC CAAAATACGG CGAATATAGA TTACCGTGTA
ATTGGGAATC AATTAGTGCT TACTCCAAAC TCTAATTCCA AATCAGGAAC ATTAACATTG
AAAAAATCAG ATGGTACTGG AACTCCAGTC GCTTATAAAA AAGCAGGACT TCAAACGTG
ATGGCTGGTG CGCTTGATAA GCCCAATACC TACGCTATTA AAATTAATGT GGAAACTAAG
GGTTCTTTAA AGATCAAAAA AATCGATAAA GAATCAGGTG ATATTGTACC AGAAACGGTT
TTCCATTTAG ATTTTGGGAA AGCTTTACCT TCAAAAGATG TGACAACAGA TAAAGATGGG
ATTTCTATTT TGGATGGAAT TCCCCATGGT ACAAAGGTAA CTATTACTGA AAAATCGGTG
CCAGATCCTT ATATGATTGA TACCACACCC ATGGCTGCCA CCATTAAAGC GGGCGAGACC
ATTTCCATGA CTTCGAAAAA TATGCGACAA AAAGGTCAAA TTCTTTTAGA GAAGACTGGG
GTAGAAACAG GTACTGATCT TTGGAATGAC AATTATTCTC TAGCTGGAAA TACATTTGCC
ATTCGTAAAG ACAGCCCAGC TGGTGAAATT GTCCAAGAAA TAACAACGGA TGAAAAAGGT
CGTGCGGAAA CACCAAAAGA GCTTGCTAAT GCTTTGGAAC TGGGAACCTA TTACGTGACA
GAAACTAAAT CTAGTAATGG TTTCGTGAAT ACCTTCAAAC CAACAAAAGT CGAGTTAAAA
TATGCCAATC AAACCGTGGC TCTTGTTACC AGTAACGTAA AAGGGCAAAA CCAAGAAATT
ACTGGGGAAA CCACTTTGAC AAAAGAAGAC AAAGATACCG GTAATGAGAG TCAAGGGAAA
GCTGAGTTTA AAGGAGCTGA ATATACTCTC TTTACTGCAA AAGATGGTCA AGCTGTTAAA
TGGAGTGAAG CTTTTTAAAC AGAATTAGTG AAGGGAACGA AAGCTTCTGA TGAAACAGTG
ACTTTGGCTT TAGATGAAAA GAACCAAGTT GCCGTAAAC ACCTAGCAAT TAACGAGTAT
TTCTGGCAAG AAACCAAAGC ACCTGAAGGA TATACTTTGG ATGAAACGAA GTATCCTGTA
TCCATCAAAA AAGTTGATAA TAACGAAAAA AATGCCGTAA TTACTCGAGA TGTTACGGCA
AAAGAACAAG TTATTCGCTT TGGCTTTGAT TTCTTTAAAT TTGCTGGATC GGCTGATGGC
ACTGCCGAAA CTGGATTTAA CGACTTATCT TTTAAAGTGT CGCCATTGGA AGGGACCAAN
GAAATCACAG GTGCTGAAGA TAAAGCGACC ACAGCTTGTA ACGAGCAATT AGGTTTTGAT
GGCTATGGTA AGTTTGAAAA TCTTCCTTAT GGGGATTATT TACTTGAAGA AATAGAGGCT
CCAGAAGGAT TTCAAAAGAT TACACCACTA GAAATCCGTT CTACATTTAA GGAAAACAAA
GACGACTATG CGAAGAGTGA GTATGTCTTT ACCATTACCG AAGAAGGACA AAAACAACCA
ATTAAGATGG TGACCGTTCC TTACGAGAAA CTAAC TAACA ACGAGTTTTC TGTTAGTCTG
AACCGTTTGA TGCTTTATGA TTTGCCCGAG AAAGAAGATA GTTTGACTTC TCTTGCGACT
TGGAAGACG GAAATAAAAA ATTGAATACC CTTGATTTTA CCGAGCTAGT TGATAAATTG
AGATGAACT TGCATGAAAT CAAAGAAGAC TGGTATGTCG TAGCTCAAGC CATTTGATGTG
GAAGCCACAA AAGCTGCCCA AGAAAAAGAC GAAAAAGCCA AACCGGTGGT GATTGCCGAA
ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ACTGGAACCT GGAAAAATTCT GCATAAATTA
ACCGCTGAAC AAGTTTTGGA TAAAAGCATC GTCTTGTTCA ATTATGTGTA TGAAAACAAG
GTAGCCTTTG AAGCAGGCAA TGAGCCAGTA GCGAAGGATG CTAGCTTGAA CAATCAAGCA
CAAACCGTCA ATTGTACGAT TGAACGCCAT GTTTCCATCC AAACAAAAGC CCACCTAGAA
GATGGTTCGC AAACTTTTAC TCATGGTGAC GTGATGGATA TGT'TTGATGA TGTGTCGGTT
ACCCATGATG TACTGGATGG CTCAAAAGAA GCTTTCGAAA CAATTCTGTA TGCTTTACTA
CCAGATGGTA CGAACAAAGA AATTTGGAAA TCTGGCAAAA TTGAGCATGA AGTGAATGAT
AAAGAATTTA CCAAAACCGT ACTTGCGGAA AAAGTAGATA CCGGAAAGTA TCCAGAAGGA
ACTAAGTTTA CTTTTACGGA AATCAATTAC GAAAAAGATG GAAACGTGAA TGGAAAAACAC
AATGAAGATT TGAAAGAAAA ATCTCAAACC TTAACACCAA AAGAAGTGCC AACCATACCG
AGTACGCCAA AACAACCGGA AACACCAGCT GTTCCAAGTA ATTCTCAAGA ATCTAGTCCC
ACAGTGAAGA CATTCCCGCA AACTGGGGAG AAAAATTCCA ACGTTCTACT GTTAGTTGGC
TTTATCTTGA TTTTTTCGAC TGCTGGGTAT TATTTCTGGA ATCGCCGCAA TTAA

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EF102-2 (SEQ ID NO:394)

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MKKTTFFKN WSLFATLALL SQTIGGTIGP TIAFADEITH
PQEVTHYDV SKLYEVDGTF SDGSTLSERT TSLYAEYNGA KQTVFCIEPG VSIPTEVTHG
YQKNPLPSMS DKAKLVSVLW EKAGTDIDTN MVAQKMIWEE VNGYKLHSIK RLGGASVDIK
SIEGKINKAI EEYQKKPSFH NTTVKITLQG STTLIDKNEL NLSEFDKVVQ NTANIDYRVI
GNQLVLTPNS NSKSGTLTLK KSAGTGTPVA YKKAGLQTM AGALDKPNTY AIKINVETKG

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

```

SLKIKKIDKE SGDIVPETVF HLDGFGKALPS KDVTDDKDI SILDGIPHGT KVTITEKSVP
DPYIMIDTTPM AATIKAGETI SMTSKNMRQK GQILLEKTGV ETGTDLWNDN YSLAGNTFAI
RKDSPAGEIV QEITTDKGR AETPKELANA LELGTYVTE TKSSNGFVNT FKPTKVELKY
ANQTVLVTLS NVKGQNEIT GETTLTKEDK DTGNESQGA EFKGAEYTLF TAKDGQAVKW
SEAFKTELVK GTKASDETVT LALDEKNQVA VKHLAINEYF WQETKAPEGY TLDETKYPVS
IKKVDNNEKN AVITRDVTAK EQVIRFGFDF FKFAGSADGT AETGFNDLSF KVSPLGTXE
ITGAEDKATT ACNEQLGFDG YGKFENLPYG DYLLLEEIEAP EGFQKITPLE IRSTFKENKD
DYAKSEYVFT ITEEGQKQPI KMTVPYEKL TNNEFSVSLN RLMLYDLPEK EDSLTSLATW
KDGNNKLNLT DFTLVDKLR YNLHEIKEDW YVVAQAIDVE ATKAAQEKDE KAKPVVIAET
TATLANKEKT GTWKILHKLT AEQVLDKSIV LFNYVYENKV AFEAGNEPVA KDASLNNQAQ
TVNCTIERHV SIQTKAHLED GSQTFTHGDV MDMFDDVSVT HDVLDGSKEA FETILYALLP
DGTNKEIWKS GKIEHEVNDK EFTKTVLAEK VDTGKYPEGT KFTFTEINYE KDGNNVGKHN
EDLKEKSQTL TPKEVPTIPS TPKQPETPAV PSNSQESSPT VKTFPQTGEK NSNVLLLVGF
ILIFSTAGYY FWNRRN

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EF102-3 (SEQ ID NO:395)

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TTCTGGCAAG AAACCAAAGC ACCTGAAGGA TATACTTTGG ATGAAACGAA GTATCCTGTA
TCCATCAAAA AAGTTGATAA TAACGAAAAA AATGCCGTAA TTA CTGAGA TGTTACGGCA
AAAGAACAAG TTATTCGCTT TGGCTTTGAT TTCTTTAAAT TTGCTGGATC GGCTGATGGC
ACTGCCGAAA CTGGATTTAA CGACTTATCT TTTAAAGTGT CGCCATTGGA AGGGACCAAN
GAAATCACAG GTGCTGAAGA TAAAGCGACC ACAGCTTGTA ACGAGCAATT AGGTTTTGAT
GGCTATGGTA AGTTTGAAAA TCTTCCTTAT GGGGATTATT TACTTGAAGA AATAGAGGCT
CCAGAAGGAT TTCAAAAGAT TACACCACTA GAAATCCGTT CTACATTTAA GGAAAACAAA
GACGACTATG CGAAGAGTGA GTATGTCCTT ACCATTACCG AAGAAGGACA AAAACAACCA
ATTAAGATGG TGACCGTTCC TTACGAGAAA CTAAC TAACA ACGAGTTTTT TGTTAGTCTG
AACCGTTTGA TGCTTTATGA TTTGCCCGAG AAAGAAGATA GTTTGACTTC TCTTGCGACT
TGGAAGACG GAAATAAAAA ATTGAATACC CTTGATTTTA CCGAGCTAGT TGATAAATTG
AGATATAACT TGCATGAAAT CAAAGAAGAC TGGTATGTCG TAGCTCAAGC CATTGATGTG
GAAGCCACAA AAGCTGCCCA AGAAAAAGAC GAAAAAGCCA AACCGGTGGT GATTGCCGAA
ACAACCGCAA CGTTGGCGAA CAAAGAGAAA ACTGGAACCTT GGAAAATTCT GCATAAATTA
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GTAGCCTTTG AAGCAGGCAA TGAGCCAGTA GCGAAGGATG CTAGCTTGAA CAATCAAGCA
CAAACCGTCA ATTGTACGAT TGAACGCCAT GTTCCATCC AAACAAAAGC CCACCTAGAA
GATGGTTCGC AAAC TTTTAC TCATGGTGAC GTGATGGATA TGTTTGATGA TGTGTCGGTT
ACCCATGATG TACTGGATGG CTCAAAAGAA GCTTTCGAAA CAATTCTGTA AGCTTTACTA
CCAGATGGTA CGAACAAGAA AATTTGGAAA TCTGGCAAAA TTGAGCATGA AGTGAATGAT
AAAGAATTTA CCAAAACCGT ACTTGCGGAA AAAGTAGATA CCGGAAAGTA TCCAGAAGGA
ACTAAGTTTA CTTTTACGGA AATCAATTAC GAAAAAGATG GAAACGTGAA TGGAAAACAC
AATGAAGATT TGAAAGAAAA ATCTCAAACC TTAACACCAA AAGAAGTGCC AACCATACCG
AGTACGCCAA AACAACCGGA AACACCAGCT GTTCCAAGTA ATTCTCAAGA ATCTAGTCCC
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EF102-4 (SEQ ID NO:396)

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LDEKNQVA VKHLAINEYF WQETKAPEGY TLDETKYPVS
IKKVDNNEKN AVITRDVTAK EQVIRFGFDF FKFAGSADGT AETGFNDLSF KVSPLGTXE
ITGAEDKATT ACNEQLGFDG YGKFENLPYG DYLLLEEIEAP EGFQKITPLE IRSTFKENKD
DYAKSEYVFT ITEEGQKQPI KMTVPYEKL TNNEFSVSLN RLMLYDLPEK EDSLTSLATW
KDGNNKLNLT DFTLVDKLR YNLHEIKEDW YVVAQAIDVE ATKAAQEKDE KAKPVVIAET
TATLANKEKT GTWKILHKLT AEQVLDKSIV LFNYVYENKV AFEAGNEPVA KDASLNNQAQ
TVNCTIERHV SIQTKAHLED GSQTFTHGDV MDMFDDVSVT HDVLDGSKEA FETILYALLP
DGTNKEIWKS GKIEHEVNDK EFTKTVLAEK VDTGKYPEGT KFTFTEINYE KDGNNVGKHN

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EDLKEKSQTL TPKEVPTIPS TPKQPETPAV PSNSQESSPT VK

EF103-1 (SEQ ID NO:397)

TAAGATAGGT TTATCAAAGA AAAGGAGCGA TGCTTTATGA AAAAGAAAGT ATTAAGTTCCG
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GATCATGCAG CCAATCCAAA TAGTGCTACA GCAAATTTAG GCAAACATCA AAACAATGGC
CAAACAAGAG GCGACAAGGC GACTAAGATT TTATCTGGCA CGGACTGGCA AGGAACCCGT
GTTTATGATG CTGCTGGTAA TGATTTAACG GCAGAAAATG CTAATTTTAT TGGTTTAGCA
AAATATGATG GTGAAACCGG TTTTACGAG TTTTTCGACA AAAATACTGG GGAAACCCGT
GGTGACGAAG GAACATTTTT TGTGACAGGT GATGGCACA AACGAATTTT AATTTCCGCG
ACACAAAATT ATCAAGCCGT AGTGGATTTA ACCGAAGTGA GTAAAGACNA ATTTACTTAC
AAGCGTTTAG GGAAAGATAA ACTGGGGAAT GATGTTGAAG TTTACGTGGA ACACATCCCT
TATCATGGGA AAAAATTAGC TTTTACAAAT GGACGTGAAG CATTAAACCA TCAAACTGGC
AAAATTGTGA CAAATAAATC AGGGGATAAA ATTTTAGGAA CAACCTTGTG GAATGGCACA
AAAGTCGTAG ATAAAAACGG TAATGATGTG ACAGCGGCCA ATCAAAATTT CATTAGTTTA
GCGAAATTTG ATCCAAACAC AAGTAAATAT GAATTTTTC AATTACAAAC AGGTGAAACC
CGCGGCGACT TTGGGTACTT CCAAGTGGTG GACAATAACA AGATTCTGGG CCATGTATCT
ATTGGTACGA ATCGTTACGG CGCGGCGCTA GAATTAACGG AACTAAACAA TGATCGATTT
ACGTATACTC GAATGGGTAA AGATAATGCT GGTAAATGATA TTCAAGTGTT CGTGAACAT
GAACCTTACC AAGGCACATA TCATCCAGCC TTTACTTTCT AA

EF103-2 (SEQ ID NO:398)

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DEGTFVVTGD GTKRILISRT QNYQAVVDLT EVSKDXFTYK RLKDKLND VEVYVEHIPY
HGKKLAFNG REALTNQTKG IVTNKSGDKI LGTTLWNGTK VVDKNGNDVT AANQNFISLA
KFDPNSTSKYE FFLNQTGETR GDFGYFQVVD NNKIRAHVSI GTNRYGAAL LTELNNDRFT
YTRMGKDNAG NDIQVFVEHE PYQGTYPFAF TF

EF103-3 (SEQ ID NO:399)

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CAAACAAGAG GCGACAAGGC GACTAAGATT TTATCTGGCA CGGACTGGCA AGGAACCCGT
GTTTATGATG CTGCTGGTAA TGATTTAACG GCAGAAAATG CTAATTTTAT TGGTTTAGCA
AAATATGATG GTGAAACCGG TTTTACGAG TTTTTCGACA AAAATACTGG GGAAACCCGT
GGTGACGAAG GAACATTTTT TGTGACAGGT GATGGCACA AACGAATTTT AATTTCCGCG
ACACAAAATT ATCAAGCCGT AGTGGATTTA ACCGAAGTGA GTAAAGACNA ATTTACTTAC
AAGCGTTTAG GGAAAGATAA ACTGGGGAAT GATGTTGAAG TTTACGTGGA ACACATCCCT
TATCATGGGA AAAAATTAGC TTTTACAAAT GGACGTGAAG CATTAAACCA TCAAACTGGC
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AAAGTCGTAG ATAAAAACGG TAATGATGTG ACAGCGGCCA ATCAAAATTT CATTAGTTTA
GCGAAATTTG ATCCAAACAC AAGTAAATAT GAATTTTTC AATTACAAAC AGGTGAAACC
CGCGGCGACT TTGGGTACTT CCAAGTGGTG GACAATAACA AGATTCTGGG CCATGTATCT
ATTGGTACGA ATCGTTACGG CGCGGCGCTA GAATTAACGG AACTAAACAA TGATCGATTT
ACGTATACTC GAATGGGTAA AGATAATGCT GGTAAATGATA TTCAAGTGTT CGTGAACAT
GAACCTTACC AAGGCACATA TCATCCAGCC T

EF103-4 (SEQ ID NO:400)

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DEGTFVVTGD GTKRILISRT QNYQAVVDLT EVSKDXFTYK RLKDKLND VEVYVEHIPY

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

HGKKLAFTNG REALTNQTGK IVTNKSGDKI LGTTLWNGTK VVDKNGNDVT AANQNFIsla
 KFDPNITSKYE FFLNLQTGETR GDFGYFQVVD NNKIRAHVSI GTNRYGAALe LTELNNDRFT
 YTRMGKDNAG NDIQVFVEHE PYQGTYPHA

EF104-1 (SEQ ID NO:401)

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 GCACAAAATT TCGGGTTTGC CGTAAATGCC TATGCTGTAA CAACGACAGA AGCACAAACA
 GAGACCACTG ATACAGCAAA AAAAGAGGCA GAGTTATCGA ACTCAACACC ATCTTTACCT
 TTAGCAACAA CGACTACTTC AGAAATGAAT CAACCAACTG CAACAACTGA ATCGCAAACC
 ACAGAGGCCG GCACAACAGC TTCCAGTGAT GCTGCTACAC CATCTGAACA ACAAACAACG
 GAGGACAAGG ACACCTCACT TAATGAAAAA GCCCTGCCAG ATGTTCAAGC GCCAATTACA
 GATGAACTAC TTGACAGTAT GAGTCTTGCG CCGATTGGTG GAACAGAATA CAGCCAAACA
 GAGGTTCCACC GCGAATTAAA TACAACACCG GTAACCGCTA CGTTCCAATT TGCTGTTGGA
 AACACAGGTT ATGCACCTGG ATCAGTTTAT ACAGTTCAAT TACCAGAACA TTTAGGTTAT
 TCAACTGTCA GCGGAGAAGT GACAGGCATT GCGCCAACTT GGGCAGTCGA TCGCGCGACC
 AAAACATTAA GTATTACGTT TAATCAACGA GTTTCAGATA CTTCCTTTAA AGTAGAAGTA
 AAAAGTTATC TAACAACAGA GCGGGAACCA TTAATCAAAA TTGAAACTCC AGGAAAAAAT
 AAAAAAACCT ACTCGTTTGA TTTATATGAA CAAGTGAAC CAATTCAATA TAACGAACGA
 ACCGAAACGA CGGGGTTAGA TGGCGAAATT TTTTATAATT TAGACCGGAC GTTAAC'TGGC
 AATCAAACAT TAGAATTATT AACAACAGAG ACGCCAGGCG CTGTCTTTGG AAAACAAGAT
 AACTTTGGAAC CTCAAGTTTT CAGTTACGAT GTCGACATTA ATGGTCAAAT TTTACCAGAA
 ACGCAAACCT TGTTAACACC TGGCAAAGAT TATACATTAA GCGATAATTC ACTCGGGCGG
 ATTGCTGTAA CTGTTCCAAA CATGAATCAA CAAAAAGCCT ATTCCTTATC GATTAATCGG
 ACAATTTATT TAGAGAGTGC TTCGGACTAT AACTACTTAT ATTTCGAGCA GTATCCAACA
 AAAAAATTG GGTCAATTTT TTTGAAAAGT ACGACAGGAA CTAAACAAAC AACCATTTTT
 ACTGCTAAGA CGAGTCAAAC AAGTAAAGTA ATTGCTGATC GTGAAATGCG TAGTATGTCC
 TATATCAGTT TTCAAAGCAA AGGGAAATAT TATGTAACAA TTTATGGCAC GTTAACAGAA
 ACAAAGTGG GTCAACAAAT CGTATTAGAG AGTACAAACG GTCAAGAAAT TAAGAATCCT
 AAATTTACGG CGTATGGTCC TTTATATGAA AATGTAAAT TGAAGACTA TTTTGATATT
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 GTTGTTAATC CTTTGAATGC TGAAACTGCT TGGGGTAATT ATGATCAAAA TGGTGCCTAT
 TCATCAAGAA CAACTGTCTC AGTTATGGGA AGCAAAGAGA AACCATTCA AAATTTAGAA
 ATTAAAGTAA AGCATCCTAA TTATCTTTCA TTACGAGCTA CAAAAGAAAT TTATTTTAT
 TACAAGTTAG GAACGGATTA TACAGTAACG CCAACGTCAG ATGGTTCAGT TATTAAGTTC
 ACTACGCCAA TAACCAACGA AATCCAAATT CCAATTGGTT TTAATTATGT GCCAGATAGT
 TTGCCAAAAG ATAAAAGTAT CCCAGTCGAT ACGATACCGA TAACAATGAG TGCTGAAGGT
 TTAACCTCAG TTGATACGAC AGTAACTACT AATAGTAAGC GTGGTTCTGA ACGAACACTT
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 AATGAAGGCT CTGCTTCGGT TTCTGTTCAA AATGAAGCGT TAGACATTTT GAGTGAACA
 CAAGCGGCCG ATCCAACATT AAAAAATGTA ACAAACCGA CAGTAACAAC AAAAAATATT
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 ATTACGATTG AATACAATAC GGTCTCTGCA AACGCTGGCC AAATCTATAC AGAAACAACA
 ATCGACTCTG AAACATTGAA CCAGATGTCT GCTAGCAAGA AAAAAGTCAC CACTGCGCCA
 ATCACATTGA AATCTCAGA AGGTGATGCG GAAGGTATTG TTTATTTAGC AACTGCCACA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTCTACACGC	ATAACGTAGA	GGATGAAAAC	CAAGCAATTG	CGAAGGTTTC	TTTGAACATA
ATTGATAATG	TCACGCATAC	AGCAACCGAA	TTTACAACAG	ATGAAAAAGG	TCAATACTCC
TTTGATGCCA	TCATGACAGG	TGATTATACT	TTGCGAGTAA	CGAATGTACC	GCAGGAATAT
TCCGTGGATG	AAGAGTATTT	GACAGGAAAA	GCCATTAAGC	TGGTCAAAGG	AGACAACCAA
CTAAAAATTC	CATTAACGAA	AACAATTGAT	CACAGTCGTT	TACAAGTCAA	AGATTCAACG
ATTTATGTCTG	GCGATTTCATG	GAAACCAGAA	GAGAACTTTG	TTTCAGCAAC	AGATAAAACA
GGTCAAGACG	TTCCCTTCGA	AAAAATCACT	GTTTCAGGTC	AAGTTGATAA	CANCAAAAGCA
GGCGTTTATC	CAATTATTTA	CAGTGACGAA	GGTAAAGAAG	AAACAGCCTA	TGTGACCGTC
AAACCCGACC	AATCTAAGTT	AGAGGTCAAA	GATACAACGA	TTTATGTTGG	TGATTTCGTGG
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AAAAATTGATG	TTCAGGGAAC	AGTGAATGTT	GATAAAATAG	GCGATTATGA	AATTGTCTAT
AAAAATGGCA	NAAAAGAAGC	GAAAGCAATC	GTTTCATGTCC	GTGATGACAG	TCAGTTAGAG
GTTAAAGATA	CAACGATTTA	TGTTGGTGAT	TCGTGGAAAC	CAGAAGATAA	TTTCGTTTCA
GCAACAGACA	AAACAGGCCA	AGACGTTCCG	TTTGAAAAAA	TCAGTGTTC	AGGTCAAGTT
GATACTAGCA	AAGCAGGCGT	TTATCCAATC	GTTTACAGTT	ACGAAGGTAA	AGAAGAAACA
GCTAATGTGA	CTGTCAAACC	CGACCAATCT	AAGTTAGAGG	TTAAAGATAC	AACGATTTAT
GTGGGCGATA	AATGGGAACC	AGAAGATAAT	TTCGTTTCAG	CAACAGACAA	AACAGGTCAA
GATGTCCCGT	TTGAAAAAAT	TGACGTTTCAG	GGAACAGTGA	ATGTTGATAA	AATAGGCGAT
TATGAAATTG	TCTATAAAAA	TGGCACAAAA	GAAGCGAAAG	CAATCGTTCA	TGTCCGTGAT
GACAGTCAGT	TAGAGGTCAA	AGATACAACA	ATTTATGTGG	GTGATAAATG	GGAAGCAGAA
GATAACTTCG	TTTCCGCGAC	AGACAAAAACA	GGTCAAGACG	TTCCGTTTGA	AAAAATTGAT
GTTACAGGGA	CAGTGAATGT	TGATAAAATA	GGCGATTATG	AAATTGTCTA	TAAAAATGGC
ACAAAAAGAAG	CGAAAGCAAT	CGTTTCATGTC	CGTGATGATA	GTCGTTTACA	AGTCAAGGAT
ACAACGATTT	ATGTCGGCGA	TTCNTGGANA	CCAGAAGNGA	ACTTTGTTTC	AGCNACAGAT
AAAAACAGGTC	AAGATGTCCC	ATTCGAAAAA	ATCACTGTT		

EF104-2 (SEQ ID NO:402)

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 ELLDSMSLAP IGGTEYSQTE VHRELNTTPV TATFQFAVGN TGYAPGSVYT VQLPEHLGYS
 TVSGEVTGIG ATWAVDAATK TLSITFNQRPV SDTSFKVELK SYLTTEAEPL IKIETPGKNK
 KTYSFDLYEQ VEPIQYNERT RTTGLDGEIF YNLDRTLTGN QTLELLTTET PGAVFGKQDN
 LEPQVFSYDV DINGQILPET QTLTPGKDY TLDNSLGR I AVTPNMMNQ KAYSLSINRT
 IYLESASDYN YLYSQYPTT KIGSISLKST TGTKQTTDFT AKTSQTSKVI ADREMRMSY
 ISFQSKGKYY VTIYGTLTET KVGQQIVLES TNGQEIKNPK FTAYGPLYEN VKLEDYFDIK
 TEGGKLTLTA TKDSYLRINI SDLTMDFDKK DINLSLSTPV IGPKNKAIQLV SDQYIEPISV
 VNPLNAETAW GNYDQNGAYS SRTTVSVMGS KEKPIQNLEI KVKHPNYLSL RATKEIFYFY
 KLGTDTYVTP TSDGSVIKFT TPITNEIQIP IGFNYVPDSL PKDKSIPVDT IPITMSAEGL
 TPVDTTVTN SKRGSERTLQ SSKNQFLVNA RNSFDSL SV RTKIPAGADV LFDIYDVSND
 QVDSIYPQYW DRGQYFDKPM TPNSPGYPTI TFDENTNSYT FDFGKTNKRY IIEYKNANGW
 IDVPTLYITG TAKEPQSNNN EGSASVSVQN EALDILSATQ AANPTLKNVT KTTVTTKNID
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 TIEYNTVSAN AGQIYTETTI DSETLNQMSA SKKKVTAPI TLKFSEGD AE GIVYLATATF
 YTHNVEDENQ AIAKVSFELI DNVHTATEF TTDEKGQYSF DAIMTG DYTL RVTNVPQEYS
 VDEEYLTGKA IKLVKGDNQL KIPLTKTIDH SRLQVKDSTI YVGDSWKPEE NFVSATDKTG
 QDVPFEKITV SGQVDNKKAG VYPIIYSDG KEETAYVTVK PDQSKLEVKD TTIYVGDSWK
 PEDNFVSATD KTGQDVPFEK IDVQGTVNVD KIGDYEIVYK NGXKEAKAIV HVRDDSQLEV
 KDTTIYVGDS WKPEDNFVSA TDKTGQDVVF EKITVSGQVD TSKAGVYPIV YSYEGKEETA
 NVTVPKPDQSK LEVKDTTIYV GDKWEPEDNF VSATDKTGQD VPFEKIDVQG TVNVDKIGDY
 EIVYKNGTKE AKAIVHVRDD SQLEVKDTTI YVGDKWEAED NFVSATDKTG QDVPFEKIDV
 QGTNVNDKIG DYEIVYKNGT KEAKAIVHVR DDSRLQVKDT TIYVGDSWXP EXNFVSATDK
 TGQDVPFEKI TV

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF104-3 (SEQ ID NO:403)

TGTAA CAACGACAGA AGCACAAACA
 GAGACCACTG ATACAGCAAA AAAAGAGGCA GAGTTATCGA ACTCAACACC ATCTTTACCT
 TTAGCAACAA CGACTACTTC AGAAATGAAT CAACCAACTG CAACAACCTGA ATCGCAAACC
 ACAGAGGCGA GCACAACAGC TTCCAGTGAT GCTGCTACAC CATCTGAACA ACAAAACAACG
 GAGGACAAGG ACACCTCACT TAATGAAAAA GCCCTGCCAG ATGTTCAAGC GCCAATTACA
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 ACGCAAACCT TGTTAACACC TGGCAAAGAT TATACATTAA GCGATAATTC ACTCGGGCGG
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 ACAATTTATT TAGAGAGTGC TTCGGACTAT AACTACTTAT ATTCGCAGCA GTATCCAACA
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 TTAAGTCCAG TTGATACGAC AGTAACTACT AATAGTAAGC GTGGTTCTGA ACGAACACTT
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 GTCCGTACAA AAATTCACGC TGGCGCCGAT GTTCTTTTTG ACATTTATGA TGTTTCAAAC
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 TTTGATGCCA TCATGACAGG TGATTATACT TTGCGAGTAA CGAATGTACC GCAGGAATAT
 TCCGTGGATG AAGAGTATTT GACAGGAAAA GCCATTAAAG TGGTCAAAGG AGACAACCAA
 CTAAAAATTC CATTAACGAA AACAATTGAT CACAGTCGTT TACAAGTCAA AGATTCAACG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GGCGTTTATC CAATTATTTA CAGTGACGAA GGTAAGAAG AAACAGCCTA TGTGACCGTC
AAACCCGACC AATCTAAGTT AGAGGTCAAA GATACAACGA TTTATGTTGG TGATTGCTGG
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GCAACAGACA AAACAGGCCA AGACGTTCCG TTTGAAAAAA TCACTGTTTC AGGTCAAGTT
GATACTAGCA AAGCAGGCGT TTATCCAATC GTTTACAGTT ACGAAGGTAA AGAAGAAACA
GCTAATGTGA CTGTCAAACC CGACCAATCT AAGTTAGAGG TTAAAGATAC AACGATTTAT
GTGGGCGATA AATGGGAACC AGAAGATAAT TTCGTTTCAG CAACAGACAA AACAGGTCAA
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TATGAAATTG TCTATAAAAA TGGCACAAAA GAAGCGAAAG CAATCGTTCA TGTCCGTGAT
GACAGTCAGT TAGAGGTCAA AGATACAACA ATTTATGTGG GTGATAAATG GGAAGCAGAA
GATAACTTCG TTTCCGCGAC AGACAAAACA GGTCAAGACG TTCCGTTTGA AAAAATTGAT
GTTTCAGGGA CAGTGAATGT TGATAAAATA GGCGATTATG AAATTGTCTA TAAAAATGGC
ACAAAAGAAG CGAAAGCAAT CGTTCATGTC CGTGATGATA GTCGTTTACA AGTCAAGGAT
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AAAACAGGTC AAGATGTCCC ATTC

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EF104-4 (SEQ ID NO:404)

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ELLDSMSLAP IGGTEYSQTE VHRELNTTPV TATFQFAVGN TGYAPGSVYT VQLPEHLGYS
TVSGEVTGIG ATWAVDAATK TLSITFNQRV SDTSFKVELK SYLTTEAEPL IKIETPGKNK
KTYSFDLYEQ VEPIQYNERT RTTGLDGEIF YNLDRTLGN QTLELLTET PGAVFGKQDN
LEPQVFSYDV DINGQILPET QLLTPGKDY TLSDNSLGR I AVTPNMNQ KAYSLSINRT
IYLESASDYN YLYSQQYPTT KIGSISLKST TGTKQTTDFT AKTSQTSKVI ADREMRSMSY
ISFQSKGKYY VTIYGTLTET KVGQQIVLES TNGQEIKNPK FTAYGPLYEN VKLEDYFDIK
TEGGKLTLTA TKDSYLRLNI SDLTMDFDKK DINLSLSTPV IGPNKAIQLV SDQYIEPISV
VNPLNAETAW GSYDQNGAYS SRTTVSVMGS KEKPIQNLEI KVKHPNYLSL RATKEIYFYY
KLGTDTYVTP TSDGSVIKFT TPITNEIQIP IGFNYVPDSL PKDKSIPVDT IPITMSAEG
TPVDTTVTN SKRGSERTLQ SSKNQFLVNA RNSDFSLSV RTKIPAGADV LFDIYDVSND
QVDSIYPQYW DRGQYFDKPM TPNSPGYPTI TFDENTNSYT FDFGKTNKRY IIEYKNANGW
IDVPTLYITG TAKEPQSNNN EGSASVSVQN EALDILSATQ AANPTLKNVT KTTVTTKNID
NKTHRVRKNT IELTPKGTTN AQIDLNSITV KGVPEDAYSL EKTNGAKVI FKDYTLTENI
TIEYNTVSAN AGQIYTETTI DSETLNQMSA SKKKVTTAPI TLKFSEGD AE GIVYLATATF
YTHNVEDENQ AIAKVSFELI DNVHTATEF TTDEKGQYSF DAIMTG DYTL RVTNVPQEYS
VDEEYLTGKA IKLVKGDNL KIPLT KTIDH SRLQVKDSTI YVGDSWKPEE NFVSATDKTG
QDVPFEKITV SGQVDNXXKAG VYPIIYSDEG KEETAYVTVK PDQSKLEVKD TTIYVGDSWK
PEDNFVSATD KTGQDVPFEK IDVQGTVNVD KIGDYEIVYK NGXKEAKAIV HVRDDSQLEV
KDTTIYVGDS WKPEDNFVSA TDKTGQDVFP EKITVSGQVD TSKAGVYPIV YSYEGKEETA
NVTVPDQSK LEVKDTTIYV GDKWEPEDNF VSATDKTGQD VPFEKIDVQG TVNVDKIGDY
EIVYKNGTKE AKAIVHVRDD SQLEVKDTTI YVGDKWEAED NFVSATDKTG QDVPFEKIDV
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TGQDVPF

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EF105-1 (SEQ ID NO:405)

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AGCACAGATG GGACGGATCC AGTAAATCCA GAAAATCCCG ATCCAGAAAA ACCAGTTCCA

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

CCAGTCGATC CAACGAATCC TGATGGACCT AATCCAGGTA CCCCTGGTCC ACTTTCCATC
 GATTATGCCT CAAGTTTGGG TTTTGGGAGT AATGAGATAT CGAATAAGGA TCAAACGTAT
 TTTGCCAGAG CGCAAACCTA TAGAAATCCA GATGGTTCAG CAAGTGAATT GGCAACTGCT
 AATTATGTAC AAGTAAGTGA TTTACGGGGA ACCAATGCTG GCTGGGTTTT AAAAGTGAAA
 CAAAATGGTC AATTTTCGTAA TGCAGAAACA TTACACAAAG AATTAACAGG CGCCACCGTC
 GCCTTTACTG AGCCCAGTGT TCGCTCAAAT GCGACGGACG TATTGCCGCC AACTGCTACC
 GCAAACATTC AATTAGATGC TCGGGGCGCA GAAACTGTTG TCATGCAAGC CCCAGAAAAG
 ACCGGCGCCG GAACGTGGAT CACGCTGTGG GGGCAAGCAG AAAAAGTGAC CGAAAAAAT
 CAACAAGGAC AGCAAGTAAA TGCCACAATC ACACGGGCAA TCTACTAAC TGTTCCTGGG
 AAAACCCCTA AGGATGCAGT ACAATATAAA ACAACATTGA CTTGGCTACT TTCAGATGTA
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EF105-2 (SEQ ID NO:406)

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 VDPTNPDGPN PGTPGPLSID YASSLDFGSN EISNKDQTYF ARAQTYRNP GSASELATAN
 YVQVSDLRGT NAGWVLKVKQ NGQFRNAETL HKELTGATVA FTEPSVRSNA TDVLPPTATA
 NIQLDAAGAE TVVMQAPEKT GAGTWITLWG QAEKVTEKNQ QGQVQVNAIT RAISLTVPGK
 TPKDAVQYKT TLTWLLSDVP VNNGGK

EF105-3 (SEQ ID NO:407)

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 AGCACAGATG GGACGGATCC AGTAAATCCA GAAATCCCCG ATCCAGAAAA ACCAGTTCGA
 CCAGTCGATC CAACGAATCC TGATGGACCT AATCCAGGTA CCCCTGGTCC ACTTTCCATC
 GATTATGCCT CAAGTTTGGG TTTTGGGAGT AATGAGATAT CGAATAAGGA TCAAACGTAT
 TTTGCCAGAG CGCAAACCTA TAGAAATCCA GATGGTTCAG CAAGTGAATT GGCAACTGCT
 AATTATGTAC AAGTAAGTGA TTTACGGGGA ACCAATGCTG GCTGGGTTTT AAAAGTGAAA
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 GCCTTTACTG AGCCCAGTGT TCGCTCAAAT GCGACGGACG TATTGCCGCC AACTGCTACC
 GCAAACATTC AATTAGATGC TCGGGGCGCA GAAACTGTTG TCATGCAAGC CCCAGAAAAG
 ACCGGCGCCG GAACGTGGAT CACGCTGTGG GGGCAAGCAG AAAAAGTGAC CGAAAAAAT
 CAACAAGGAC AGCAAGTAAA TGCCACAATC ACACGGGCAA TCTACTAAC TGTTCCTGGG
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EF105-4 (SEQ ID NO:408)

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 VDPTNPDGPN PGTPGPLSID YASSLDFGSN EISNKDQTYF ARAQTYRNP GSASELATAN
 YVQVSDLRGT NAGWVLKVKQ NGQFRNAETL HKELTGATVA FTEPSVRSNA TDVLPPTATA
 NIQLDAAGAE TVVMQAPEKT GAGTWITLWG QAEKVTEKNQ QGQVQVNAIT RAISLTVPGK
 TPKDAV

EF106-1 (SEQ ID NO:409)

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 AATCCCAATA ATTTAGGGGA TTTACCTGAG TATTTACGTT CAGTTGGTAT TAGACAAGAT
 GAAGGATTAT CAGAAAAAGA TTGGGCTGGA ACACGCGTTT ATGATCGAAA TGGGAATGAC
 TTAACAGATG AAAATCAAAA CCTATTACAT GCAATCAAAT TTGATGCAAC CACTAGTTTC
 TATGAATTTT TTGATAAAGA GACTGGAGAA TCAACAGGAG ATGAAGGAAC CTTCTTTATG
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 GGTGTATACC CACTTAGAAC TTTATACCAA GATACTTTTA CGTATAGACA GATGGGGAAA
 GATAAAAACG GAAATGATAT TGAAGTTTTT GTAGAAAACA AAGCAACCTC AGGACCAGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TATGGTCGTC CGCAGCCATA CCCCAATAAT CGTCCCAGAA CACTAGAATT CACGAATGGA
 CGCCGTGCCA TGACAGAACA AACAGGCCAG ATTGATGTAA ATCGACAAGG GGATGAAATT
 ATTGGTAAAA CTTCTTTTGA TGGGACACCG CAACTTCTTT GGAATGGCAC AAAAGTAGTG
 GATAAAGATG GCAATGACGT AACTTCGGCC AACCAAACT TTATCAGCTT AGCGAAATTT
 GACCAAGATA GCAGCAAATA TGAATTTTTC AATTTACAAA CTGGTGAAAC TCGTGCGGAC
 TATGGCTACT TTAAAGTAGG AAATCAAAAT AAATTCCGTG CCCATGTTTC CATTTGGAACC
 AATCGCTATG GCGCTGTCTT AGAGTTAACA GAATTGAATG ATAATCGTTT TACGTACACA
 CGAATGGGTA AAGATAACGA AGGAAACGAT ATCCAAGTCT ATGTGGAACA TGAACCATAC
 CAAGGAACTT TTAATCCTGA ATTTACCTTT TAA

EF106-2 (SEQ ID NO:410)

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 GLSEKDWAGT RYVDRNGNDL TDENQNLHA IKFDATTSFY EFFDKETGES TGDEGTFMT
 AGITDVSRV IISSETKNYQG VYPLRTLYQD TFTYRQMGKD KNGNDIEVFV ENKATSGPVY
 GRPQYPNNR PRTLEFTNGR RAMTEQTGQI DVNRQGEII GKTSFDGTPQ LLWNGTKVVD
 KDGNDVTSAN QNFISLAKFD QDSSKYEFFN LQTGETRGDY GYFKVGNQNK FRAHVSIGTN
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EF106-3 (SEQ ID NO:411)

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 GAAGGATTAT CAGAAAAAGA TTGGGCTGGA ACACGCGTTT ATGATCGAAA TGGGAATGAC
 TTAACAGATG AAAATCAAAA CCTATTACAT GCAATCAAAAT TTGATGCAAC CACTAGTTTC
 TATGAATTTT TTGATAAAGA GACTGGAGAA TCAACAGGAG ATGAAGGAAC CTCTTTTATG
 ACCGCTGGTA TTACAGATGT TTCCCGTCTT GTAATTATTT CTGAAACCAA AAATTATCAA
 GGTGTATACC CACTTAGAAC TTTATACCAA GATACTTTTA CGTATAGACA GATGGGGAAA
 GATAAAAACG GAAATGATAT TGAAGTTTTC GTAGAAAACA AAGCAACCTC AGGACCAGTT
 TATGGTCGTC CGCAGCCATA CCCCAATAAT CGTCCCAGAA CACTAGAATT CACGAATGGA
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EF106-4 (SEQ ID NO:412)

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 GRPQYPNNR PRTLEFTNGR RAMTEQTGQI DVNRQGEII GKTSFDGTPQ LLWNGTKVVD
 KDGNDVTSAN QNFISLAKFD QDSSKYEFFN LQTGETRGDY GYFKVGNQNK FRAHVSIGTN
 RYGAIVLELTE LNDNRFTYTR MGKDNEGNDI QVYVEHEPYQ GT

EF107-1 (SEQ ID NO:413)

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 CTTTATAGAG ACTATAGATT GAATTTTAC ATAGAAAGAA GGAGCAAGAT GAAGCGAGTA
 AATTGAAAA GATGGCTAGT TGTGGGTTA AGTTGTTCTT TGTTCATGGA TTCAGTGGTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GGTGTGACTG TGTTAGCGGA AACGATTACT GGGGCGACGG AGCAAGGAGT AGCAACATCT
CAGTCGAGTG ACGAAGCGAG CCAGACGACG CAAACAACCG AAGAGTCACA GGCAACGGTC
GCTAGTGAAG CGAAAACAGT ACCGCCACAG GAAACGGCAA GAATGCTTC TCGAGCGATT
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TTGTTTGATC CCGACCGAAT TACGATGGCG GTCAATCTTT CCACGTTTTC GTTTTATGAA
GAGAAATTAC AACGAACCCC CCTTGAGCCC ACCACTGTGA ATGGCGGAAA GTTACTGTCT
ATTCCAACGT CACCAGCTTT TAAATATGAT ACAAATAACC AGAATCCAAG TAATATTTAT
GGCGTTTCTG AAGTGTCTGT TACTATTCCT AAGGAGTATC AAAGCCTGGA CATTCGACCA
AGTACGTTTT ATACAGGAGA CACTACGCAA TATCCAGTGC CAACGTTTTT TCGGAACGTT
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GATGACAATG ACGATTTGCA TGTGGTCTAT GAAGAAGCAG TGATGAAAAC CTATACGTTG
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AAGCCAACGG CACTTGGGC GGCTGGCATC GGCGCACCCA ACACGATATT TGTACAAGGA
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ACGAGTCCTG ACGGCGACGG CTTTATTAGT ACCCGACAT TTGATTTTGG TAAACTAGCA
ATTTACAGGA GTAAGCAACA ATATGGTTTG AAGAAGGCCG CAGATTACTA CGGCAATGGC
ACTCGCAACC CTTATTTACG CCTGAATACT AGCCAAGCCA ATTGGAGTTT AACGGCCCAG
CTATCGCAAC CAAAATCAGC CACAGACAGC TTGCCAACA CGACCCGCTT GTTGCTAGGA
ACGGCCGCTG CTGCCAGCTT TACCGATTAC AACCACCAA CAGAAACCAG GACACCACTT
GGCAAGACCA GCACCGTGAC TTTAACCGCC GACAATACCG CAACAGCGGT GGTGCGAAAC
CAACAGTTCA CAGGCAGTGA CGTCTATCAG TTGGACTTCA CGTTTGCTAA CATCAAATA
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EF107-2 (SEQ ID NO:414)

MKRVN

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SEAKTVPPQE TARIASRAIG YSSVEGREIP FFFVEEDGTL FDPDRITMAV NLSTFSFYEE

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KLQRTPLEPT	TVNGGKLLSI	PTSPAIFYDT	NNQNPSNIYG	VSEVSFTIPK	EYQSLDIRPS
TFYTGDTTQY	PVPTVFANVG	GKVTNYVGAN	AETEELELTNE	KMPNKLTFGP	KKTFKYTVAT
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QDKKTIVTGE	DFTFTQEGTL	PERYTGSDGK	TYLFGWYK	NAKPSTLETT	KTPSYAVTYD
DNDDLHVVE	EAVMKYTLTP	AREALFGYVD	EQGNLINPAK	FKLSATMGES	DGATGEMTTF
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DKTKYPVPNE	VRRGIENPDN	IVSSLVGXXA	YNLTQKSATR	YTARRSYWXW	GPTKTLYSMS
IYSGTAGGNY	NLSTPDGTIY	YYLENRRVTE	HFVDESGAKI	TPPTGFTQGN	QLVVDSENYV
YTVAKALPKI	YQAGEKTYIF	QGWFKGKTKP	ATLKTITTPS	FTPTFNDDED	MTAVYQEAIP
TAELTLTGAV	DIENGATMD	YWEALLKNTG	EAPLTITIKI	PTATWAAGIG	APNTIFVQGT
GQNTKAFPVT	KEQWTTGAGV	SITLDQPLPA	GGQLKMNLLG	TAVTGNPGQV	LTADVEVTGN
FGSLTAKDTV	RIKDLQDEIT	SPDGDGFIST	PTFDGKLA	SGSKQYGLK	KAADYYNGNT
RNPYLRLNTS	QANWSLTAQL	SQPKSATDSL	PTTTRLLLTG	AAAASFTDYN	QPTETRTPLG
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VTGP					

EF107-3 (SEQ ID NO:415)

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GCTAGTGAAG	CGAAAACAGT	ACCGCCACAG	GAAACGGCAA	GAATTGCTTC	TCGAGCGATT
GGTTATTCTT	CTGTGGAAGG	GCGCGAGATT	CCCTTTTCTT	TTGTGGAGGA	AGACGGGACG
TTGTTTGATC	CCGACCGAAT	TACGATGGCG	GTCAATCTTT	CCACGTTTTT	GTTTTATGAA
GAGAAATTAC	AACGAACCCC	CCTTGAGCCC	ACCACTGTGA	ATGGCGGAAA	GTTACTGTCT
ATTCCAACGT	CACCAGCTTT	TAAATATGAT	ACAAATAACC	AGAATCCAAG	TAATATTTAT
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GGGGATAAAA	CCAAGTATCC	AGTACCAAT	GAAGTGCGCC	GTGGCATCGA	AAACCCCGAC
AACATTGTTA	GTAGTTTAGT	GGGAANCNCT	GCGTATAACT	TGACCCAAAA	AAGTGCCACA
CGCTATACTG	CCCGCCGTTT	TTACTGGANG	TGGGGCCCCA	CGAAGACACT	TTACTCAATG
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TATTATTACT	TAGAAAATCG	GCGGGTCACT	GAACATTTTG	TAGACGAAAG	TGGCGCAAAA
ATCACGCCAC	CAACTGGCTT	TACACAAGGA	AATCAGCTAG	TGGTGGACAG	TGAAAACATAT
GTCTACACTG	TCGCAAAAGC	TTTGCCGAAG	ATCTACCAAG	CTGGTGAAAA	AACCTATATC
TTCCAAGGCT	GGTTTAAAGG	CAAAACCAAG	CCAGCAACAT	TAAAGACGAC	AACGACCCCA
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CCCACCGCGG	AACATAACGTT	AACAGGTGCC	GTGACATAA	TCGAAAATGG	CGCCACAATG
GATTACTGGG	AGGCGCTACT	GAAGAACACA	GGCGAAGCGC	CGTTAACCAC	CATTAAAATC
AAGCCAACGG	CAACTTGGGC	GGCTGGCATC	GGCGCACCCA	ACACGATATT	TGTACAAGGA
ACGGGTCAAA	ACACCAAAGC	TTTTCTCTGC	ACCAAAGAAC	AATGGACGAC	CGGTGCAGGA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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GTGTCCATCA CGTTGGATCA GCCTTTACCA GCTGGCGGTC AATTAAAAAT GAACTTATTA
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ACGAGTCCTG ACGGCGACGG CTTTATTAGT ACCCCGACAT TTGATTTTGG TAAACTAGCA
ATTTCAAGAA GTAAGCAACA ATATGGTTTG AAGAAGGCCG CAGATTACTA CGGCAATGGC
ACTCGCAACC CTTATTTACG CCTGAATACT AGCCAAGCCA ATTGGAGTTT AACGGCCCAG
CTATCGCAAC CAAAATCAGC CACAGACAGC TTGCCAACAA CGACCCGCTT GTTGCTAGGA
ACGGCCGCTG CTGCCAGCTT TACCGATTAC AACCAACCAA CAGAAACCAG GACACCCTT
GGCAAGACCA GCACCGTGAC TTTAACCGCC GACAATACCG CAACAGCGGT GGTCCGAAAC
CAACAGTTCA CAGGCAGTGA CGTCTATCAG TTGGACTTCA CGTTTGCTAA CATCAAATA
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EF107-4 (SEQ ID NO:416)

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PTIDGIDMPA SQLKKLAIPQ KVTYTRPDDGT IVTYGPQEVs VEIPKYYQTI SISPTTAYTG
DKTKYPVPNE VRRGIENPDN IVSSLVGXXA YNLTKQK SATR YTARRSYWXW GPTKTLYSMS
IYSGTAGGNY NLSTPDGTIY YYLENRRVTE HFVDESGAKI TPPTGFTQGN QLVVDSENYV
YTVAKALPKI YQAGEKTYIF QGWFKGKTKP ATLKTITTPS FTPTFNDEDD MTAVYQEAIP
TAELTLTGAV DIIENGATMD YWEALLKNTG EAPLTTIKIK PTATWAAGIG APNTIFVQGT
GQNTKAFPV T KEQWTTGAGV SITLDQPLPA GGQLKMNLG TAVTGNPGQV LTADVEVTGN
FGSLTAKDTV RIKDLDEIT SPDGDGFIST PTFDFGKLAI SGSKQYGLK KAADYYNGT
RNPYLRLNTS QANWSLTAQL SQPKSATDSL PTTTRLLLG AAAASF TDYN QPTETRTPLG
KTSTVTLTAD NTATAVVANQ QFTGSDVYQL DFTFANIKLE VPANQGMAGQ QYQAAVTWNL
VTGP

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EF108-1 (SEQ ID NO:417)

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CAACGATTAG CAACCATGG CTTGTGTAGT TCTTTAGTAA TTAACGCCTT TTCTGGTG TG
ACGGCAGTTG CGGAAACCGT GACGATTGAA AGTAGTCCGA CCGCCGAAAG TAGTGCCAAG
GAAGAGACGC AAGCAAGTAG CGTGAAGGAA GAAACAACGA AAGCCAGTAC GGAAAATAGT
CAAGTAACAA CTGACACGAG TCAGGAAGAA GCAACGAAAAG AAGCGGAGAA AGAAGAACCG
CAAGCAGAAG TGAACAAGC AGAAACACCA ATCATTCCTA AACCAAAAAA AATCAATATG
AAGGCAACTT ATTCATTTTC TGCAGAACT TATCAGTTTG GATTTGTGAA TGAATCAGGT
CAATTAATAA ATCCAGATAT TATACCAATT ACGTATAGCT ATGCCAAAGG ATCATGGAAG
ACAGATGGTT ATAATCGAAA GTGGACTAGT ATGGTTCAAG GGAGTGCTTC AACCGTAGGA
AACTTAAAGA ATGTAATAAT GCCAGCAACT TCTGTAGTTA TGCCACCAGG ACCGTCATAT
GAAGGAAC TC AAGAGGTGTA CACAACTTT TCAATTCGCA TACCAAAATA TTATGCATCA
GCGAGTCTCT ACAATAGAGA AGGTAAAATT GATTCTACTT ATCCGTTACC TGCTATTGCA
CTAGCAGGTA CTAGACCGCT ATCTTTGACT CAAAGTAGTG TAATTAGTGC ATTGGCGCTG
ACCA GTAAAG GAGACAATGT TTATACACCA CGGGAACAT TTTTGGAGG AGATCCTGCA
GGTGTAAGT TTAATAATTT TTTGTATCGT ATAAATGACT TTGATGTGAA AGGTAATAAC
ATAGGTTATA AGACTGTGAG TAGCCCAATC TATTACCATC TGACCAACCG CCGTGTACC
GAAAAC TTTCG TAGATACAAG TGGCGCCAAA ATCACGCCAC CAAGTAATTT CACCCAAGGG
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ACCTACAAAG TTGGCACGAA ATCTTACCGA TTCAAAGGCT GGTACAAAGG GAAAACCAAA

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACCGAGCCTT TGGCCACCAC TAAACACCT AGCTATAAAG TCACGTATGA TGACAATGAT
 GATTTGACGG TGGTCTATGA GGAGTTTTC GGGTACGAGC TGCCTGCTTC GACCAATCAA
 TTTGGCTTTG TGGATGAAGC GACGAACAAA TTAATTGCC CCGACCAAGT GCAGATGAAG
 TATAATCTTA CTTTAAATGA AAATAATAAA AAAACAGTAA TGAGCAGTAA CTTAACGGGG
 ACAGATACAG CGACACTGAA AAACCTGTCC GTGCCTGTCA ACTATTTTGA ACAATATCGC
 GTCAATACGT TTTATGGCGC GAGTGACATT ACGTTTACAT TGCCCAAACG GTACAAATCA
 ATCAATATTA CCAAATCAGA TGGCAAAACC GACCCAGCTT TTCTCTTCC TAAAATCTAT
 AATATAGATC AAGTAGAAAT GTCACACATG CCTGTGACCA CTTATAACAA GTTGAAACAG
 CTGTCGGGCC AAACGTTTGG CTTTAATGCT TTAGCCGATC AACCTGAATT TTATACGAAA
 ACGTTATTTG GGACAGAGTC TGGCATCGAT GACCCAGTCA ATTATTATAC AATGAGTGGC
 CCTGTTTACT ATTATTTAGA AAACCGCAAA GTCACCGAGA ACTTCGTAGA CACCAACGGC
 GCTAAAACCT CACCGCCAAC AGGTTTCACC CAAGGTAAAA AAACGGTGTAG TACAAGCGAC
 GCCTACACTT TCAAACAAGC AGGCACCTTA CCAGACACTT ACACAACAGG CGGTAAGGACC
 TACAAGTTCA AAGGTTGGTA CAAAGGCAAG TCCATACTCA ACACATTGAC AACTACCAAA
 GCGCCAAGTT ATCAAGTGAC CTACGATGAC AATGATGATT TGAATGTGGT GTATGAAGAA
 GAAACAGTTA CGACAGTGTA TCCATCAGTC GATATGAACT TTGTGAATGA AAAAGGCGGG
 GCTTTCACAC CGGCGTTAAC TTTTAGTGGT AAGTACTATG CGCAAAGTAC GAGTGCCTAC
 TTAAGAACCG ATTTATATGA CGTGACCTCA AAAAATAATG GTAATGGGCA ATATACGGTA
 AGTATTAATA ATGGTAGTAT GCCATTGTCC CAAGAATTAT TGAAAAATA TAATAATGGA
 CAACCAATCA GTGCTACCAA CAGATTACAG TTTAATGTTG ATAAATTAGC CATCGACCAA
 CAACTAAAT ATGTTGACAG CATTCAAATTA GACACAGCTC AAAGTAGCAA TCTGAAATCC
 TATAGATATG TGTACACGAA CAATAGCTCA CTGGTTTTCG ACCCAAATGT AGCACCAGCA
 GAGGTTGACC TTAGTTCAGA ATCTCTTAAC TTGCTTAATT TTGATTGAGA TGGCACCTAT
 TTTCTAATG CAAATAATAG ACTTTTTTTAC ACGCATTTAG GATATAGTGG CACACCAGGA
 GTTAECTATC TTCTCGTAAT GTTTCTTTT AAGCCAAAC CTGCGGATAA GTCAAACTT
 GTCTACAAAG TCACTCGCAA ACAAGTCACC GAAACCTTCG TGGATGTCAA CGGTGCCAAA
 ATCACTGCAC CAACAGGCTT CACCAAGGT AaccaagTAC CAATGAACAG TAACACCTTC
 AAGTACACAG CGGCAAAAGC TTTACCAGCG ACGTATACTA CAGGTGGCAA AGTCTATACG
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 ACGTTCAATG CGACCTTTGA TGGCAATGAC GATATGACCG CCATGTATAA GGAAGAAATA
 CCAACAGCTA GTGTCACATT AACTCGACCA AAAGAAGTGA TTGATACGAA TACCAATGTA
 ATCTGGACAA CAACGATCAC GAATACTAGC AAAGCACCTT TACAAAATCT CACCTTGAAA
 AAAGGGCCCA ATTGGTCAGC TGGTCTGACG ATCCCGACCT TTATGGAAGT GACACCAGAA
 GGAGAAACGA CAAAATCAAT CCCAGTAAAT AGTACACTTT GGACAGAGGG GGTTCCTTTA
 CCAATGCGG TTCCTATCGG CAAAAAGTT TCAGTTGCTT TCACAACCTG CGCAACAGGG
 AAACCAAACA CTGTTTTGAA AGCAGAAGTT GTAGTATTTG GTGGTATTAA AGATAGTACA
 GTGGATAACT TCGTGAGAAT TCGTCCAAAT GATCAAGAAG TAGTCACACC AACGACCGAA
 GGCTTCATCA GTGTGCCAAC CTTCGACTTC GGCCAAGTGG GCGTTGCAGG AACTAAGCAA
 CAACACAGCT TGAACAAGC CGCGGATTAC TACGGTAACG GCACACGGAA TCCGTATCTG
 CGGATTAAGA AAACGCAACC CAATTGGAGC TTAACAGCGC AACTGTCACA ACCAAAATCA
 GCGACAGACA CCTTGCCCTAC AGCGACCCGC TTATTATTAG GGGCGGCGCC TGTCTCTAGC
 TTACCAATT ACAATCAACC AACCAGTTG AAAAATACGG TCGGTACCAC GAGTGCCATT
 AGCTTAACAG CCAACAACAC AGCAACGAGT ATTATTGCCA ACAAGCAATT CACAGGTAGT
 AATGTTTATC AGTTGGACTT CACCTTCAAT AATGTCAAAC TTGAAGTGCC AGCCAATCAA
 GGTGTTAAAG GGCAACAATA CAAGGCCGCA GTTACATGGA ACCTAGTTAC AGGTCCCTAA

EF108-2 (SEQ ID NO:418)

MKQTKWQ RLATIGLCSS LVINAFSGVT AVAETVTIES SPTAESSAKE
 ETQASSVKEE TTKASTENSQ VTTDTSQEEA TKEAEKEEPQ AEVEQAETPI IPKPKKINMK
 ATYSFSAETY QFGFVNESGQ LINPDIIPIT YSYAKGSWKT DGYNRKWTSM VQGSASTVGN
 LKNVIMPATS VVMPGPSYE GTQEVYTNFS IRIPKYASA SLYNREGKID STYPLPAIAL
 AGTRPLSLTQ SSVISALALT SKGDNVYTPR ETFFGGDPAG VKFTNFLYRI NDFDVKGNNI
 GYKTVSSPIY YHLTNRRVTE NFVDTSAGAKI TPPSNFTQGK QTVINSDPYT FQSGFLPET

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

YKVGTKSYRF	KGWYKGKTKT	EPLATTKTPS	YKVTYDDNDD	LTVVYEEFSG	YELPASTNQF
GFVDEATNKL	IAPDQVQMKY	NLTLNENNKK	TVMSSNLGT	DTATLKNLSV	PVNYFEQYRV
NTFYGASDIT	FTLPKRYKSI	NITKSDGKTD	PAFPLPKIYN	IDQVEMSHMP	VTYTNKLKQL
SGQTFGFNAL	ADQPEFYTKT	LFGTESGIDD	PVNYTMSGP	VYYYLENRKV	TENFVDTNGA
KITPPTGFTQ	GKKTIVITSDA	YTFKQAGTLP	DTYTTGGKTY	KFKGWYKGKS	ILNLTLT'TTKA
PSYQVTYDDN	DDLNVVYEEE	TVTTVYPSVD	MNFVNEKGGA	FTPALTFS GK	YYAQST SAYL
RTDLYDVTSK	NNGNGQYTVS	INNGSMPLSQ	ELLKKYNNGQ	PISATNRLQF	NVDKLAI DQQ
LKYVDSIQLD	TAQSSNLKSY	RYVYTNNSSL	VFDPNVAPAE	VDLSSES LNL	LNFDSDGTYF
SNANNRLFYT	HLGYS GTPGV	NYLLVMFLFN	AKPADKSKLV	YKVRTRKQVTE	NFVDVNGAKI
TAPTGTQGN	QVPMNSNTFK	YTAAKALPAT	YTTGGKVYTF	QGWYKGKTKP	STLNKTTTPT
FNATFDGND	MTAMYKEEIP	TASVTLTRPK	EVIDTNTNVI	WTTTITNTSK	APLQNLTLKK
GPNWSAGLTI	PTFMEVTPEG	ETTKSIPVNS	TLWTEGVPLP	NAVPIGKKVS	VAFTTRATGK
PNTVLKAEVV	VFGGIKDSTV	DNFVRIRPND	QEVVTPTEG	FISVPTFDFG	QVG VAGTKQQ
HSLKQAADYY	GNGTRNPYLR	IKKTQPNWSL	TAQLSQPKSA	TDSLPTATRL	LLGAAPVSSF
TNYNQPTLTK	NTVGT TSAIS	LTANNTATS I	IANKQFTGSN	VYQLDFTFNN	VKLEVPANQG
VKGQQYKAAV	TWNLV TGP				

EF108-3 (SEQ ID NO:419)

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GAAGAGACGC AAGCAAGTAG CGTGAAGGAA GAAACAACGA AAGCCAGTAC GGAAAATAGT

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CAAGCAGAAG TGGAACAAGC AGAAACACCA ATCATTCCCTA AACCAAAAAA AATCAATATG

AAGGCAACTT ATTCATTTTC TGCAGAACT TATCAGTTTG GATTTGTGAA TGAATCAGGT

CAATTAATAA ATCCAGATAT TATACCAATT ACGTATAGCT ATGCCAAAGG ATCATGGAAG

ACAGATGGTT ATAATCGAAA GTGGACTAGT ATGGTTCAAG GGAGTGCTTC AACC GTAGGA

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GAAGGAAGTC AAGAGGTGTA CACAACTTT TCAATTCGCA TACCAAAATA TTATGCATCA

GCGAGTCTCT ACAATAGAGA AGGTAAAATT GATTCTACTT ATCCGTTACC TGCTATTGCA

CTAGCAGGTA CTAGACCGCT ATCTTTGACT CAAAGTAGTG TAATTAGTGC ATTGGCGCTG

ACCAGTAAAG GAGACAATGT TTATACACCA CGGGAAACAT TTTTGGAGG AGATCCTGCA

GGTGTAAGT TACTAATTT TTTGTATCGT ATAAATGACT TTGATGTGAA AGGTAATAAC

ATAGGTTATA AGACTGTGAG TAGCCCAATC TATTACCATC TGACCAACCG CCGTGTACCC

GAAAAC'TTCG TAGATACAAG TGGCGCCAAA ATCACGCCAC CAAGTAATTT CACCCAAGGG

AAACAAACGG TCATTAACAG TGATCCTTAC ACGTTCCAAC AAAGTGGTTT TTTACCCGAG

ACCTACAAAG TTGGCACGAA ATCTTACCGA TTCAAAGGCT GGTACAAAGG GAAAACCAAA

ACCGAGCCTT TGGCCACCAC TAAAACACCT AGCTATAAAG TCACGTATGA TGACAATGAT

GATTTGACGG TGGTCTATGA GGAGTTTTC A GGTACGAGC TGCTTGCTTC GACCAATCAA

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TATAATCTTA CTTTAAATGA AAATAATAAA AAAACAGTAA TGAGCAGTAA CTTAACGGGG

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GTCAATACGT TTTATGGCGC GAGTGACATT ACGTTTACAT TGCCCAAACG GTACAAATCA

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CTGTGCGGCC AAACGTTTGG CTTTAATGCT TTAGCCGATC AACCTGAATT TTATACGAAA

ACGTTATTTG GGACAGAGTC TGGCATCGAT GACCCAGTCA ATTATTATAC AATGAGTGGC

CCTGTTTACT ATTATTTAGA AAACCGCAAA GTCACCGAGA ACTTCGTAGA CACCAACGGC

GCTAAAATCA CACCGCCAAC AGGTTTCACC CAAGGTAAAA AAACGGTGAT TACAAGCGAC

GCCTACACTT TCAAACAAGC AGGCACCTTA CCAGACACTT ACACAACAGG CCGTAAGACC

TACAAGTTCA AAGGTTGGTA CAAAGGCAAG TCCATACTCA ACACATTGAC AACTACCAAA

GCGCCAAGTT ATCAAGTGAC CTACGATGAC AATGATGATT TGAATGTGGT GTATGAAGAA

GAAACAGTTA CGACAGTGTA TCCATCAGTC GATATGAACT TTGTGAATGA AAAAGGCGGG

GCTTTCACAC CGGCGTTAAC TTTTAGTGGT AAGTACTATG CGCAAAGTAC GAGTGC GTAC

TTAAGAACCG ATTTATATGA CGTGACCTCA AAAAATAATG GTAATGGGCA ATATACGGTA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AGTATTAATA ATGGTAGTAT GCCATTGTCC CAAGAATTAT TGAAAAAATA TAATAATGGA
CAACCAATCA GTGCTACCAA CAGATTACAG TTTAATGTTG ATAAATTAGC CATCGACCAA
CAACTAAAAT ATGTTGACAG CATTCAATTA GACACAGCTC AAAGTAGCAA TCTGAAATCC
TATAGATATG TGTACACGAA CAATAGCTCA CTGGTTTTCG ACCCAAATGT AGCACCAGCA
GAGGTTGACC TTAGTTCAGA ATCTCTTAAC TTGCTTAATT TTGATTCAGA TGGCACCTAT
TTTTCTAATG CAAATAATAG ACTTTTTTAC ACGCATTTAG GATATAGTGG CACACCAGGA
GTTAACATATC TTCTCGTAAT GTTTCTTTTT AACGCCAAAC CTGCGGATAA GTCAAAACTT
GTCTACAAAG TCACTCGCAA ACAAGTCACC GAAAACCTCG TGGATGTCAA CGGTGCCAAA
ATCACTGCAC CAACAGGCTT CACCCAAGGT AACCAAGTAC CAATGAACAG TAACACCTTC
AAGTACACAG CGGCAAAAAGC TTTACCAGCG ACGTATACTA CAGGTGGCAA AGTCTATACG
TTCCAAGGGT GGTATAAAGG GAAAACCAAG CCAAGTACGT TGAACAAAAC AACAACCTCA
ACGTTCAATG CGACCTTTGA TGGCAATGAC GATATGACCG CCATGTATAA GGAAGAAATA
CCAACAGCTA GTGTCACATT AACTCGACCA AAAGAAGTGA TTGATACGAA TACCAATGTA
ATCTGGACAA CAACGATCAC GAATACTAGC AAAGCACCCCT TACAAAATCT CACCTTGAAA
AAAGGGCCCA ATTGGTCAGC TGGTCTGACG ATCCCGACCT TTATGGAAGT GACACCAGAA
GGAGAAACGA CAAAATCAAT CCCAGTAAAT AGTACACTTT GGACAGAGGG GGTTCTCTTTA
CCAAATGCCG TTCTATCGG CAAAAAAGTT TCAGTTGCTT TCACAACCTCG CGCAACAGGG
AAACCAACA CTGTTTGTGA AGCAGAAGTT GTAGTATTTG GTGGTATTAA AGATAGTACA
GTGGATAACT TCGTGAGAAT TCGTCCAAAT GATCAAGAAG TAGTCACACC AACGACCGAA
GGCTTCATCA GTGTGCCAAC CTTGCACTTC GGCCAAGTGG GCGTTGCAGG AACTAAGCAA
CAACACAGCT TGAAACAAGC CGCGGATTAC TACGGTAACG GCACACGGAA TCCGTATCTG
CGGATTAAGA AAACGCAACC CAATTGGAGC TTAACAGCGC AACTGTCACA ACCAAAATCA
GCGACAGACA GCTTGCTTAC AGCGACCCGC TTATTATTAG GGGCGGCGCC TGTCTCTAGC
TTTACCAATT ACAATCAACC AACCAGAGTG AAAAATACGG TCGGTACCAC GAGTGCCATT
AGCTTAACAG CCAACAACAC AGCAACGAGT ATTATTGCCA ACAAGCAATT CACAGGTAGT
AATGTTTATC AGTTGGACTT CACCTTCAAT AATGTCAAAC TTGAAGTGCC AGCCAATCAA
GGTGTTAAAG GGCAACAATA CAAGGCCGCA GTTACATGGA ACCTAGTTAC AG

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EF108-4 (SEQ ID NO:420)

VTIES SPTAESSAKE

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ATYSFSAETY QFGFVNESGQ LINPDIIPIT YSYAKGSWKT DGYNRKWTSM VQGSASTVGN
LKNVIMPATS VVMPGPSYE GTQEVYTNFS IRIPKYASA SLYNREGKID STYPLPAIAL
AGTRPLSLTQ SSVISALALT SKGDNVYTPR ETFFGGDPAG VKFTNFLYRI NDFDVKGNNI
GYKTVSSPIY YHLTNRRVTE NFVDTSAGAKI TPPSNFTQ GK QTVINS DPYT FQQSGFLPET
YKVGTSYRF KGWYKGKTKT EPLATTKTPS YKVTYDDNDD LTVVYEEFSG YELPASTNQF
GFVDEATNKL IAPDQVQMKY NLTLNENNNK TVMSSNLTGT DTATLKNLSV PVNYFEQYRV
NTFYGASDIT FTLPKRYKSI NITKSDGKTD PAFPLPKIYN IDQVEMSHMP VTTYNKLKQL
SGQTFGFNAL ADQPEFYTKT LFGTESGIDD PVNYYTMSGP VYYYLENRKV TENFVDTNGA
KITPPTGFTQ GKKTIVITSDA YTFKQAGTLP DTYTTGGKTY KFKGWYKGKS ILNTLTITTKA
PSYQVTYDDN DDLNVVYEEE TVTTVYPSVD MNFVNEKGGA FTPALTFSGK YYAQSTSAYL
RTDLYDVTSK NNGNGQYTVS INNGSMPLSQ ELLKKYNNQ PISATNRLQF NVDKLAIDQQ
LK YVDSIQLD TAQSSNLKSY RYVYTNNSSL VFDPNVAPAE VDLSSSESLNL LNFDSGTYF
SNANNRLFYT HLGYSCTPGV NYLLVMFLFN AKPADKSKLV YKVRKQVTE NFVDVNGAKI
TAPTGTQGN QVPMNSNTFK YTAALPAT YTTGGKVYTF QGWYKGKTKP STLNKTTTPT
FNATFDGND MTAMYKEEIP TASVTLTRPK EVIDTNTNVI WTTTTINTSK APLQNLTLKK
GPNWSAGLTI PTFMEVTPEG ETTKSIPVNS TLWTEGVPLP NAVPIGKVS VAFTRATGK
PNTVLKAEVV VFGGIKDS TV DNFVRIRPND QEVVTPTEG FISVPTDFG QVGVAGTKQQ
HSLKQAADYY GNGTRNPYLR IKKTQPNWSL TAQLSQPKSA TDSLPTATRL LLGAAPVSSF
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VKGQQYKAAV TWNLV T

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EF109-1 (SEQ ID NO:421)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 GAAATGAACC CAAGCATCAT AAATTCTCAA GAGGAAACAG AAACAACGTC CACTTCCTCA
 ACCTCCGATT CCACCACTGA AGTTTCTACA TCAGAAGTAA CAACTGTTAA TGATACAGAA
 NATAGTAGCG ACGTACTGAA ACTACTTTGG NAACATCACN AAGTAATGAG GACACACCTA
 TAG

EF109-2 (SEQ ID NO:422)

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EF109-3 (SEQ ID NO:423)

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 GAAACGGTGG CTTCAGAAAC ATCTCTAACG GAGCGACAAA TGAGTAGCGG TGCTACTGAA
 GAAATGAACC CAAGCATCAT AAATTCTCAA GAGGAAACAG AAACAACGTC CACTTCCTCA
 ACCTCCGATT CCACCACTGA AGTTTCTACA TCAG

EF109-4 (SEQ ID NO:424)

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EF110-1 (SEQ ID NO:425)

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 GACCCTGAGG ACAGAAGACA AGAAGTGGCA GATACAACCG AAGCGCCTTT TGCGTCAATC
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 GTTGGAACCA ATACAATTGT CACCAATAAT CATGTGGCTG AAAGTTTAA GAATGCCAAA
 GTATTAAATC CGAATGCCAA AGATGATGCT TGGTTTTATC CAGGTCGAGA TGGCAGTGCG
 ACACCATTTG GCAAATTCOA AGTGATTGAT GTAGCTTTT CCCCGAATGC GGATATTGCG
 GTAGTGACTG TCGGCAAACA AAACGATCGT CCAGATGGCC CAGAGTTGGG AGAAATTTTA
 ACGCCATTTG TTTTGAAAAA GTTTGAATCT TCAGATACCC ATGTCACAAT ATCAGGCTAT
 CCAGGTGAGA AAAACACAC ACAATGGTCT CATGAAAATG ATTTGTTTAC ATCTAACTTT
 ACAGACTTAG AAAATCCATT ACTATTTTAT GATATCGATA CAACCGCGG TCAATCTGGT
 TCACCAATCT ATAATGATCA GGTGAAGTA GTTGGTGTTT ATTCCAATGG CGGCATTAAG
 CAAACAGGAA ATCATGGTCA AAGACTAAAT GAAGTGAATT ATAACTTTAT TGTTAATCGA
 GTGAATGAAG AAGAAAATAA ACGTTTATCC GCTGTGCCAG CAGCGTAA

EF110-2 (SEQ ID NO:426)

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 PEDRRQEVAD TTEAPFASIG RIISPASKPG YISLGTGFVV GTNTIVTNNH VAESFKNAKV
 LNPNAKDDAW FYPGRDGSAT PFGKFKVIDV AFSPNADIAV VTVGKQND RP DGPELGEILT
 PFVLKKFESS DTHVTISGYP GEKNHTQWSH ENDLFTSNFT DLENPLLFYD IDTTGGQSGS
 PIYNDQVEVV GVHSNGGIQ TGNHGQRLNE VNYNFIVNRV NEEENKRLSA VPAA

EF110-3 (SEQ ID NO:427)

AG AGTATATCGT TCCTGCCGAA AGTCATTAC GACAAAAAAG ATCGTTACTG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GACCCTGAGG ACAGAAGACA AGAAGTGGCA GATACAACCG AAGCGCCTTT TGC GTCAATC
 GGAAGAATCA TTTCCCCTGC CAGTAAACCA GGCTATATTT CTTTAGGAAC AGGCTTTGTT
 GTTGGAACCA ATACAATTGT CACCAATAAT CATGTGGCTG AAAGTTTTAA GAATGCCAAA
 GTATTAAATC CGAATGCCAA AGATGATGCT TGGTTTTATC CAGGTCGAGA TGGCAGTGCG
 ACACCATTTC GCAAATTCAA AGTGATTGAT GTAGCTTTTT CCCC GAATGC GGATATTGCG
 GTAGTGACTG TCGGCAACAA AAACGATCGT CCAGATGGCC CAGAGTTGGG AGAAATTTTA
 ACGCCATTTC TTTTGAAAAA GTTTGAATCT TCAGATACCC ATGTCACAAT ATCAGGCTAT
 CCAGGTGAGA AAAACCACAC ACAATGGTCT CATGAAAATG ATTTGTTTAC ATCTAACTTT
 ACAGACTTAG AAAATCCATT ACTATTTTAT GATATCGATA CAACCGCGG TCAATCTGGT
 TCACCAATCT ATAATGATCA GGTTGAAGTA GTTGGTGTC ATTCCAATGG CGGCATTAAG
 CAAACAGGAA ATCATGGTCA AAGACTAAAT GAAGTGAATT ATAACTTTAT TGTTAATCGA
 GTGAATGAAG AAGAAAATAA ACGTTTATCC GCTGTGCCAG CAGCGT

EF110-4 (SEQ ID NO:428)

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PEDRRQEVAD TTEAPFASIG RIISPASKPG YISLGTGFVV GTNTIVTNNH VAESFKNAKV
 LNPNAKDDAW FYPGRDGSAT PFGKFKVIDV AFSPNADIAV VTVGKQND RP DGPELGEILT
 PFVLKKFESS DTHVTISGYP GEKNHTQWSH ENDLFTSNFT DLENPLLFYD IDTTGGQSGS
 PIYNDQVEVV GVHSNGGIKQ TGNHGQRLNE VNYNFIVNRV NEEENKRLSA VPAA

EF111-1 (SEQ ID NO:429)

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 AAAAAGGGAT AACTCCATT TGGCATAGTC CTTGCTGATA ATAAATCAGT GTATAAAGCG
 CTATCATTTT ATAGGAGGGG TTTTATGAAG GGTTTATCAA AAAAGAAACG GGTGTCTACT
 TGGTTAGCGT TAGGAATCAC CGTAGTCAGC TGTTTTGCGT TAAGCAGGGA AGTGCAAGCA
 AGTGTTGAAA GAACAAAAGT TGATGAATTT GCAAATGTTT TAGATGTGAG TGCATCACCA
 ACCGAACGGA CGAATGGCGT ATACGATACC AATTATTTTA ATAATTTTTT TGATTTAGGT
 GCATGGCATG GCTACTATTT ACCTGAAAAA AGCAATAAAG AGCTACTGGG TGGTTTTGCG
 GGGCCATTGA TTATTGCGGA AGAATATCCA GTAAACTTGG CGGCAAGTTT AAACAAATTA
 ACGGTCAAAA ATAAAAAAC GGGAGAAACC TATGATTTAA GCCAAAGCAA CCGCATGGAC
 CTGTCTTATT ATCTGGGCG CCTAGAGCAA ACCTATGAAT TAGACGATTT AACGATTCAT
 TTAGCTTTAA TTTTGTGTCAG CAATCGAAGC GCGCTTATCC AAACGACACT TGAAAACACT
 GGTGAAGAGC CCTGTGCACT TGGAGCAAGC TGGACAGGTG CGGCTTTTGA CAAAATTCOA
 GAGGGAACGG AAACCTTAGA TATTGGCACT CGTTTAACTG CTAAAGACAA TGACATTCOA
 GTGAATTTTG GTGAAGTCAG AGAAACGTGG AATTATTTTG CTACGAAAGA CACAAAATAT
 ACGATTCATC ATGCGGATAA AGTTTCAACA AAAATTGATA ATCGGAATTA TACAGCAACC
 GCTGAACCAA TTGAATTGAA GCCTAAACAA ACGTACAACA CCTATACGAC AGAAAGCTAT
 ACTTTTACAA AAGAAGAAGA GGCAAAGGAA CAACAACAAG CACCCGAATA TACCAAAAAT
 CGGCGCGCCT ATTTCAAAGA GAACAAGCAA AGATGGCAAG GATATCTAGA TAAAACGTTT
 GATCAAAAAGA AAACAGCAGA ATTTCTTGAA TATCAAAATG CGCTAGTCAA ATCGATTGAA
 ACGATTAATA CCAATTGGCG AAGTGCGGCA GGTGCCTTTT AGCATGACGG GATTGTTCCG
 TCCATGTCTT ATAAATGGTT TATTGGTATG TGGGCTTGGG ATTCGTGGAA AGCGGATGTA
 GCAACGGCTG ATTTTAATCC TGAGTTAGCT AAAAATAATA TGCGGGCCTT GTTTGATTAT
 CAAATTCAAA AAGATGATAC CGTACGTCCA CAAGATGCAG GAGCGATCAT TGATGCTGTC
 TTTTACAATC AAGACAGTGC GCGTGGTGGT GAAGGTGGCA ACTGGAATGA ACGAAATTC
 AAACCACCAT TGGCTGCATG GGCAGTTTGG CATATTTATC AAGAAACCAA AGATAAGGAA
 TTTTAAAAG AAATGTATCC CAACTTGTG GCTTATCATA ATTGGTGGTA TACCAACAGA
 GACCACAATA AAAATGGGAT AGCAGAATAT GGAAGCATGG TCAGTGATGC TCACTGGCAA
 AAAGACGACA AGGATCAAAT CATTAAGAT AAAAATGGCC ACCTAAAGTG GATGATGATG
 CTGTTATTGA AGCAGCCGCG TGGGAAAGTG GCATGGATAA CGCTACACGG TTTGACAAAG
 AAGGTGTGGG CAAAGCGCAC GTTGGAGTTA AAGTTTTTGA AAACAAAAT AAAGGAAAAG
 TAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF111-2 (SEQ ID NO:430)

MKG LSKKKRVSTW

LALGITVWSC FALSREVQAS VERTKVDEFA NVLDVSASPT ERTNGVYDTN YFNNFSDLGA
 WHGYLPEKS NKELLGGFAG PLIIAEEYPV NLAASLNKLT VKNKKTGETY DLSQSNRMDL
 SYYPGRLEQT YELDDLTIHL ALIFVSNRTA LIQTTLENTG EEPLSLGASW TGAVFDKIQE
 GTETLDIGTR LTAKDNDIQV NFGEVRETWN YFATKDTKYT IHHADKVSTK IDNRNYTATA
 EPIELKPKQT YNTYTTESYT FTKEEEAKEQ QQAPEYTKNA ARYFKENKQR WQGYLDKTFD
 QKKTAEFPEY QNALVKSJET INTNWRSAAG AFKHDGIVPS MSYKWFIMGW AWDSWKADVA
 TADFNPELAK NNMRALFDYQ IQKDDTVRPQ DAGAIIDAVF YNQDSARGGE GGNWNERNNSK
 PPLAAWAVWH IYQETKDKEF LKEMYPKLVA YHNWWTNRD HNKNGLAEYG SMVSDAHWQK
 DDKDQIIKDK NGHLKWMML LLKQPRGKVA WITLHGLTKK VWAKATLELK FLKTKIKEK

EF111-3 (SEQ ID NO:431)

TGATGAATTT GCAAATGTTT TAGATGTGAG TGCATCACCA
 ACCGAACGGA CGAATGGCGT ATACGATACC AATTATTTTA ATAATTTTTC TGATTTAGGT
 GCATGGCATG GCTACTATTT ACCTGAAAAA AGCAATAAAG AGCTACTGGG TGGTTTTGCG
 GGGCCATTGA TTATTGCGGA AGAATATCCA GTAAACTTGG CGGCAAGTTT AAACAAATTA
 ACGGTCAAAA ATAAAAAAC GGGAGAAACC TATGATTTAA GCCAAAGCAA CCGCATGGAC
 CTGTCTTATT ATCCTGGGCG CCTAGAGCAA ACCTATGAAT TAGACGATTT AACGATTCAT
 TTAGCTTTAA TTTTGTCTAG CAATCGAACG GCGCTTATCC AAACGACACT TGAAAACACT
 GGTGAAGAGC CTTGTCTACT TGGAGCAAGC TGGACAGGTG CGGTCTTTGA CAAAATTCAA
 GAGGGAACGG AAACCTTAGA TATTGGCACT CGTTTAACTG CTAAAGACAA TGACATTCAA
 GTGAATTTTG GTGAAGTCAG AGAAACGTGG AATTATTTTG CTACGAAAGA CACAAAATAT
 ACGATTCATC ATGCGGATAA AGTTTCAACA AAAATTGATA ATCGGAATTA TACAGCAACC
 GCTGAACCAA TTGAATTGAA GCCTAAACAA ACGTACAACA CCTATACGAC AGAAAGCTAT
 ACTTTTACAA AAGAAGAAGA GGCAAAGGAA CAACAACAAG CACCCGAATA TACCAAAAAT
 GCGGCGCGCT ATTTCAAAGA GAACAAGCAA AGATGGCAAG GATATCTAGA TAAAACGTTT
 GATCAAAAGA AAACAGCAGA ATTTCTTGAA TATCAAAATG CGCTAGTCAA ATCGATTGAA
 ACGATTAATA CCAATTGGCG AAGTGCAGCA GGTGCCTTTA AGCATGACGG GATTGTTCCG
 TCCATGTCTT ATAAATGGTT TATTGGTATG TGGGCTTGGG ATTCGTGGAA AGCGGATGTA
 GCAACGGCTG ATTTTAATCC TGAGTTAGCT AAAAATAATA TGCGGGCCTT GTTTGATTAT
 CAAATTCAAA AAGATGATAC CGTACGTCCA CAAGATGCAG GAGCGATCAT TGATGCTGTC
 TTTTACAATC AAGACAGTGC GCGTGGTGGT GAAGGTGGCA ACTGGAATGA ACGAAATTCT
 AAACCACCAT TGGCTGCATG GGCAGTTTGG CATATTTATC AAGAAACCAA AGATAAGGAA
 TTTTAAAAG AAATGTATCC CAACTTGTG GCTTATCATA ATTGGTGGTA TACCAACAGA
 GACCACAATA AAAATGGGAT AGCAGAATAT GGAAGCATGG TCAGTGATGC TCACTGGCAA
 AAAGACGACA AGGATCAAAT CATTAAGATG AAAAATGGCC ACCTAAAGTG GATGATGATG
 CTGTTATTGA AGCAGCCGCG TGGGAAAGTG GCATGGATAA CGCTACACGG TTTGACAAAG
 AAGGTGTGGG CAAAGGCGAC GTTGGAGTTA AAGTT

EF111-4 (SEQ ID NO:432)

DEFA NVLDVSASPT ERTNGVYDTN YFNNFSDLGA

WHGYLPEKS NKELLGGFAG PLIIAEEYPV NLAASLNKLT VKNKKTGETY DLSQSNRMDL
 SYYPGRLEQT YELDDLTIHL ALIFVSNRTA LIQTTLENTG EEPLSLGASW TGAVFDKIQE
 GTETLDIGTR LTAKDNDIQV NFGEVRETWN YFATKDTKYT IHHADKVSTK IDNRNYTATA
 EPIELKPKQT YNTYTTESYT FTKEEEAKEQ QQAPEYTKNA ARYFKENKQR WQGYLDKTFD
 QKKTAEFPEY QNALVKSJET INTNWRSAAG AFKHDGIVPS MSYKWFIMGW AWDSWKADVA
 TADFNPELAK NNMRALFDYQ IQKDDTVRPQ DAGAIIDAVF YNQDSARGGE GGNWNERNNSK
 PPLAAWAVWH IYQETKDKEF LKEMYPKLVA YHNWWTNRD HNKNGLAEYG SMVSDAHWQK
 DDKDQIIKDK NGHLKWMML LLKQPRGKVA WITLHGLTKK VWAKATLELK

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF117-1 (SEQ ID NO:433)

TAATTCGATG GAGAAGGTGG TTTAGTGAAA AGATTTTCAT TTTTTTTACT AATTTTACTT
 GCTTTAACAG GTTGTAATC CGGTGAAAAA GAATTTGATG AAGAATCTCT TCAAAATCTA
 AAGGAAACGN CACAGTCTTA NTCAGAAACA GAATTACAAA ATGGTGACGT TCGTTTAAAT
 GAATATATTT CTTTGAAAGG GGAGATTGTT GAGAGTGACA GTCGTTCCAG TTTAATAAAA
 AAAGGTGATC GTTTTATTTT GAAAAGTGGT TCTAGTAAAT ATCAAGTTTN TAATGAGCAA
 AAGAAAAAAT TGAAGATTGG TGACGAAGTG ACAGTTTACG GAGAATATTA CGGCTTTTTG
 AAAGGGACAT TAATTGAAAG TGAGGAGAAT CATGATTCAG CCACGAATTA G

EF117-2 (SEQ ID NO:434)

VKR FSFFLLILLA LTGCKSKEKE FDEESLQNLK ETXQXSETE LQNGDVRLNE
 YISLKGEIVE SDSRSSLIKK GDRFILKSGS SKYQVXNEQK KKLKIGDEVT VYGEYYGFLK
 GTLIESEENH DSATN

EF117-3 (SEQ ID NO:435)

TG AAGAATCTCT TCAAAATCTA
 AAGGAAACGN CACAGTCTTA NTCAGAAACA GAATTACAAA ATGGTGACGT TCGTTTAAAT
 GAATATATTT CTTTGAAAGG GGAGATTGTT GAGAGTGACA GTCGTTCCAG TTTAATAAAA
 AAAGGTGATC GTTTTATTTT GAAAAGTGGT TCTAGTAAAT ATCAAGTTTN TAATGAGCAA
 AAGAAAAAAT TGAAGATTGG TGACGAAGTG ACAGTTTACG GAGAATATTA CGGCTTTTTG
 AAAGGGACAT TAATTGAAAG TGAGGAGAAT CATGATTCAG CCACGAA

EF117-4 (SEQ ID NO:436)

EESLQNLK ETXQXSETE LQNGDVRLNE YISLKGEIVE SDSRSSLIKK GDRFILKSGS
 SKYQVXNEQK KKLKIGDEVT VYGEYYGFLK GTLIESEENH DSATN

EF118-1 (SEQ ID NO:437)

TGAGGGGGAA AAAGTGTGTT AAAAAGAAAA GTGGGGATTG TCGCAGGCGT TTTCTGTTC
 GCTTTGTAC TGACAGGTTG TGGCAAAAGT GCGAAAGATG AGTTCATTCA AGGAATCGGC
 AATCANAACG CACAAGAATC TGGGGTTTGN GATTTCTCTA TGTCATTAG TGACATGAAA
 TTTTCACAAG AAGATGGTGC ACAAACGAAT CCTATGATTG GGATGCTCAT CACGCAAATC
 AAAGACGCAT CGCTTCTG GGAAGATTCA AGTAGATGCC AAAAAAGAAA AAGCATTCAA
 CTTAGAGATG AAATTAAAAG CGATGGGAAT GGATGTACCG ATTTCAATTG TTGGATCGTT
 AGATAA

EF118-2 (SEQ ID NO:438)

VLKRKV GIVAGVFCSA LLLTGCGKSA KDEFIQGIGN XNAQESGVXD FSMSISDMKF
 SQEDGAQTNP MIGMLITQIK DASLGEDSS RCQKRKSIQL RDEIKSDGNG CTDFIGWIVR

EF118-3 (SEQ ID NO:439)

GAAAGATG AGTTCATTCA AGGAATCGGC
 AATCANAACG CACAAGAATC TGGGGTTTGN GATTTCTCTA TGTCATTAG TGACATGAAA
 TTTTCACAAG AAGATGGTGC ACAAACGAAT CCTATGATTG GGATGCTCAT CACGCAAATC
 AAAGACGCAT CGCTTCTG GGAAGATTCA AGTAGATGCC AAAAAAGAAA AAGCATTCAA
 CTTAGAGATG AAATTAAAAG CGATGGGAAT GGATGTACCG ATTTCAATTG TTGGATCGTT
 AGAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

EF118-4 (SEQ ID NO:440)

KDEFIQGIGN XNAQESGVXD FSMSISDMKF SQEDGAQTNP MIGMLITQIK DASLSGEDSS
RCQKRKSIQL RDEIKSDGNG CTDFIGWIVR

EF119-1 (SEQ ID NO:441)

TAAAGAATAC CGAGTAAAT TTTCGGAAGG CTTTTTTTCA AAAATTGTAT ATGCAAAAGA
AGTGCAACGG AAAGGAGCTC GGAAATCGTG AATAAGCTAC CTTTACTTAT TTTATTGTTA
GGCGGAGTGT TGCTTGTTAG TGGCTGTCAA AGCCATAAGG AAGAAAACAA GTCTAGTAAA
GTATCGACAG AAGAAACGAC AGTGATTGAA ACAGTAGCAA GGGAACAATC GAAGGAATCG
TTTACGAGTG AAGCAACTAA AAAACAGACA GAAACAACGA AATTAGAAGA ACCAGATCAT
GTAAAGCTTC TAGAAGCTTA TGGAAATGCG TATGCGAACT TTACAAGTAT TAATGATCGC
AATGAAAAGC TAAAGCCCCCT CATGACTGAA AAATGTATCA AAAAAAATGG AATTGATGTT
AAAACCTGGAG TAGCGTTAGT TTCCGTAGGA AAGGTTACAA CGATTTATAA AAATGATCAA
CATGAATATG CTTTACTTTT GGATTGTGAA CAAAATGGAA CGCAGACACG AGTGTTACTT
TTGGCTAAGG TGAAGAACAA TAAAATTTCT GAAATGACCT ATAATTCAGT TAAGCAAGAG
TATTAG

EF119-2 (SEQ ID NO:442)

VN KLPLLLLLG GVLLVSGCQS HKEENKSSKV STEETTVIET VAREQSKESF TSEATKKQTE
TTKLEEPDHV KLEAYGNAY ANFTSINDRN EKLKPLMTEK CIKKNIDVK TGVALVSVGK
VTIYKNDQH EYALLLDCEQ NGTQTRVLLL AKVKNNKISE MTYNSVKQEY

EF119-3 (SEQ ID NO:443)

AGAAAACAA GTCTAGTAAA
GTATCGACAG AAGAAACGAC AGTGATTGAA ACAGTAGCAA GGGAACAATC GAAGGAATCG
TTTACGAGTG AAGCAACTAA AAAACAGACA GAAACAACGA AATTAGAAGA ACCAGATCAT
GTAAAGCTTC TAGAAGCTTA TGGAAATGCG TATGCGAACT TTACAAGTAT TAATGATCGC
AATGAAAAGC TAAAGCCCCCT CATGACTGAA AAATGTATCA AAAAAAATGG AATTGATGTT
AAAACCTGGAG TAGCGTTAGT TTCCGTAGGA AAGGTTACAA CGATTTATAA AAATGATCAA
CATGAATATG CTTTACTTTT GGATTGTGAA CAAAATGGAA CGCAGACACG AGTGTTACTT
TTGGCTAAGG TGAAGAACAA TAAAATTTCT GAAATGACCT ATAATTCAGT TAAGCAAGAG
TAT

EF119-4 (SEQ ID NO:444)

ENKSSKV STEETTVIET VAREQSKESF TSEATKKQTE TTKLEEPDHV KLEAYGNAY
ANFTSINDRN
EKLKPLMTEK CIKKNIDVK TGVALVSVGK VTIYKNDQH EYALLLDCEQ NGTQTRVLLL
AKVKNNKISE MTYNSVKQEY

EF120-1 (SEQ ID NO:445)

TGAATAGGCG TGAAAAGGG AATGTTAGCG TTTTTTGTGCG TGCTAGCGGT TTTATCATTA
ACTGCTTGTC GGGAACCAAA AGNAAAGAAA GTAACCGCTT CAACGGAGGC ATCCTCTAAA
GTTGAAGAGA CGAATGAAAA AACGAGTGAA ACAATTGATA AGACAAACGA ACAAGCGAGC
AGCAGTGTG AGTCTAACGA ATCAGTGAAA AATGAAGAGC CGACAGCTGA TGGAAACAA
AGTCAGCTAA CTGTAGCTGA TTTAGATACT ACAGCGATTA ATGCTGGCGA TTTTACTACT
TTAGTTGGAA TATGGAAAAA TGGTAAAGGA GAGAGTTTGA TCATTCATCC TGATGGTAGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACAAATACCG GAGGAATGAT TACGAAGGAT TCACCTACTG ATGAGTCGCG ACCAATTACA
AGCTTAAGTA TTAGGTGGGG GCCTACTGGT GCTGCGCTAT TATTATATAA AATTGGTGT

EF120-2 (SEQ ID NO:446)

VKKGMLAF FVVLAVLSLT ACREPKXKKV TASTEASSKV EETNEKTSET IDKTNEQASS
SVESNESVKN EEPTADGNNS QLTVADLDTT AINAGDFTTL VGIWKNGKGE SLIIHPDGST
NTGGMITKDS PTDESRPITS LSIRWGPTGA ALLLYKIGV

EF120-3 (SEQ ID NO:447)

AAGAAA GTAACCGCTT CAACGGAGGC ATCCTCTAAA
GTTGAAGAGA CGAATGAAAA AACGAGTGAA ACAATTGATA AGACAAACGA ACAAGCGAGC
AGCAGTGTGCG AGTCTAACGA ATCAGTGAAA AATGAAGAGC CGACAGCTGA TGGAAACAAT
AGTCAGCTAA CTGTAGCTGA TTTAGATACT ACAGCGATTA ATGCTGGCGA TTTTACTACT
TTAGTTGGAA TATGGAAAAA TGGTAAAGGA GAGAGTTTGA TCATTTCATCC TGATGGTAGT
ACAAATACCG GAGGAATGAT TACGAAGGAT TCACCTACTG ATGAGTCGCG ACCAATTACA
AGCTTAAGTA TTAGGTGGGG GCCTACTGGT GCTGCGCTAT TATTATATAA AATTGGTGT

EF120-4 (SEQ ID NO:448)

KKV TASTEASSKV EETNEKTSET IDKTNEQASS
SVESNESVKN EEPTADGNNS QLTVADLDTT AINAGDFTTL VGIWKNGKGE SLIIHPDGST
NTGGMITKDS PTDESRPITS LSIRWGPTGA ALLLYKIGV

EF121-1 (SEQ ID NO:449)

TGAAACACAA GGAGGAAATT TGTGAAAAAG TTGAGCTTTA AAAAAGTGAA GTGGGGCATG
CATTTTTTAA TGGCTGTTGC GTTGATAGCG CCAAGTGTTA CTAGTACGGC ATATGCAGTA
GAAACAACGA GTCAACAAAG TTCAGAAGCA GTAACAAGTA CCACCGATTC AAGTAGAAAA
CAAGAACCAG TCATTACACA GGAAACAACA GACATCAAAC AAGAAGCACC AAATCAGGCT
ACGAGTGACA TGTCTAAGCA GTCACAAGAA ACCACAGCAC CAACAGAGAC GACGAATTTA
GAAACGTCAA TCGCTGAAAA AGAAGAAACG AGCACGCCGC AAAAAATAAC AATTTTAGGT
ACGTCAGATG TTCATGGTCA ATTATGGAAT TGGTCTTATG AAGATGATAA AGAACTACCA
GTTGGTTTTGT CCCAAGTAAG TACAGTCGTT AACCAAGTCC GGGCACAAAA CCCAGCAGGC
ACCGTTTTAA TTGATAATGG CGACAATATT CAAGGCACTA TTTTAACAGA TGACTTGTAT
AATAAAGCGC CTTTAGTGAA TGAAAAGACC CATCCAATGA TCACCGCCAT GAATGTGATG
AAGTATGATG CAATGGTTTT GGGAAATCAT GAGTTTAATT TTGGTTTACC GTTAATCAAA
AAAATTCAAC AAGAAGCCAC TTTTCCAATC TTGTCTGCGA ATACCTACAA TAAGGAAGAT
GGTCTTCGTT TTGTTGAAGG GACTACCACG AAGGAACTTG ATTTTAATCA AGATGGGCAG
CCAGATTTAA AAGTTGGGAT TATCGGCTTA ACAATTCCGC ACATTCCTTT GTGGGATGGC
CCTCGTGTTA CTTGCTTAA TTTTTTACCT TTGAAAGAAG AAGCAGAAAA AGCAGTTACT
GAGTTGAAAG CTAACGATCA GGCTGACATT ATTGTTGCCT CGATTCATGC GGGACAACAA
AATAGTGATC CGGCTGCCAG TGCCGACCAA GTAATTGAAA ATGTCGCGGG GATTGATGCG
TATATTCTGG GTCATGACCA CCTTCTTTT ACCAAGCAAG GAGCAGCGCC GAATGGAAAA
ACTGTACCGG TAGGGGGACC GAAAGATACG GGGACAGAAG TTGTCAAAAT TGATCTTTCA
GTTGCTAAAA ATGCCGATAA GTGGGAAGTG CAAGAAGGTA CAGCAACGAT TGTACCAACA
ACGAATGTTT CAGCAGATGA AGCAGTTAAG GCAGCGACAA AAGAATACCA TGAAAAAACG
CGAGCGTTTA TTCAGGAGGA GATCGGCACA GCAACAGCTG ATTTTTTACC AAAACAAGAA
ATTAAAGGAA TTCCCGAAGC ACAATTACAA CCAACAGCGA TGATTTCTTT AATTAATAAC
GTTCAAAAAG AAGTAACGGG CGCACAATTA AGTGCGGCAG CGCTGTTTAA ATACGACAGT
AAATTACCTG CGGGGAAGAT TTCTATGCC ACGATTTTTG ATATCTACAA ATACCCGAAT
ACCTTAGTGA GTGTTCCCAT TAACGGTGAA AACTTACTGA AGTATTTAGA AAAACAAGGG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCGTACTATA ACCAAACACA GCCAGATGAT TTGACCATTA GTTTTAATCC AAACATTCGT
 GTATATAACT ATGACATGAT TTCTGGAGTG GACTACAAGA TTGACATTTC AAAACCAGTG
 GGTGAACGAA TTGTAGATGC GAAAATTGAC GGCCAACCGC TGGATCCTGC CAAAGAATAT
 ACGATTGCTA TGAATAATTA TCGTTACGGC GGTTTAGCTA GCCAAGGGAT TCAAGTAGGG
 GAACCTATTA AAAATTCTGA TCCAGAAACC TTACGAGGAA TGATTGTTGA TTATATTAAG
 AAAAAAGGAA CTCTTGATCC AGAACAAGAA ATCGAACGAA ATTGGTCAAT TATTGGGACA
 AATTTTGATG AAAAAATGGCG TGCCAAAGCA ATCGAATTAG TGAATGACGG CACTCTTCAA
 ATTCCGACTT CTCTTGATGG ACGTACACCA AACGCCGCCG CTATTACGAA ACAAGATGTC
 CGTAATTGCGG GCTTTGATTT AGATAATGCA TATACCATTA TGCACACAAA TGACGTTTAT
 GGCCGACTAG AAGCAGGGAA AGGCGAATTA GGTATGGCGC GTCTAAAAAC CTTTAAAGAC
 CAAGAAAACC CAACCTTGAT GGTGGATGCA GGGGATGTTT TCCAAGGATT ACCAATCTCC
 AATTTCTCCA AAGGCGCGGA TATGGCCAAA GCAATGAAATG AAGTTGGTTA TGTATGCCATG
 GCGGTGGGAA ATCACGAGTT TGATTTTGGT TTAGAGATTG CACTAGGTTA TAAAGACCAA
 CTGAATTTTC CGATTTTATC TAGTAATACG TATTACAAAG ATGGCAGTGG ACGGGTTTTT
 GATCCGTATA CAATCGTAGA AAAATCCGGG AAAAAGTTTG CCATTGTAGG TGTGACGACC
 CCAGAAACAG CAACGAAAAC ACACCCGAAA AACGTAGAGA AGGTGACATT TAAAGACCCG
 ATTCCAGAAG TAGAAGCAGT GATTAAGGAA ATTAAAGAGA AGTACGCGGA TATNCAAGCT
 TTCGTGGTTA CTGGGCATTT AGGCGTAGAT GAAACGACGC CGCATATCTG GCGTGGTGAT
 ACGCTAGCAG AAACCCCTAG TCAAACATAT CCTGAGTTAG ATATCACTGT GATTGATGGA
 CATTCGCATA CAGCCGTCGA AAGTGGCAAA CGTTATGGCA AAGTGATCTA TGCTCAAACA
 GGTAATTATT TAAATAATGT TGGGATCGTC ACAGCACCAG AGAGTGAACC AACTAAGAAA
 ACAACAAAAT TGATTTACGC AGCAGAGCTG CTAGAATTGC CAGAAAACCC GGCAGTTAAA
 GCCATCGTTG ATGAAGCAG TACGAATTTT AACGCTGAAA ATGAAAAAGT AATTGTCGAT
 TATATTCCAT TCACATTGGA TGGACAACGA GAAAATGTGC GCACACGAGA GACCAACTTA
 GGGAATTTGA TTGGTGATGC GATTATGTCA TATGGCCAAG ACGCGTTTAG CCAACCTGCT
 GATTTTGCAG TAACTAATGG TGGCGGCATT CGCGCTGATA TTAAACAAGG GCCAATTAAA
 GTTGGGGATG TCATTGCTGT GTTACCTTTT GGCAATAGCA TTGCGCAAAT TCAAGTAACC
 GGCGCCCAAG TTAAAGAAAT GTTTGAAATG TCTGTTCTGT CGATTCCACA AAAAGATGAG
 AATGGCACAA TTTTACTAGA TGATGCTGGC CAACCAAAAC TTGGCGCAAA TGGTGGTTTC
 CTACATGTTT CAAGCTCCAT TCGTATCCAC TATGATTCCA CAAAACCAGG TACTCGCTTG
 GCTAGTGACG AAGGCAATGA AACAGGACAA ACGATTGTCT GTAGTCGCGT ATTAGGAATA
 GAAATTAAAA ATCGGCAAAAC ACAAAGTTT GAACCATTTG ATGAGAAGAA ACAATACCGG
 ATGGCTACCA ATGATTCTT AGCTGCTGGT GGTGATGGTT ACGATATGCT AGGTGGTGAA
 CGAGAAGAAG GGATTTCACT AGATTCTGTC TTAATTGAAT ACTTGAAAAG TGCAACCAGC
 TTGCGGTTGT ATCGTGACG AACGACGATT GATTTAGCAC AATATAAAGA ACCATTCCCA
 GGCGAACGAA TTGTTTCTAT TTCGGAAGAA GCTTACAAAG AGTTAATCGG TGGAGGAGAG
 ACGCCAAAAC CAGATCCAA ACCAGACCCG AAACCAACAC CAGAAACACC AGTAGCAACC
 AATAAACAAA ACCAAGCGGG AGCAAGACAG AGCAATCCAT CCGTAACAGA GAAGAAAAAG
 TATGGCGGCT TTTTACCTAA AACGGGTACA GAAACAGAAA CGCTTGCAAT ATATGGTTTA
 CTGTTCTGTTG GACTTTCTTC TTCTGGCTGG TATATTTATA AACGACGTAA CAAAGCTAGT
 TAG

EF121-2 (SEQ ID NO:450)

VKKL SFRKVKWGMH FLMAVALIAP SVTSTAYAVE TTSQQSSEAV TSTTDSSRKQ
 EPVITQETTD IKQEAPNQAT SDSVKQSQET TAPTETTNLE TSIAEKEETS TPQKITILGT
 SDVHGQLWNW SYEDDKELPV GLSQVSTVVN QVRAQNPAQT VLIDNGDNIQ GTILTDLLYN
 KAPLVNEKTH PMITAMNVMK YDAMVLGNHE FNFGLPLIKK IQQEATFPIL SANTYNKEDG
 LRFVEGTTTK ELDFNQDGQP DLKVGIIIGLT IPHIPLWDGP RVTSLNFLPL KEEAEKAVTE
 LKANDQADII VASIHAGQQN SDPAASADQV IENVAGIDAY ILGHDHLSFT KQGAAPNGKT
 VPVGGPKDTG TEVVKIDLSV AKNADKWEVQ EGTATIVPTT NVPADAEVKA ATKEYHEKTR
 AFIQEEIGTA TADFLPKQEI KGIPEAQLQP TAMISLINNV QKEVTGAQLS AAALFKYDSK
 LPAGKISYAT IFDIYKYPNT LVSVPINGEN LLKYLEKQGA YYNQTQPDLL TISFNPNIQV
 YNYDMISGVD YKIDISKPVG ERIVDAKIDG QPLDPAKEYT IAMNNYRYGG LASQGIQVGE

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PIKNSDPETL	RGMIVDYIKK	KGTLDPEQEI	ERNWSIIGTN	FDEKWRAKAI	ELVNDGTLQI
PTSPDGRTPN	AAAITKQDVR	NAGFDLDNAY	TIMHTNDVHG	RLEAGKGELG	MARLKTFKDQ
ENPTLMVDAG	DVFQGLPISN	FSKGADMAKA	MNEVGVDAMA	VGNHEFDGFL	EIALGYKDQL
NFPILSSNTY	YKDGSGRVFD	PYTIVEKSGK	KFAIVGVVTP	ETATKTHPKN	VEKVTFKDPI
PEVEAVIKEI	KEYYADXQAF	VVTGHLGVDE	TTPHIWRGDT	LAETLSQTYT	ELDITVIDGH
SHTAVESGKR	YGKVIYAQTG	NYLNNVGIVT	APESEPTKKT	TKLISAAELL	ELPENPAVKA
IVDEARTNFN	AENEKVIVDY	IPFTLDGQRE	NVRTRETNLG	NLIGDAIMSY	GQDAFSQPAD
FAVTNGGGIR	ADIKQGPIKV	GDVIAVLPG	NSIAQIQVTG	AQVKEMFEMS	VRSIPQKDEN
GTILLDDAGQ	PKLGANGGFL	HVSSSIRIHY	DSTKPGTRLA	SDEGNETGQT	IVGSRVLGIE
IKNRQTQKFE	PLDEKKQYRM	ATNDFLAAGG	DGYDMLGGER	BEGISLDSVL	IEYLKSATSL
RLYRAATTID	LAQYKEPFP	ERIVSISEEA	YKELIGGGET	PKPDPKDPK	PTPETPVATN
KQNQAGARQS	NPSVTEKKKY	GGFLPKTGTE	TETLALYGLL	FVGLSSSGWY	IYKRRNKAS

EF121-3 (SEQ ID NO:451)

ACAAAG TTCAGAAGCA GTAACAAGTA CCACCGATTC AAGTAGAAAA

CAAGAACCAG TCATTACACA GGAAACAACA GACATCAAAC AAGAAGCACC AAATCAGGCT

ACGAGTGACA GTGTCAAGCA GTCACAAGAA ACCACAGCAC CAACAGAGAC GACGAATTTA

GAAACGTCAA TCGCTGAAAA AGAAGAAACG AGCACGCCGC AAAAAATAAC AATTTTAGGT

ACGTCAGATG TTCATGGTCA ATTATGGAAT TGGTCTTATG AAGATGATAA AGAACTACCA

GTTGGTTTTGT CCCAAGTAAG TACAGTCGTT AACCAAGTCC GGGCACAAAA CCCAGCAGGC

ACCGTTTTAA TTGATAATGG CGACAATATT CAAGGCACTA TTTTAACAGA TGACTTGTAT

AATAAAGCGC CTTTAGTGAA TGAAAAGACC CATCCAATGA TCACCGCCAT GAATGTGATG

AAGTATGATG CAATGGTTTT GGGAAATCAT GAGTTTAATT TTGGTTTACC GTTAATCAAA

AAAATTCAAC AAGAAGCCAC TTTTCCAATC TTGTCTGCGA ATACCTACAA TAAGGAAGAT

GGTCTTCGTT TTGTTGAAGG GACTACCACG AAGGAACTTG ATTTTAATCA AGATGGGCAG

CCAGATTTAA AAGTTGGGAT TATCGGCTTA ACAATTCCGC ACATTCCCTT GTGGGATGGC

CCTCGTGTTA CTTCGCTTAA TTTTTTACCT TTGAAAGAAG AAGCAGAAAA AGCAGTTACT

GAGTTGAAAG CTAACGATCA GGCTGACATT ATTGTTGCCCT CGATTTCATGC GGGACAACAA

AATAGTGATC CGGCTGCCAG TGCCGACCAA GTAATTGAAA ATGTCGCGGG GATTGATGCG

TATATTCCTGG GTCATGACCA CCTTCTTTTT ACCAAGCAAG GAGCAGCGCC GAATGGAAAA

ACTGTACCGG TAGGGGGACC GAAAGATACG GGGACAGAAG TTGTCAAAAT TGATCTTTCA

GTGCTAAAA ATGCCGATAA GTGGGAAGTG CAAGAAGGTA CAGCAACGAT TGTACCAACA

ACGAATGTTT CAGCAGATGA AGCAGTTAAG GCAGCGACAA AAGAATACCA TGAAAAAACG

CGAGCGTTTA TTCAGGAGGA GATCGGCACA GCAACAGCTG ATTTTTTACC AAAACAAGAA

ATTAAAGGAA TTCCCGAAGC ACAATTACAA CCAACAGCGA TGATTTCTTT AATTAATAAC

GTTCAAAAAG AAGTAACGGG CGCACAATTA AGTGCGGCAG CGCTGTTTAA ATACGACAGT

AAATTACCTG CGGGGAAGAT TTCTTATGCC ACGATTTTGT ATATCTACAA ATACCCGAAT

ACCTTAGTGA GTGTTCCCAT TAACGGTGAA AACTTACTGA AGTATTTAGA AAAACAAGGG

GCGTACTATA ACCAAACACA GCCAGATGAT TTGACCATTA GTTTTAATCC AAACATTCGT

GTATATAACT ATGACATGAT TTCTGGAGTG GACTACAAGA TTGACATTTT AAAACCAGTG

GGTGAACGAA TTGTAGATGC GAAAATTGAC GGCCAACCGC TGGATCCTGC CAAAGAATAT

ACGATTGCTA TGAATAATTA TCGTTACGGC GGTTTAGCTA GCCAAGGGAT TCAAGTAGGG

GAACCTATTA AAAATTCTGA TCCAGAAACC TTACGAGGAA TGATTGTTGA TTATATTAAG

AAAAAAGGAA CTCTTGATCC AGAACAAGAA ATCGAACGAA ATTGGTCAAT TATTGGGACA

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ATTCCGACTT CTCTGATGG ACGTACACCA AACGCCC

EF121-4 (SEQ ID NO:452)

QSSEAV TSTTDSSRKQ

EPVITQETTD IKQEAPNQAT SDSVKQSQET TAPTETTNLE TSIAEKEETS TPQKITILGT

SDVHGQLWNW SYEDDKELPV GLSQVSTVVN QVRAQNPAGT VLIDNGDNIQ GTILTDDLYN

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

KAPLVNEKTH	PMITAMNVMK	YDAMVLGNHE	FNFGPLPLIKK	IQQEATFPIL	SANTYNKEDG
LRFVEGTTTK	ELDFNQDGQP	DLKVGIIIGLT	IPHIPLWDGP	RVTSNLNPL	KEEAEKAVTE
LKANDQADII	VASIHAGQQN	SDPAASADQV	IENVAGIDAY	ILGHDHLSFT	KQGAAPNGKT
VPVGGPKDTG	TEVVKIDLSV	AKNADKWEVQ	EGTATIVPTT	NVPADEAVKA	ATKEYHEKTR
AFIQEEIGTA	TADFLPKQEI	KGIPEAQLQP	TAMISLINNV	QKEVTGAQLS	AAALFKYDSK
LPAGKISYAT	IFDIYKYPNT	LVSVPINGEN	LLKYLEKQGA	YYNQTPDDL	TISFNPNIHV
YNYDMISGVD	YKIDISKPVG	ERIVDAKIDG	QPLDPAKEYT	IAMNNYRYGG	LASQGIQVGE
PIKNSDPETL	RGMIVDYIKK	KGTLDPQEIE	ERNWSIIGTN	FDEKWRAKAI	ELVNDGTLQI
PTSPDGRTPN	A				

EF122-1 (SEQ ID NO:453)

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GAAACAACGA	GTCACAAAG	TTCAGAAGCA	GTAACAAGTA	CCACCGATTC	AAGTAGAAAA
CAAGAACCAG	TCATTACACA	GGAAACAACA	GACATCAAAC	AAGAAGCACC	AAATCAGGCT
ACGAGTGACA	GTGTCAAGCA	GTCACAAGAA	ACCACAGCAC	CAACAGAGAC	GACGAATTTA
GAAACGTCAA	TCGCTGAAAA	AGAAGAAACG	AGCACGCCGC	AAAAAATAAC	AATTTTAGGT
ACGTCAGATG	TTTATGGTCA	ATTATGGAAT	TGGTCTTATG	AAGATGATAA	AGAACTACCA
GTTGGTTTTGT	CCCAAGTAAG	TACAGTCGTT	AACCAAGTCC	GGGCACAAAA	CCCAGCAGGC
ACCGTTTTTAA	TTGATAATGG	CGACAATATT	CAAGGCACTA	TTTTAACAGA	TGACTTGTAT
AATAAAGCGC	CTTTAGTGAA	TGAAAAGACC	CATCCAATGA	TCACCGCCAT	GAATGTGATG
AAGTATGATG	CAATGGTTTT	GGGAAATCAT	GAGTTTAATT	TTGGTTTACC	GTTAATCAAA
AAAATTCAAC	AAGAAGCCAC	TTTTCCAATC	TTGTCTGCGA	ATACCTACAA	TAAGGAAGAT
GGTCTTCGTT	TTGTTGAAGG	GACTACCACG	AAGGAACTTG	ATTTTAATCA	AGATGGGCAG
CCAGATTTTAA	AAGTTGGGAT	TATCGGCTTA	ACAATTCCGC	ACATTCCCTT	GTGGGATGGC
CCTCGTGTTA	CTTCGCTTAA	TTTTTTTACCT	TTGAAAGAAG	AAGCAGAAAA	AGCAGTTACT
GAGTTGAAAG	CTAACGATCA	GGCTGACATT	ATTGTTGCCT	CGATTTCATG	GGGACAACAA
AATAGTGATC	CGGCTGCCAG	TGCCGACCAA	GTAATTGAAA	ATGTCGCGGG	GATTGATGCG
TATATTCTGG	GTCTAGACCA	CCTTTCTTTT	ACCAAGCAAG	GAGCAGCGCC	GAATGGAAAA
ACTGTACCGG	TAGGGGGACC	GAAAGATACG	GGGACAGAAG	TTGTCAAAAT	TGATCTTTCA
GTTGCTAAAA	ATGCCGATAA	GTGGGAAGTG	CAAGAAGGTA	CAGCAACGAT	TGTACCAACA
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CGAGCGTTTA	TTCAGGAGGA	GATCGGCACA	GCAACAGCTG	ATTTTTTACC	AAAACAAGAA
ATTAAAGGAA	TTCCCGAAGC	ACAATTACAA	CCAACAGCGA	TGATTCTTTT	AATTAATAAC
GTTCAAAAAG	AAGTAACGGG	CGCACAAATTA	AGTGCGGCAG	CGCTGTTTAA	ATACGACAGT
AAATTACCTG	CGGGGAAGAT	TTCTATGACC	ACGATTTTTG	ATATCTACAA	ATACCCGAAT
ACCTTAGTGA	GTGTTCCCAT	TAACGGTGAA	AACTTACTGA	AGTATTTAGA	AAAACAAGGG
GCGTACTATA	ACCAAACACA	GCCAGATGAT	TTGACCATT	GTTTAAATCC	AAACATTCGT
GTATATAACT	ATGACATGAT	TTCTGGAGTG	GACTACAAGA	TTGACATTTT	AAAACCAGTG
GGTGAACGAA	TTGTAGATGC	GAAAATTGAC	GGCCAACCGC	TGGATCCTGC	CAAAGAATAT
ACGATTGCTA	TGAATAATTA	TCGTTACGGC	GGTTTAGCTA	GCCAAGGGAT	TCAAGTAGGG
GAACCTATTA	AAAATTCTGA	TCCAGAAACC	TTACGAGGAA	TGATTGTTGA	TTATATTAAG
AAAAAAGGAA	CTCTTGATCC	AGAACAAGAA	ATCGAACGAA	ATTGGTCAAT	TATTGGGACA
AATTTTGATG	AAAAATGGCG	TGCCAAAGCA	ATCGAATTAG	TGAATGACGG	CACTCTTCAA
ATTCCGACTT	CTCCTGATGG	ACGTACACCA	AACGCCGCCG	CTATTACGAA	ACAAGATGTC
CGTAATGCGG	GCTTTGATTT	AGATAATGCA	TATACCATT	TGCACACAAA	TGACGTTTAT
GGCCGACTAG	AAGCAGGGAA	AGGCCAATTA	GGTATGGCGC	GTCTAAAAAC	CTTTAAAGAC
CAAGAAAACC	CAACCTTGAT	GGTGGATGCA	GGGGATGTTT	TCCAAGGATT	ACCAATCTCC
AATTTCTCCA	AAGGCGCGGA	TATGGCCAAA	GCAATGAATG	AAGTTGGTTA	TGATGCCATG
GCGGTGGGAA	ATCACGAGTT	TGATTTTGGT	TTAGAGATTG	CACTAGGTTA	TAAAGACCAA
CTGAATTTTC	CGATTTTATC	TAGTAATACG	TATTACAAAG	ATGGCAGTGG	ACGGGTTTTT
GATCCGTATA	CAATCGTAGA	AAAATCCGGG	AAAAAGTTTG	CCATTGTAGG	TGTGACGACC

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CCAGAAACAG CAACGAAAAC ACACCCGAAA AACGTAGAGA AGGTGACATT TAAAGACCCG
ATTCCAGAAG TAGAAGCAGT GATTAAAGGAA ATTAAAGAGA AGTACGCGGA TATNCAAGCT
TTCGTGGTTA CTGGGCATTT AGGCGTAGAT GAAACGACGC CGCATATCTG GCGTGGTGAT
ACGCTAGCAG AAACCCCTAG TCAAACATAT CCTGAGTTAG ATATCACTGT GATTGATGGA
CATTGCGATA CAGCCGTCGA AAGTGGCAAA CGTTATGGCA AAGTGATCTA TGCTCAAACA
GGTAATTATT TAAATAATGT TGGGATCGTC ACAGCACCAG AGACTGAACC AACTAAGAAA
ACAAACAAAT TGATTTTCAGC AGCAGAGCTG CTAGAATTGC CAGAAAACCC GGCAGTTAAA
GCCATCGTTG ATGAAGCAG TACGAATTTT AACGCTGAAA ATGAAAAAGT AATTGTCGAT
TATATTCCAT TCACATTGGA TGGACAACGA GAAAATGTGC GCACACGAGA GACCAACTTA
GGGAATTTGA TTGGTGATGC GATTATGTCA TATGGCCAAG ACGCGTTTAG CCAACCTGCT
GATTTTGCAG TAACTAATGG TGGCGGCATT CGCGCTGATA TTAAACAAGG GCCAATTAAA
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GGCGCCCAAG TTAAAGAAAT GTTTGAAATG TCTGTTTCGTT CGATTCCACA AAAAGATGAG
AATGGCACAA TTTTACTAGA TGATGCTGGC CAACCAAAAC TTGGCGCAAA TGGTGGTTTC
CTACATGTTT CAAGCTCCAT TCGTATCCAC TATGATTCCA CAAAACCAGG TACTCGCTTG
GCTAGTGACG AAGGCAATGA AACAGGACAA ACGATTGTCT GTAGTCGCGT ATTAGGAATA
GAAATTAAAA ATCGGCAAAAC ACAAAGTTT GAACCATTTG ATGAGAAGAA ACAATACCGG
ATGGCTACCA ATGATTCTCT AGCTGCTGGT GGTGATGGTT ACGATATGCT AGGTGGTGAA
CGAGAAGAAG GGATTTCACT AGATTCTGTC TTAATTGAAT ACTTGAAAAG TGCAACCAGC
TTGCGGTTGT ATCGTGCAGC AACGACGATT GATTTAGCAC AATATAAAGA ACCATTCCCA
GGCGAACGAA TTGTTTCTAT TTCGGAAGAA GCTTACAAAG AGTTAATCGG TGGAGGAGAG
ACGCCAAAAC CAGATCCAAA ACCAGACCCG AAACCAACAC CAGAAACACC AGTAGCAACC
AATAACAAA ACCAAGCGGG AGCAAGACAG AGCAATCCAT CCGTAACAGA GAAGAAAAAG
TATGGCGGCT TTTTACCTAA AACGGGTACA GAAACAGAAA CGCTTGCATT ATATGGTTTA
CTGTTTCGTTG GACTTCTTTC TTCTGGCTGG TATATTTATA AACGACGTAA CAAAGCTAGT
TAG

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EF122-2 (SEQ ID NO:454)

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VKKL SFKKVKWGMH FLMAVALIAP SVTSTAYAVE TTSQQSSEAV TSTTDSSRKQ
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SDVHGQLWNH SYEDDKELPV GLSQVSTVVN QVRAQNPAGT VLIDNGDNIQ GTILTDDLNY
KAPLVNEKTH PMITAMNVMK YDAMVLGNHE FNFGLPLIKK IQQEATFPIL SANTYNKEDG
LRFVEGTTTK ELDFNQDGQP DLKVGIIGLT IPHIPLWDGP RVTSLNFLPL KEEAEKAVTE
LKANDQADII VASIHAGQQN SDPAASADQV IENVAGIDAY ILGHDHLSFT KQGAAPNGKT
VPVGGPKDTG TEVVKIDLSV AKNADKWEVQ EGTATIVPTT NVPADAEVKA ATKEYHEKTR
AFIQEEIGTA TADFLPKQEI KGIPEAQLQP TAMISLINNV QKEVTGAQLS AAALFKYDSK
LPAGKISYAT IFDIYKYPNT LVSVPINGEN LLKYLEKQGA YYNQTQPDLL TISFNPNIHV
YNYDMISGVD YKIDISKPVG ERIVDAKIDG QPLDPAKEYT IAMNNYRYGG LASQGIQVGE
PIKNSDPETL RGMIVDYIKK KGTLDPQEIE ERNWSIIGTN FDEKWRKAI ELVNDGTLQI
PTSPDGRTPN AAATKQDVR NAGFDLDNAY TIMHTNDVHG RLEAGKGELG MARLKTFKDQ
ENPTLMVDAG DVFQGLPISN FSKGADMAKA MNEVGYDAMA VGNHEFDGFL EIALGYKDQL
NFPILSSNTY YKDGSGRVFD PYTIVEKSGK KFAIVGVTPP ETATKTHPKN VEKVTFKDPI
PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIWRGDT LAETLSQTYP ELDITVIDGH
SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APESEPTKKT TKLISAAELL ELPENPAVKA
IVDEARTNFN AENEKVIDY IPFTLDGQRE NVRTRETNLG NLIGDAIMSY GQDAFSQPAD
FAVTNGGGIR ADIKQGPICK GDVIAVLPFG NSIAQIQVTG AQVKEMFEMS VRSIPQKDEN
GTILLDDAGQ PKLGANGGFL HVSSSIRIHY DSTKPGTRLA SDEGNETGQT IVGSRVLGIE
IKNRQTQKFE PLDEKKQYRM ATNDFLAAGG DGYDMLGGER EEGISLDSVL IEYLKSATSLS
RLYRAATTID LAQYKEPFPG ERIVSISEEA YKELIGGET PKPDPKDPK PTPETPVATN
KQNQAGARQS NPSVTEKKKY GGFLPKTGTE TETLALYGLL FVGLSSSGWY IYKRRNKAS

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EF122-3 (SEQ ID NO:455)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TG AAAAATGGCG TGCCAAAGCA ATCGAATTAG TGAATGACGG CACTCTTCAA
 ATTCCGACTT CTCCTGATGG ACGTACACCA AACGCCGCCG CTATTACGAA ACAAGATGTC
 CGTAATGCGG GCTTTGATTT AGATAATGCA TATACCATTG TGCACACAAA TGACGTTTCAT
 GGCCGACTAG AAGCAGGGAA AGGCGAATTA GGTATGGCGC GTCTAAAAAC CTTTAAAGAC
 CAAGAAAACC CAACCTTGAT GGTGGATGCA GGGGATGTTT TCCAAGGATT ACCAATCTCC
 AATTTCTCCA AAGGCGCGGA TATGGCCAAA GCAATGAATG AAGTTGGTTA TGATGCCATG
 GCGGTGGGAA ATCACGAGTT TGATTTTGGT TTAGAGATTG CACTAGGTTA TAAAGACCAA
 CTGAATTTTC CGATTTTATC TAGTAATACG TATTACAAAG ATGGCAGTGG ACGGGTTTTT
 GATCCGTATA CAATCGTAGA AAAATCCGGG AAAAAGTTTG CCATTGTAGG TGTGACGACC
 CCAGAAACAG CAACGAAAAC ACACCCGAAA AACGTAGAGA AGGTGACATT TAAAGACCCG
 ATTCCAGAAG TAGAAGCAGT GATTAAGGAA ATTAAAGAGA AGTACGCGGA TATNCAAGCT
 TTCGTGGTTA CTGGGCATTT AGGCGTAGAT GAAACGACGC CGCATATCTG GCGTGGTGAT
 ACGCTAGCAG AAACCCCTAG TCAAACATAT CCTGAGTTAG ATATCACTGT GATTGATGGA
 CATTCGCATA CAGCCGTCGA AAGTGGCAAA CGTTATGGCA AAGTGATCTA TGCTCAAACA
 GGTAAATTATT TAAATAATGT TGGGATCGTC ACAGCACCAG AGAGTGAACC AACTAAGAAA
 ACAACAAAAT TGATTTTCAGC AGCAGAGCTG CTAGAATTGC CAGAAAACCC GGCAGTTAAA
 GCCATCGTTG ATGAAGCACG TACGAATTTT AACGCTGAAA ATGAAAAAGT AATTGTCGAT
 TATATTCCAT TCACATTGGA TGGACAACGA GAAAATGTGC GCACACGAGA GACCAACTTA
 GGGAAATTTGA TTGGTGATGC GATTATGTCA TATGGCCAAG ACGCGTTTAG CCAACCTGCT
 GATTTTGCAG TAACTAATGG TGGCGGCATT CGCGCTGATA TTAAACAAGG GCCAATTAAA
 GTTGGGGATG TCATTGCTGT GTTACCTTTT GGCAATAGCA TTGCGCAAAT TCAAGTAACC
 GGCGCCCAAG TTAAAGAAAAT GTTTGAAATG TCTGTTCTGT CGATTCCACA AAAAGATGAG
 AATGGCACAA TTTTACTAGA TGATGCTGGC CAACCAAAAC TTGGCGCAAA TGGTGGTTTC
 CTACATGTTT CAAGCTCCAT TCGTATCCAC TATGATTCCA CAAAACCAGG TACTCGCTTG
 GCTAGTGACG AAGGCAATGA AACAGGACAA ACGATTGTCT GTAGTCGCGT ATTAGGAATA
 GAAATTAAAA ATCGGCAAAAC ACAAAGTTT GAACCATTTG ATGAGAAGAA ACAATACCGG
 ATGGCTACCA ATGATTTCTT AGCTGCTGGT GGTGATGGTT ACGATATGCT AGGTGGTGAA
 CGAGAAGAAG GGATTTCACT AGATTCTGTC TTAATTGAAT ACTTGAAAAG TGCAACCAGC
 TTGCGGTTGT ATCGTGACG AACGACGATT GATTTAGCAC AATATAAGA ACCATTCCCA
 GGCGAACGAA TTGTTTCTAT TTCGGAAGAA GCTTACAAAG AGTTAATCGG TGGAGGAGAG
 ACGCCAAAAC CAGATCCAAA ACCAGACCCG AAACCAACAC CAGAAACACC AGTAGCAACC
 AATAAACAAA ACCAAGCGGG AGCAAGACAG AGCAATCCAT CCGTAACAGA GAAGAAAAAG
 TATGGCGGCT TT

EF122-4 (SEQ ID NO:456)

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 PTSPDGRTPN AAAITKQDVR NAGFDLDNAY TIMHTNDVHG RLEAGKGELG MARLKTFKQDQ
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 NFPILSSNTY YKDGSGRVFD PYTIVEKSGK KFAIVGVVTP ETATKTHPKN VEKVTFKDPI
 PEVEAVIKEI KEKYADXQAF VVTGHLGVDE TTPHIWRGDT LAETLSQTYP ELDITVIDGH
 SHTAVESGKR YGKVIYAQTG NYLNNVGIVT APESEPTKKT TKLISAAELL ELPENPAVKA
 IVDEARTNFN AENEKVIVDY IPFTLDGQRE NVRTRETNLG NLIGDAIMSY GQDAFSQPAD
 FAVTNGGGIR ADIKQGPIKV GDVIAVLPGF NSIAQIQVTG AQVKEMFEMS VRSIPQKDEN
 GTILLDDAGQ PKLGANGGFL HVSSSIRIHY DSTKPGTRLA SDEGNETGQT IVGSRVLGIE
 IKNRQTQKFE PLDEKKQYRM ATNDFLAAGG DGYDMLGGER EEGISLDSVL IEYLKSATSLS
 RLYRAATTID LAQYKEPFPF ERIVSISEEA YKELIGGGET PKPDPKDPK PTPETPVATN
 KQNQAGARQS NPSVTEKKKY GGF

EF123-1 (SEQ ID NO:457)

TAAAATAAAA AATTGGTACG AAGTGAACGT TCTCTTCTAT GTGTCGTTAG TAGAGGAAGG
 ATGAAAGAAA TGAGAAAGAA TGGTCCAATG GTAAACCGTT GGCTCTACGG GTTGATGTGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTGTTACTTG	TTCTAAATTA	TGGCACACCA	CTCATGGCTT	TGGCGGAAGA	GGTTAACAGC
GATGGCCAGT	TAACGTTAGG	AGAAGTGAAG	CAAACCAGCC	AGCAAGAAAT	GACCTTAGCG
CTTCAAGGAA	AAGCACAACC	AGTAACACAA	GAGGTTGTAG	TGCATTATAG	TGCCAATGTG
TCAATCAAAG	CTGCACATTG	GGCAGCGCCC	AATAATACGC	GCAAGATTCA	AGTGGATGAC
CAGAAGAAAC	AGATTCAAAT	TGAATTGAAT	CAGCAAGCGT	TAGCAGATAC	GTTAGTCTTA
ACGTTGAACC	CTACAGCTAC	AGAAGATGTG	ACGTTTTCTT	ATGGACAACA	GCAACGAGCG
TTGACGTTAA	AGACTGGTAC	TGATCCGACA	GAATCAACGG	CAATCACGAG	TTCCGCCAGCC
GCATCAGCGA	ATGAAGGTTC	AACAGAAGAA	GCATCTACAA	ACTCCTCTGT	TCCTCGTTTCG
TCCGAAGAAA	CTGTCGCCAG	CACGACAAAA	GCGATAGAAA	GTAATAACAAC	TGAATCGACG
ACTGTCAAAC	CGCGCGTAGC	AGGACCAACA	GATATCAGTG	ATTATTTTAC	AGGTGATGAA
ACAACGATTA	TCGATAATTT	TGAAGATCCG	ATTTATTTAA	ATCCTGATGG	AACACCAGCA
ACACCGCCGT	ATAAAGAAGA	TGTGACCATT	CATTGGAACT	TTAACTGGTC	GATTCCAGAA
GATGTGCGAG	AACAAATGAA	AGCAGGCGAT	TACTTCGAGT	TTCAATTACC	TGGCAATTTG
AAACCTAATA	AACCAAGTTC	AGGTGATTTA	GTTGATGCAG	AAGGCAATGT	CTATGGAACC
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GAGTACCAAA	CGACGATTGA	CGAGGCGGTT	ATTCCAGATG	GCGGCGGCGA	TGTGCCTTTT
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GCAGTCATTA	CAGACACAAT	GGGGGATAAT	TTAACGTTTG	AACCAGATTTC	TTTACATTTA
TATTCAGTGA	CATTTGATGA	CAAAGGAAAT	GAAGTCGTTG	GAGCAGAACT	TGTGGAAGGA
AAAGATTACA	AAGTGGTAAT	CAACGGAGAC	GGTTCCTTTG	CAATTGACTT	TTTACATGAT
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ACCCTGGTGT	CTCAGTTGAC	GTTAGGCAAG	GATTTTCATGG	TAGAAATAAC	TCGTAATGCA
GATGGTGAAA	CAGGCTTTAA	GGTAAGTTTT	ATAGGGGCGT	ATGCCAAAAC	AAGTGATGCC
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GTTGATGAAA	AAGTTATCGA	AGGTTCGGCT	AGTTATGACA	ATACCGCATC	TTATACAAAC
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AATGGCGCCC	AATCGGTTTT	AGACGATGTG	GTTATTACTG	ATACACCCCTC	ACCAAACCAA
GTGCTAGATC	CCGAGTCATT	GGTGATTTAC	GGTACCAACG	TAACAGAAGA	CGGAACCTATT
ACGCCAGATA	AATCTGTTAT	TTTAGAAGAA	GGAAAAGATT	ACACACTGGA	AGTTACCACC
GATAATGAAA	CAGGACAACA	AAAAATTGTC	GTTAAAATGG	CCCATATTGA	AGCACCTTAT
TATATGGAAT	ATCGTAGTTT	AGTGACTTCT	TCAGCGGCGG	GGAGTACAGA	CACGGTATCC
AACCAAGTGT	CAATTACTGG	AAATGGTTCA	GAAGTCGTTT	ATGGGGATGA	CAATGGCGAT
GTGGTCGTTG	ACATTGATCA	CAGTGGCGGG	CATGCCACAG	GGACTAAAGG	CAAAATTCAG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CTGAAGAAAA CAGCCATGGA TGAGACGACT ATTTTAGCAG GCGCCCATTT CCAAATTTGG
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ACAGTTTCGG ACGAATTAGC TAAAGGCCGA GTCATTACTA TTGATGAAGA AACTTCAGCC
GAAGGAGCAC AACCAACCAT TATTA AAAAC GATGTCAATA AAGTATTTTT AGAAAAATG
GATGAGAAGG GTAAAAAGTT AGTCAATGCT CGCTTTAAAT TAGAGCATGC CGTAACCACG
CCGTTTACTC ATTGGGAAGA AGTTCCCTTT GCGCCGATC GAACCAACGC GAATGGCCAG
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EF123-2 (SEQ ID NO:458)

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SANEGSTEEA STNSSVPRSS EETVASTTKA IESKTTESTT VKPRVAGPTD ISDYFTGDET

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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EFTWEIN YNY	GEQTIPKDQA	VITDTMG DNL	TFEPDSLHLY	SVTFDDK GNE	VVGAELVEGK
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SQQNI I KNTG	AVDYQNSTIG	WTLAVNQNNY	LMENAVITDT	YEPVPGLTMV	PNSLVVKDTT
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KGGEYHKDDP	DHVVYWHVMIN	GAQSVLDDVV	ITDTPSPNQV	LDPESLVIYG	TNVTEDGTIT
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QAGNPLAGAE	FSVLDTTGQA	VREHLVSDAN	GKVTVTD LAP	GKYQFVETKA	PAGYLLNTEP
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KGAFQIVKTN	SADQPLAGAV	FELYDHNKQS	LGITATSGKD	GKIIFRDLAP	GTYYYYKEIKA
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NDKQPLDELE	FDVNYQAEVMG	RKVNEQGQTL	AGAVFAIYNA	DEQNQPQ GSP	ITFLNRAGEK
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EF123-3 (SEQ ID NO:459)

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CAGAAGAAAC	AGATTCAAAT	TGAATTGAAT	CAGCAAGCGT	TAGCAGATAC	GTTAGTCTTA
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TTGACGTTAA	AGACTGGTAC	TGATCCGACA	GAATCAACGG	CAATCACGAG	TTCCGCCAGCC
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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CAAGAATTCA CTTGGGAAAT TAACTACAAC TATGGTGAAC AAACCATTCC AAAAGACCAA
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EF123-4 (SEQ ID NO:460)

EEVNSD

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PNKPGSGDLV DAEGNVYGTY TISEDGTVRF TFNERITSES DIHGDFSLDT HLNDSDGRGP
GDWVIDIPTQ EDLPPVVIPI VPDTEQQIDK QGHFDRTPNP SAITWTV DIN QAMKDQTNPT
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EFTWEINYNY GEQTIPKDQA VITDTMGDNL TFEPLSLHLY SVTFDDKGNE VVGAELVEGK
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SQQNIKNTG AVDYQNSTIG WTLAVNQNNY LMEHAVITDT YEPVPLTMV PNSLVVKDTT
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EF124-1 (SEQ ID NO:461)

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GATGTGCGAG AACAAATGAA AGCAGGCGAT TACTTCGAGT TTCAATTACC TGGCAATTTG

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AAACCTAATA	AACCAGGTTTC	AGGTGATTTTA	GTTGATGCAG	AAGGCAATGT	CTATGGAACC
TACACAATTA	GTGAAGATGG	TACGGTTCGT	TTTACCTTTA	ATGAGCGAAT	CACGTCTGAA
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CCAGGAAAAT	ATCAATTTGT	GGAAACCAAA	GCGCCAGCAG	GGTACCTTTT	AAACACTGAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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CCAAGTGCCTT TCACGATTGC AGCAAGCGAT CGGGGCAAAC CAGCAACAGT TATAGCAACG
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EF124-2 (SEQ ID NO:462)

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PNKPGSGDLV DAEGNVYGTY TISEDGTVRF TFNERITSES DIHGDFSLDT HLNDSGDRGP
GDWVIDIPTQ EDLPPVVIPI VPDTEQQIDK QGHFDRTPNP SAIWTVDIN QAMKDQTNPT
VTETWPTGNT FKS VKVYELV MNLDGTIKEV GRELSPDEYT VDKNGNVTIK GDTNKAYRLE
YQTTIDEAVI PDGGGDVPPK NHATLTSDNN PNGLDAEATV TATYGMKLDK RNIDYDEANQ
EFTWEINYN YGEQTI PKDQA VITDTMGDNL TFEPDSLHLY SVTFDDKGNE VVGAE LVEGK
DYKVVINGDG SFAIDFLHDV TGAVKIDYKT KVDGIVEGDV AVNNRVVDVGT GQHS EDDGTA
SQQNI IKNTG AVDYQNSTIG WTLAVNQNNY LMENAVITDT YEPVPGLTMV PNSLVVKDTT
TGAQLTLGKD FMVEITRNAD GETGFKVSFI GAYAKTSDAF HITYTTFFDV TELDANNPAL
DHYRNTAAID WTDEAGNNHH SEDSKPFKPL PAFDLNAQKS GYNAVTKET TWTI AVNLSN
NRLVDAFLTD PILTNQTYLA GSKVYEGNT KPDGSVEKVK PTQPLDITM EEPSEKNQNT
WRVDFPNDSR TYVIEFKTSV DEKVI EGSSAS YDNTASYTNQ GSSRDVTGKV SIQHGGESVK
KGGEYHKDDP DHVYWHVMIN GAQSVLDDV ITDTPSPNQV LDPESLVIYG TNVTEDGTIT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

PKDSVILEEG	KDYTLEVTTD	NETGQKIVV	KMAHIEAPYY	MEYRSLVTSS	AAGSTDVTSN
QVSITGNGSE	VVHGDDNGDV	VVDIDHSGGH	ATGTKGKIQL	KKTAMDETTI	LAGAHFQIWD
QAKTQVLREG	TVDATGVITF	GGLPQGQYIL	VETKAPEGYT	VSDELAKGRV	ITIDEETSAE
GAQPTIIKND	VNKVFLEKMD	EKGKKLVNAR	FKLEHAVTTP	FTHWEEVPLA	PDRTNANGQL
EVDSLKPGLY	QFTEIEAPTG	YLLDTPPKRF	IVTQNTSGQI	RDVHVKMLNY	QGSaelIKKD
QAGNPLAGAE	FSVLDTTGQA	VREHLVSDAN	GKVTVTDLAP	GKYQFVETKA	PAGYLLNTEP
SAFTIAASDR	GKPATVIATA	NFVNYQGTA	LIKKDvNGHL	LSGATFKVLD	AKGETIQTGL
TTNNQGEIVA	EHLAPGKYRF	VETKAPTGYL	LNTTPVPFEI	AEKNAGKPAV	VVASDNFVSY
KGAFQIVKTN	SADQPLAGAV	FELYDHNKQS	LGITATSGKD	GKIIFRDLAP	GTYYYKEIKA
PKLPDGADYI	IYPELVKVEI	RGDFKGDPEI	FQLGAFANFK	GRAVFKKIDA	NANPLPGTIF
KLYRIENGEK	IFEREVTAEK	DGSLAMEDLG	AGSYELDELD	ATDGYIVNKQ	PIYFVVKNS
NDKQPLDELE	FVNYQAEVMG	RKVNEQGQTL	AGAVFAIYNA	DEQNQPQGS	ITFLNRAGEK
VSEITTDKGT	EIYAKGLNEG	HYVLVETKAP	TGYLLDITLH	PFDVTAQLGK	EQPIALGDLI
NYQGTaQLTK	ENETGEALAG	AVFKVIDETG	QTVDGQTNLM	SDKQGKVIK	NLAPGTYRFV
ETQAPTSYLL	NETPSASFTI	AKDNQGKPAT	VVLKAPFINY	QGAAKLVKID	QQKNALAGAE
FKVTDaETGQ	TVARSLRSDN	QGLVQVNLH	PGKYTFVETK	APDGYQLSKQ	AVAFTIAATA
KDKPELVNAG	TFVNEKQPV	KKTKPNQPTT	KQAARETGWL	GLPKTNTQVN	YFFVFIGLML
VGLASWLFYK	KSKK				

EF124-3 (SEQ ID NO:463)

TGCCTTCCACATAACTTATACTACCTTTTTGACG GATCCAATTT TAACCAATCA AACCTATTTG
 GCTGGGAGCT TGAAAGTCTA TGAAGGCAAT ACAAAGCCAG ATGGTTCGGT TGAAAAAGTG
 AAACCAACGC AACCGTTGAC GGATATCACA ATGGAAGAAC CAAGCGAGAA AAACCAAAT
 ACTTGGCGTG TTGATTTTCC TAATGATAGT CGTACGTATG TGATTGAATT TAAGACGTCT
 GTTGATGAAA AAGTTATCGA AGGTTCCGCT AGTTATGACA ATACCGCATC TTATACAAAC
 CAAGGTTCTT CACGTGATGT GACAGGAAAA GTTTCATATC AACATGGTGG CAGATCATG
 AAAAAAGGTG GCGAATACCA CAAAGATGAT CCAGATCATG TGTACTGGCA TGTAATGATC
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 GATAATGAAA CAGGACAACA AAAAATTGTC GTTAAAATGG CCCATATTGA AGCACCTTAT
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 GACCAAGCAG GCAATCCATT AGCAGGTGCT GAATTTTCAG TCCTTGACAC CACAGGACAA
 GCAGTTCGAG AACACTTAGT TTCGGATGCA AACGGAAAAG TCACAGTGAC GGATTTAGCC
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 CCAAGTGCTT TCACGATTGC AGCAAGCGAT CGGGGCAAAC CAGCAACAGT TATAGCAACG
 GCTAACTTTG TTAACATATCA AGGCACGGCT AAATTAATCA AAAAAAGATG GAATGGACAC
 TTATTAAGTG GTGCGACATT TAAAGTGCTT GATGCGAAGG GAGAAACGAT TCAAACAGGC
 TTGACGACAA ATAATCAAGG G

EF124-4 (SEQ ID NO:464)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AF HITYTTFFDV TELDANNPAL

DHYRNTAAID	WTDEAGNNHH	SEDSKPFKPL	PAFDLNAQKS	GVYNAVTKEI	TWTIAVNLSN
NRLVDAFLTD	PILTNQTYLA	GSLKVYEGNT	KPDGSVEKVK	PTQPLTDITM	EEPSEKNQNT
WRVDFPNDSR	TYVIEFKTSV	DEKVIEGSAS	YDNTASYTNQ	GSSRDVTGKV	SIQHGGESVK
KGGEYHKDDP	DHVVWHVMIN	GAQSVLDDVV	ITDTPSPNQV	LDPESLVIYG	TNVTEDGTIT
PDKSVILEEG	KDYTLEVTTD	NETGQQKIVV	KMAHIEAPYY	MEYRSLVTSS	AAGSTDVTSN
QVSITGNGSE	VVHGDDNGDV	VVDIDHSGGH	ATGTKGKIQL	KKTAMDETTI	LAGAHFQIWD
QAKTQVLREG	TVDATGVITF	GGLPQQQYIL	VETKAPEGYT	VSDELAKGRV	ITIDEETSAE
GAQPTIIKND	VNKVFLEKMD	EKGKKLVNAR	FKLEHAVTTP	FTHWEEVPLA	PDRTNANGQL
EVDSLKPGLY	QFTEIEAPTG	YLLDTPPKRF	IVTQNTSGQI	RDVHVKMLNY	QGSaelIKKD
QAGNPLAGAE	FSVLDTTGQA	VREHLVSDAN	GKVTVTDLAP	GKYQFVETKA	PAGYLLNTEP
SAFTIAASDR	GKPATVIATA	NFVNYQGTA	LIKKDVNGHL	LSGATPKVLD	AKGETIQTGL
TTNNQG					

EF125-1 (SEQ ID NO:465)

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TTGTTACTTG	TTCTAAATTA	TGGCACACCA	CTCATGGCTT	TGGCGGAAGA	GGTTAACAGC
GATGGCCAGT	TAACGTTAGG	AGAAGTGAAG	CAAACCAGCC	AGCAAGAAAT	GACCTTAGCG
CTTCAAGGAA	AAGCACAACC	AGTAACACAA	GAGGTTGTAG	TGCATTATAG	TGCCAATGTG
TCAATCAAAG	CTGCACATTG	GGCAGCGCCC	AATAATACGC	GCAAGATTCA	AGTGGATGAC
CAGAAGAAAC	AGATTCAAAT	TGAATTGAAT	CAGCAAGCGT	TAGCAGATAC	GTTAGTCTTA
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TTGACGTAA	AGACTGGTAC	TGATCCGACA	GAATCAACGG	CAATCACGAG	TTCCGCCAGCC
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TCCGAAGAAA	CTGTCGCCAG	CACGACAAAA	GCGATAGAAA	GTAAACAAC	TGAATCGACG
ACTGTCAAAC	CGCGCGTAGC	AGGACCAACA	GATATCAGTG	ATTATTTTAC	AGGTGATGAA
ACAACGATT	TCGATAATTT	TGAAGATCCG	ATTTATTTAA	ATCCTGATGG	AACACCAGCA
ACACCGCCGT	ATAAGAAGA	TGTGACCATT	CATTGGAAC	TTAACTGGTC	GATTCCAGAA
GATGTGCGAG	AACAAATGAA	AGCAGGCGAT	TACTTCGAGT	TTCAATTACC	TGGCAATTG
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AGTGACATTC	ACGGGGACTT	TTCTTTAGAT	ACTCATTGTA	ATGATTTCAGA	TGGGCGGGGC
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ATTGTCCCAG	ATACCGAACA	ACAAATTGAT	AAACAAGGCC	ATTTTGATCG	AACGCCCAAT
CCTAGTGCGA	TTACTTGGAC	GGTAGATATC	AATCAAGCGA	TGAAAGATCA	AACAAATCCA
ACTGTGACGG	AAACATGGCC	AACAGGGAAT	ACCTTTAAGT	CCGTGAAAGT	CTATGAGTTA
GTGATGAATC	TTGATGGAAC	AATTAAAGAA	GTGGGTGCGG	AACCTAGTCC	AGATGAATAT
ACCGTTGATA	AAAATGGCAA	TGTGACGATT	AAAGGTGACA	CCAACAAAGC	GTATCGTCTT
GAGTACCAAA	CGACGATTGA	CGAGGCGGTT	ATTCCAGATG	GCGGCGGCGA	TGTGCCTTTT
AAAAATCACG	CGACGTTAAC	AAGTGATAAT	AATCCAAATG	GGTTAGATGC	TGAAGCAACT
GTTACCGCCA	CATATGGCAA	AATGTTAGAC	AAGCGCAATA	TAGATTACGA	CGAAGCCAAT
CAAGAATTCA	CTTGGGAAAT	TAACACAAC	TATGGTGAAC	AAACCATTCC	AAAAGACCAA
GCAGTCATTA	CAGACACAAT	GGGGGATAAT	TTAACGTTTG	AACCAGATTG	TTTACATTTA
TATTTCAGTGA	CATTTGATGA	CAAAGGAAAT	GAAGTCGTTG	GAGCAGAACT	TGTGGAAGGA
AAAGATTACA	AAGTGGTAAT	CAACGGAGAC	GGTTCCTTTG	CAATTGACTT	TTTACATGAT
GTGACTGGCG	CAGTCAAGAT	TGATTATAAA	ACCAAAGTTG	ATGGAATTGT	CGAAGGCGAT
GTGCGCGTGA	ATAATCGTGT	GGATGTTGGC	ACTGGTCAGC	ATTTCAGAAGA	TGATGGCACA
GCCAGTCAAC	AAAATATTAT	TAAAAACACT	GGTGCAGTTG	ATTATCAAAA	TTCAACGATT
GGTTGGACGT	TAGCTGTGAA	TCAAAAATAAT	TATTTGATGG	AAAATGCCGT	GATTACGGAT
ACGTACGAAC	CAGTTCCTGG	CTTAACTATG	GTACCCAATT	CGTTGGTTGT	CAAAGATACA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

ACCACTGGTG	CTCAGTTGAC	GTTAGGCAAG	GATTTTCATGG	TAGAAATAAC	TCGTAATGCA
GATGGTGAAA	CAGGCTTTAA	GGTAAGTTTT	ATAGGGGCGT	ATGCCAAAAC	AAGTGATGCC
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GCTGGGAGCT	TGAAAGTCTA	TGAAGGCAAT	ACAAAGCCAG	ATGGTTCGGT	TGAAAAAGTG
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ACTTGGCGTG	TTGATTTTCC	TAATGATAGT	CGTACGTATG	TGATTGAATT	TAAGACGTCT
GTTGATGAAA	AAGTTATCGA	AGGTTCGGCT	AGTTATGACA	ATACCGCATC	TTATACAAAC
CAAGGTTCTT	CACGTGATGT	GACAGGAAAA	GTTTCTATTC	AACATGGTGG	CGAATCAGTG
AAAAAAGGTG	GCGAATACCA	CAAAGATGAT	CCAGATCATG	TGTAATGATC	TGTAATGATC
AATGGCGCCC	AATCGGTTTT	AGACGATGTG	GTTATTACTG	ATACACCCTC	ACCAAACCAA
GTGCTAGATC	CCGAGTCATT	GGTGATTTAC	GGTACCAACG	TAACAGAAGA	CGGAACATTT
ACGCCAGATA	AATCTGTTAT	TTTAGAAGAA	GGAAAAGATT	ACACACTGGA	AGTTACCACC
GATAATGAAA	CAGGACAACA	AAAAATTGTC	GTTAAAATGG	CCCATATTGA	AGCACCTTAT
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AACCAAGTGT	CAATTACTGG	AAATGGTTCA	GAAGTCGTTT	ATGGGGATGA	CAATGGCGAT
GTGGTTCGTT	ACATTGATCA	CAGTGGCGGG	CATGCCACAG	GGACTAAAGG	CAAAATTCAG
CTGAAGAAAA	CAGCCATGGA	TGAGACGACT	ATTTTAGCAG	GCGCCCATTT	CCAAATTTGG
GACCAAGCTA	AAACACAAGT	CCTACGTGAA	GGTACAGTAG	ATGCCACCGG	GGTTATCACA
TTTGGTGGGT	TGCCACAAGG	GCAATACATT	TTGGTGGAGA	CAAAAGCACC	AGAAGGCTAT
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GAAGGAGCAC	AACCAACCAT	TATTA AAAAC	GATGTCAATA	AAGTATTTTT	AGAAAAATG
GATGAGAAGG	GTAAAAAGTT	AGTCAATGCT	CGCTTTAAAT	TAGAGCATGC	CGTAACCACG
CCGTTTACTC	ATTGGGAAGA	AGTTCCCTTT	GCGCCGGATC	GAACCAACGC	GAATGGCCAG
TTAGAGGTGG	ATAGTTTAAA	ACCAGGGCTT	TATCAGTTCA	CAGAAATCGA	AGCACCGACA
GGCTATCTTT	TAGACACGAC	CCCCAAACGA	TTCAATCGTA	CACAAAATAC	GAGCGGACAA
ATTCGTGATG	TTCATGTCAA	AATGCTTAAT	TACCAAGGTT	CTGCTGAAC	AATTA AAAA
GACCAAGCAG	GCAATCCATT	AGCAGGTGCT	GAATTTTCAG	TCCTTGACAC	CACAGGACAA
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CCAGGAAAAAT	ATCAATTTGT	GGAAACCAAA	GCGCCAGCAG	GGTACCTTTT	AAACACTGAA
CCAAGTGCTT	TCACGATTGC	AGCAAGCGAT	CGGGGCAAAAC	CAGCAACAGT	TATAGCAACG
GCTAACTTTG	TTAACTATCA	AGGCACGGCT	AAATTAATCA	AAAAAGATGT	GAATGGACAC
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TTTGTTAGAAA	CCAAAGCGCC	AACAGGCTAT	TTATTAATAA	CCACGCCAGT	CCCATTTGAA
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AAAGGACGCG	CCGTCTTTAA	GAAAATTGAT	GCCAATGCGA	ACCCACTTCC	AGGAACGATT
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GATGCAACGG	ATGGCTATAT	CGTCAATAAA	CAACCCATTT	ATTTTGTAGT	GAAGAAGAAT
TCAAAATGATA	AACAACCACT	AGATGAGTTA	GAGTTTGTA	ATTATCAAGC	AGAAGTAATG
GGACGTAAAAG	TCAACGAGCA	AGGTCAAACC	TTAGCGGGTG	CAGTTTTTGC	AATTTTACAAT
GCCGATGAGC	AGAATCAGCC	CCAAGGTTCA	CCGATAACAT	TCTTGAATCG	TGCAGGAGAA
AAAGTTTCTG	AAATAACAAC	GGATAAGACT	GGCGAAATTT	ACGCTAAAGG	GCTAAATGAA
GGGCATTACG	TTTTAGTGGA	AACGAAAGCA	CCAACAGGCT	ATCTGTTAGA	CACAACGCTA
CATCCATTTG	ATGTAACCGC	CCAATTAGGA	AAAGAGCAGC	CAATTGCTTT	AGGCGATCTT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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ATCAATTATC AAGGAACTGC TCAATTAACC AAAGAAAACG AAACAGGTGA AGCATTGGCA
GGTGC GG GTGT TTAAGGTCAT TGATGAAACA GGGCAAACCG TAGATGGACA AACCAATCTG
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GTGGAGACAC AAGCGCCAAC TAGCTATCTT CTTAATGAAA CGCCAAGCGC AAGCTTTACG
ATTGCCAAAG ACAACCAAGG CAAACCAGCC ACTGTGGTAC TTAAAGCACC TTTTATTAAT
TACCAAGGTG CTGCCAAGCT GGTGAAAATT GATCAGCAAA AGAATGCCTT AGCAGGTGCT
GAATTTAAAG TGACAGATGC AGAGACAGGG CAACTGTCTG CTCGTTCATT ACGTTC TGAC
AACCAAGGGT TAGTTCAAGT GAACCACTTA CAACCAGGAA AATATACCTT TGTGAAACA
AAAGCACCGG ATGGTTACCA ACTGTCTAAG CAAGCTGTCT CATTCACTAT TGCGGCAACA
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EF125-2 (SEQ ID NO:466)

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KKQIQIELNQ QALADTLVLT LNPTATEDVT FSYGQQQRAL TLKTGTDPTT STAITSSPAA
SANEGSTEEA STNSSVPRSS EETVASTTKA IESKTTESTT VKPRVAGPTD ISDYFTGDET
TIIDNFEDPI YLNPDPGTPAT PPYKEDVTIH WNFNWSIPED VREQMKAGDY FEFQLPGNLK
PNKPGSGDLV DAEGNVYGTY TISEDGTVRF TFNERITSES DIHGDFSLDT HLNDS DGRGP
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YQTTIDEAVI PDGGGDVPFK NHATLTS DNN PNGLDAEATV TATYGMMLDK RNIDYDEANQ
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SQQNI IKNTG AVDYQNSTIG WTLAVNQNNY LMENAVITDT YEPVPGLTMV PNSLVVKD TT
TGAQLTLGKD FMVEITRNAD GETGFKVSFI GAYAKTSDAF HITYTTFDFV TELDANNPAL
DHYRN TAAID WTDEAGNNHH SEDSKPFKPL PAFDLNAQKS GYNAVTK EI TWI AVNLSN
NRLVDAFLTD PILTNQTYLA GSKVYEGNT KPDGSVEKVK PTQPLTDITM EEPSEKNQNT
WRVDFPNSR TYVIEFKTSV DEKVI EGSA YDNTASYTNQ GSSRDVTGKV SIQHGGESVK
KGGEYHKDDP DHVYWHVMIN GAQSVLDDV ITDTPSPNQV LDPESLVIYG TNVTEDGTIT
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QAKTQVLREG TVDATGVITF GGLPQGQYIL VETKAPEGYT VSDELAKGRV ITIDEETSAE
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EVDSLKPGLY QFTEIEAPTG YLLDTPKRF IVTQNTSGQI RDVHV KMLNY QGSAELIKKD
QAGNPLAGAE FSVLDTTGQA VREHLVSDAN GKVTVDLAP GKYQFVETKA PAGYLLNTEP
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TTNNQGEIVA EHLAPGKYRF VETKAPTGYL LNTTPVPFEI AEKNAGKPAV VVASDNFVSY
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VSEITTDK TG EIIYAKLNEG HYVLVETKAP TGYLLD TTHL PFDVTAQLGK EQPIALGDLI
NYQGT AQLTK ENETGEALAG AVFKVIDETG QTV DGTNL M SDKQ GKVI AK NLAPGTYRFV
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FKVTD AETGQ TVARSLRSDN QGLVQVNHLQ PGKYTFVETK APDGYQLSKQ AVAFTIAATA
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EF125-3 (SEQ ID NO:467)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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 AAAGATGGTT CATTGCTAT GGAGGATTTA GGTGCTGGTA GCTATGAATT AGATGAAGT
 GATGCAACGG ATGGCTATAT CGTCAATAAA CAACCCATTT ATTTTGTAGT GAAGAAGAAT
 TCAAATGATA AACAACCACT AGATGAGTTA GAGTTTGTA ATTATCAAGC AGAAGTAATG
 GGACGTAAAG TCAACGAGCA AGGTCAAACC TTAGCGGGTG CAGTTTTTGC AATTTACAAT
 GCCGATGAGC AGAATCAGCC CCAAGGTTCA CCGATAACAT TCTTGAATCG TGCAGGAGAA
 AAAGTTTCTG AAATAACAAC GGATAAGACT GGCGAAATTT ACGCTAAAGG GCTAAATGAA
 GGGCATTACG TTTTAGTGGA AACGAAAGCA CCAACAGGCT ATCTGTTAGA CACAACGCTA
 CATCCATTTG ATGTAACCGC CCAATTAGGA AAAGAGCAGC CAATTGCTTT AGGCGATCTT
 ATCAATTATC AAGGAACTGC TCAATTAACC AAAGAAAACG AACAGGTGA AGCATTGGCA
 GGTGCGGTGT TTAAGGTCAT TGATGAAACA GGGCAAACCG TAGATGGACA AACCAATCTG
 ATGTCTGACA AGCAAGGCAA AGTCATTGCG AAAAATTTAG CACCGGGAAC GTATCGTTTT
 GTGGAGACAC AAGCGCCAAC TAGCTATCTT CTTAATGAAA CGCCAAGCGC AAGCTTTACG
 ATTGCCAAAG ACAACCAAGG CAAACCAGCC ACTGTGGTAC TTAAAGCACC TTTTATTAAT
 TACCAAGGTG CTGCCAAGCT GGTGAAAATT GATCAGCAAA AGAATGCCTT AGCAGGTGCT
 GAATTTAAAG TGACAGATGC AGAGACAGGG CAAACTGTCTG CTCTTCATT ACCTTCTGAC
 AACCAAGGGT TAGTTCAAGT GAACCACTTA CAACCAGGAA AATATACCTT TGTGGAAACA
 AAAGCACCGG ATGGTTACCA ACTGTCTAAG CAAGCTGTCTG CATTCACAT TGCAGGCAACA
 GCGAAAGACA AACCTGAAC TCGTAATGCG GGCACGTTTG TTAACGAGAA ACAACCTGTA
 TCCAAAAAAA CAAAACCAAA TCAGCCAACA ACGAAACAAG CAGCTAGAGA GACAGGTTGG
 CTTGGT

EF125-4 (SEQ ID NO:468)

NFVNYQGTAK LIKKDVNGHL LSGATFKVLD AKGETIQTGL
 TTNNQGEIVA EHLAPGKYRF VETKAPTGYL LNTTPVPFEI AEKNAGKPAV VVASDNFVSY
 KGAFQIVKTN SADQPLAGAV FELYDHNKQS LGITATSGKD GKIIIFRDLAP GTYYYYKEIKA
 PKLPDGADYI IYPELVKVEI RGDFKGDPEI FQLGAFANFK GRAVFKKIDA NANPLPGTIF
 KLYRIENGEK IFEREVTAEK DGSLAMEDLG AGSYELDELD ATDGYIVNKQ PIYFVVKKNS
 NDKQPLDELE FVNYQAEVMG RGVNEQGQTL AGAVFAIYNA DEQNQPQGSF ITFLNRAGEK
 VSEITTDKGT EIIYAKGLNEG HYVLVETKAP TGYLLDITLH PFDVTAQLGK EQPIALGDLI
 NYQGTALTK ENETGEALAG AVFKVIDETG QTVDGQTNLM SDKQGVIAK NLAPGTYRFV
 ETQAPTSYLL NETPSASFIT AKDNQGKPAT VVLKAPFINY QGAAKLVKID QQKNALAGAE
 FKVTDAAETGQ TVARSLRSDN QGLVQVNHQ PGKYTFVETK APDGYQLSKQ AVAFTIAATA
 KDKPELVNAG TFVNEKQPVV KKTkPNQPTT KQAARETGWLG

EF126-1 (SEQ ID NO:469)

TAGCGAAAGA AAATAGGGAG GATTAAAATG TTTAAGAAAG CAACGAAATT ATTATCGACA
 ATGGTGATTG TCGCTGGAAC AGTTGTGGGA AATTTTCAGT CCACATTGGC TTTAGCTGAA
 GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CCGTGAAAGT GAAAGACGAC
 AGTCTGGCTG ATTGTAACCG GATATTGGAA GGACAAGCTA CTTTCCCAGT TCAAGCGGGT
 GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TTTCCACATG	TAAGACAAGC	GATTGATGAA	GTGGTTCAAG	GCTTATCTGA	TCAAGACCGC
GTGATGCTGG	CTTCATATCG	CGGCGGAAAA	CAATTTATGT	TTCTTGATGG	AAAGACAAAA
ATTAATTCAG	CTGATTATGA	TATGAATGTG	CGCGTCAATA	CGCAATTGAC	TTATGATAAA
AGCCAATTTG	TCTCTGGTTT	TGGAGACGTT	CGGACGTATG	GTGGTACGCC	AACCGCCCCA
GGATTGAAAC	TCGCTTTAGA	TACGTACAAT	CAAACACACG	GAGATTTAAC	GAATCGAAAA
ACGTATTTCC	TATTAGTGAC	AGATGGGGTC	GCTAATACAC	GTTTAGATGG	TTACTTGCAT
AAGACCAATA	CCAATGATTC	AATCAATGAA	TATCCAGATC	CAAGACATCC	TTCTCAAGTC
TCAGTGGAAT	ATAGTAATGA	CTACCAAGGT	GCAGCAGCAG	AAGTTTTAGC	GTTAAACCAA
GAAATTACTA	ACCAAGGCTA	TGAAATGATT	AATGCGTATT	GGGAAAGTGT	TGAATCTTTA
AGTTCAGTGA	ATTCATACTT	TGATAAATAT	AAAACAGAAG	TGGGTCCCTT	TGTAAAACAA
GAGTTGCAAC	AAGGGTCTAG	CACACCAGAA	GATTTTATTA	CAAGCCAATC	TATTGATGAT
TTTACAACCC	AATTAAAAACA	AATTGTCAAA	GATCGTCTGG	CGCAATCGAC	ACCAGCAACA
GCTTCATTAA	CGATTGCCAA	TCAATTTGAT	ATTCAATCTG	CGACCGCTAC	GGACGATGCT
GGAAATGATG	TGCCGTGTTCA	AATTAACGGA	CAAACCATTT	CAGCAACTAG	TACAGAAGGT
TACGTAGGAA	ACATCACGAT	TCACTACGAA	GTCAAAGAAA	ATACAGCGAT	TGATGCAGCA
ACCCTTGTA	GTAAGTGGGAC	AATGAATCAA	GGAACAATTG	CTAAGGAATT	TCCAGAAGCG
ACGATTCCTA	AAAATGACAA	TGCGCATGCG	TGTGACGTGA	CGCCAGAAGA	TCCAACGATT
ACAAAAGATA	TCGAAAATCA	AGAACACTTA	GATTTAACCA	ATCGTGAAGA	TAGTTTCGAT
TGGCATGTCA	AAACAGCCTT	TGGCAACGAA	ACCAGTACTT	GGACCCAAGC	CAGCATGGTG
GATGACATTA	ATAAAGTGCT	AGATATCATT	GATGTGAAAG	TCACCGACGA	AAATGGTAAA
GATGTTACAG	CTAACGGCAC	AGTAACACAA	GAAAATAACA	AAGTAACCTT	TGAAATGAAC
AAACAAGCAG	ACAGCTATGA	CTATTTAAGT	GGTCATACGT	ATACAATGAC	TATCACCAC
AAAATTAATA	CTGACGCAAC	GGACGAAGAA	TTAGCGCCTT	ACATTGAACA	AGGCGGGATT
CCCAACCAAG	CCGACTTAAA	CTTTGGCAAT	GAAGGTGACG	TGTTACATTC	CAACAAACCA
ACCGTAACAC	CACCGCCAGT	TGATCCAAAT	ATTGCTAAAG	ACGTAGAAGG	ACAAGAACAT
TTAGATTTAA	CCAACCGCGA	TCAAGAATTT	AAATGGAACG	TCAAAAACAGC	TTTCGGTAAC
GAAACAAGCA	CTTGGACCCA	AGCCAGCATG	GTAGATGACA	TTAATAAAGT	GTTAGACATC
ACTGATGTAA	AAGTCACAGA	TGAAAATGGT	AAAGATGTTA	CAGCTAACGG	CAAAGTAACA
CAAGAAAATA	ACAAAGTAAC	TTTTGAAATG	AACAANCAAG	CNGACAGCTA	TGACTATTTA
AGTGGTCATA	CGTACACAAT	GACCATTACT	ACTAAAATCA	AAGCTAGCGC	AACGGACGAA
GAATTAGCAC	CTTATATTGA	ACAAGGTGGC	ATTCCCAACC	AAGCCGACTT	GAACCTTGGC
AACGAAGGTG	ACGTGTTGCA	TTCCAACAAA	CCAACCGTAA	CACCACCTGC	ACCAACGCCA
GAAAGTCCAA	CGATTACAAA	AGATATCGAA	GGCCAAGAAC	ATTTAGATTT	AACCAACCGT
GACCAAGAAT	TTAAATGGAA	CGTCAAAACA	GCTTTTCGGTA	ACGAAACAAG	CACATGGACC
CAAGCCAGCA	TGGTGGATGA	CATTAATAAA	TGTGTTAGACA	TCACAGACGT	GAAAGTTNCT
GANGAAAATG	GCAAAGATGT	TACAGATAAT	GGCATAGTAA	CACAAGAAAA	TAACAAAGTA
ACTTTTACTA	TGAACAAAAA	AGATGACAGC	TACTCTTACT	TAGCTGGTCA	TACATACACA
ATGACTATTA	CCACTAAAAT	TAAAACTGAC	GCAACGGATG	AAGAATTAGC	GCCTTATATT
GAACAAGGCG	GGATTCCCAA	CCAAGCCGAC	TTAAACTTTG	GCAACGAAGG	TGACGTGTTG
CATTCCAACA	AGCCAACCGT	AACACCGCCT	GCACCAACGC	CAGAAGACCC	AAAAAACCTT
GAACCTAAAC	AACCGCTAAA	ACCGAAAAAA	CCGTTGACGC	CTACAAATCA	TCAAGCACCA
ACGAACCCAG	TCAATTTTGG	AAAATCAGCA	AGTAAAGGAA	TTCATTTACC	AATGACTAAT
ACAACAGTAA	ATCCACTTTA	CATGATCGCA	GGTTTAATTG	TCCTTATAGT	GGCTATTAGC
TTTGGCATAA	CAAAAAATAA	AAAAAGAAAA	AATTAG		

EF126-2 (SEQ ID NO:470)

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LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
LKLALDITYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPVFKQE
LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGTMNQ TIAKEFPEAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

IPKNDNAHAC	DVTPEDPTIT	KDIENQEHL	LTNREDSFDW	HVKTAFGNET	STWTQASMVD
DINKVLDIID	VKVTDENGKD	VTANGTVTQE	NNKVTFEMNK	QADSYDYLSG	HTYTMITITTK
IKTDATDEEL	APYIEQGGIP	NQADLNFGNE	GDVLHSNKPT	VTPPPVDPI	AKDVEGQEHL
DLTNRDQEFK	WNVKTAFGNE	TSTWTQASMV	DDINKVLDT	DVKVTDENGK	DVTANGKVTQ
ENNKVTFEMN	XQADSYDYLS	GHTYTMITIT	KIKASATDEE	LAPYIEQGGI	PNQADLNFGN
EGDVLHSNKP	TVTPPAPTPE	DPTITKDIEG	QEHLDLTNRD	QEFKWNVKTA	FGNETSTWTQ
ASMVDDINKV	LDITDVKVXX	ENGKDVTDNG	IVTQENNKVT	FTMNKKDDSY	SYLAGHTYTM
TITTKIKTDA	TDEELAPYIE	QGGIPNQADL	NFGNEGDLH	SNKPTVTPPA	PTPEDPKKPE
PKQPLPKPKP	LTPTNHQAPT	NPVNFGKSAS	KGIHLPMTNT	TVNPLYMIAG	LIVLIVAISF
GITKNKKRKN					

EF126-3 (SEQ ID NO:471)

TGAA

GAAGCGGTTA	AAGCAGGAGA	TACAGAAGGA	ATGACCAATA	CGGTGAAAGT	GAAAGACGAC
AGTCTGGCTG	ATTGTAAACG	GATATTGGAA	GGACAAGCTA	CTTTCCAGT	TCAAGCGGGT
GAAACGGAAC	CAGTCGATTT	AGTAGTTGTT	GAAGATGCTA	GTGGTAGTTT	TTCAGATAAT
TTTCCACATG	TAAGACAAGC	GATTGATGAA	GTGGTTCAAG	GCTTATCTGA	TCAAGACCGC
GTGATGCTGG	CTTCATATCG	CGGCGGAAAA	CAATTTATGT	TTCTTGATGG	AAAGACAAAA
ATTAATTCAG	CTGATTATGA	TATGAATGTG	CGCGTCAATA	CGCAATTGAC	TTATGATAAA
AGCCAATTTG	TCTCTGGTTT	TGGAGACGTT	CGGACGTATG	GTGGTACGCC	AACCGCCCCA
GGATTGAAAC	TCGCTTTAGA	TACGTACAAT	CAAACACACG	GAGATTTAAC	GAATCGAAAA
ACGTATTTCC	TATTAGTGAC	AGATGGGGTC	GCTAATACAC	GTTTAGATGG	TTACTTGTCAT
AAGACCAATA	CCAATGATTC	AATCAATGAA	TATCCAGATC	CAAGACATCC	TCTTCAAGTC
TCAGTGGAAT	ATAGTAATGA	CTACCAAGGT	GCAGCAGCAG	AAGTTTTAGC	GTAAACCAA
GAAATTACTA	ACCAAGGCTA	TGAAATGATT	AATGCGTATT	GGGAAAGTGT	TGAATCTTTA
AGTTCAGTGA	ATTCATACTT	TGATAAATAT	AAAACAGAAAG	TGGGTCCTTT	TGTAACAA
GAGTTGCAAC	AAGGGTCTAG	CACACCAGAA	GATTTTATTA	CAAGCCAATC	TATTGATGAT
TTTACAACCC	AATTAACAA	AATTGTCAAA	GATCGTCTGG	CGCAATCGAC	ACCAGCAACA
GCTTCATTAA	CGATTGCCAA	TCAATTTGAT	ATTCAATCTG	CGACCGCTAC	GGACGATGCT
GGAAATGATG	TGCCTGTTCA	AATTAACGGA	CAAACCATTT	CAGCAACTAG	TACAGAAGGT
TACGTAGGAA	ACATCACGAT	TCACTACGAA	GTCAAAGAAA	ATACAGCGAT	TGAT

EF126-4 (SEQ ID NO:472)

EE AVKAGDTEGM TNTVKVKDDS

LADCKRILEG	QATFPVQAGE	TEPVDLVVVE	DASGSFSDNF	PHVRQAIDEV	VQGLSDQDRV
MLASYRGGKQ	FMFPDGKTKI	NSADYDMNVR	VNTQLTYDKS	QFVSGFGDVR	TYGGTPTAPG
LKLALDTYNQ	THGDLTNRKT	YFLLVTDGVA	NTRLGTYLHK	TNTNDSINEY	PDPRHPLQVS
VEYSNDYQGA	AAEVLALNQE	ITNQGYEMIN	AYWESVESLS	SVNSYFDKYK	TEVGPFVKQE
LQQGSSTPED	FITSQSIDDF	TTQLKQIVKD	RLAQSTPATA	SLTIANQFDI	QSATATDDAG
NDVPVQINGQ	TISATSTEGY	VGNITIHVEV	KENTAID		

EF127-1 (SEQ ID NO:473)

TAGCGAAAGA	AAATAGGGAG	GATTAAAATG	TTTAAGAAAG	CAACGAAATT	ATTATCGACA
ATGGTGATTG	TCGCTGGAAC	AGTTGTGGGA	AATTTCACTC	CCACATTGGC	TTTAGCTGAA
GAAGCGGTTA	AAGCAGGAGA	TACAGAAGGA	ATGACCAATA	CGGTGAAAGT	GAAAGACGAC
AGTCTGGCTG	ATTGTAAACG	GATATTGGAA	GGACAAGCTA	CTTTCCAGT	TCAAGCGGGT
GAAACGGAAC	CAGTCGATTT	AGTAGTTGTT	GAAGATGCTA	GTGGTAGTTT	TTCAGATAAT
TTTCCACATG	TAAGACAAGC	GATTGATGAA	GTGGTTCAAG	GCTTATCTGA	TCAAGACCGC
GTGATGCTGG	CTTCATATCG	CGGCGGAAAA	CAATTTATGT	TTCTTGATGG	AAAGACAAAA
ATTAATTCAG	CTGATTATGA	TATGAATGTG	CGCGTCAATA	CGCAATTGAC	TTATGATAAA

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACCGCCCCA
GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTTG CAT
AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
TCAGTGGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTAGC GTTAAACCAA
GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
AGTTTCAGTA ATTCATACCTT TGATAAATAT AAAACAGAAG TGGGTCCTTT TGTAAACAA
GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
TTTACAACCC AATTAAAACA AATTGTCAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATT T CAGCAACTAG TACAGAAGGT
TACGTAGGAA ACATCACGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
ACCTTGTA G TAGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
ACGATTCTTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
ACAAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACTTT TGAAATGAAC
AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTACATACG ATACAATGAC TATCAACCACT
AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATTC CAACAAACCA
ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAACAGC TTTCGGTAAC
GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
ACTGATGTAA AAGTCACAGA TGAAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAANCAAG CNGACAGCTA TGACTATTTA
AGTGGTCATA CGTACACAAT GACCATTACT ACTAAAATCA AAGCTAGCGC AACGGACGAA
GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
GAAGATCCAA CGATTACAAA AGATATCGAA GGCCAAGAAC ATTTAGATTT AACCAACCGT
GACCAAGAAT TTAAATGGAA CGTCAAAAACA GCTTTCGGTA ACGAAACAAG CACATGGACC
CAAGCCAGCA TGGTGGATGA CATTAATAAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
ATGACTATTA CCACTAAAAA TAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAAACCT
GAACCTAAAC AACCCTGTAAC ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
ACGAACCCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCATTTACC AATGACTAAT
ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
TTTGGCATAA CAAAAAATAA AAAAAAGAAA AATTAG

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EF127-2 (SEQ ID NO:474)

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MF KKATKLLSTM VIVAGTVVGN FSPTLALAE AVKAGDTEGM TNTVKVKDDS
LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
LKLALDITYNQ THGDLTNRKT YLLVTDGVA NTRL DGYLHK TNTNDSINEY PDPRHPLQVS
VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFPVKQE
LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGTMTNQ TIAKEFPEAT
IPKNDNAHAC DVTPEPTIT KDIENQEHLD LTNREDSFDW HVKTAFGNET STWTQASMVD
DINKVLDIID VKVTDENGKD VTANGTVTQE NNVKVFEMNK QADSYDYLGS HTYTMTITTK
IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHNSKPT VTPPPVDPNI AKDVEGQEH

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSYDYLS GHTYTMITT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHSNKP TVTPPAPTPE DPTITKDIEG QEHLDLTNRD QEFKWNVKTA FGNETSTWTQ
 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLKPKKP LTPTNHQAPT NPVNFGKSAS KGIHLPMTNT TVNPLYMIAG LIVLIVAISF
 GITKNKKRKN

EF127-3 (SEQ ID NO:475)

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 ACGATTCCTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
 ACAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
 TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
 GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACCTT TGAAATGAAC
 AAACAAGCAG ACAGCTATGA CTATTAAAGT GGTCTACGT ATACAATGAC TATCACCCT
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
 CCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTACATTC CAACAAACCA
 ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAAACAGC TTTTCGGTAAC
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAAT

EF127-4 (SEQ ID NO:476)

NQG TIAKEFPEAT
 IPKNDNAHAC DVPEDPTIT KDIENTQEHLD LTNREDSFDW HVKTAFGNET STWTQASMVD
 DINKVLDIID VKVTDENGKD VTANGTVTQE NNVKTFEMNK QADSYDYLSG HTYTMITTITK
 IKTDATDEEL APYIEQGGIP NQADLNFGNE GDVLHSNKP VTPPPVDPNI AKDVEGQEHL
 DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDIN

EF128-1 (SEQ ID NO:477)

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 ATGGTGATTG TCGCTGGAAC AGTTGTGGGA AATTTTCAGTC CCACATTGGC TTTAGCTGAA
 GAAGCGGTTA AAGCAGGAGA TACAGAAGGA ATGACCAATA CCGTGAAAGT GAAAGACGAC
 AGTCTGGCTG ATTGTAAACG GATATTGGAA GGACAAGCTA CTTTCCAGT TCAAGCGGGT
 GAAACGGAAC CAGTCGATTT AGTAGTTGTT GAAGATGCTA GTGGTAGTTT TTCAGATAAT
 TTTCCACATG TAAGACAAGC GATTGATGAA GTGGTTCAAG GCTTATCTGA TCAAGACCGC
 GTGATGCTGG CTTCATATCG CGGCGGAAAA CAATTTATGT TTCTGATGG AAAGACAAAA
 ATTAATTTCAG CTGATTATGA TATGAATGTG CGCGTCAATA CGCAATTGAC TTATGATAAA
 AGCCAATTTG TCTCTGGTTT TGGAGACGTT CGGACGTATG GTGGTACGCC AACCAGCCCCA
 GGATTGAAAC TCGCTTTAGA TACGTACAAT CAAACACACG GAGATTTAAC GAATCGAAAA
 ACGTATTTCC TATTAGTGAC AGATGGGGTC GCTAATACAC GTTTAGATGG TTACTIONCAT
 AAGACCAATA CCAATGATTC AATCAATGAA TATCCAGATC CAAGACATCC TCTTCAAGTC
 TCAGTGGAAT ATAGTAATGA CTACCAAGGT GCAGCAGCAG AAGTTTTAGC GTTAAACCAA
 GAAATTACTA ACCAAGGCTA TGAAATGATT AATGCGTATT GGGAAAGTGT TGAATCTTTA
 AGTTCAGTGA ATTCATACTT TGATAAATAT AAAACAGAAG TGGGTCCCTT TGTAACAA
 GAGTTGCAAC AAGGGTCTAG CACACCAGAA GATTTTATTA CAAGCCAATC TATTGATGAT
 TTTACAACCC AATTAAAACA AATTGTCAAA GATCGTCTGG CGCAATCGAC ACCAGCAACA
 GCTTCATTAA CGATTGCCAA TCAATTTGAT ATTCAATCTG CGACCGCTAC GGACGATGCT
 GGAAATGATG TGCCTGTTCA AATTAACGGA CAAACCATTT CAGCAACTAG TACAGAAGGT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

TACGTAGGAA ACATCACGAT TCACTACGAA GTCAAAGAAA ATACAGCGAT TGATGCAGCA
 ACCCTTGTA GTAGTGGGAC AATGAATCAA GGAACAATTG CTAAGGAATT TCCAGAAGCG
 ACGATTCCCTA AAAATGACAA TGCGCATGCG TGTGACGTGA CGCCAGAAGA TCCAACGATT
 ACAAAAGATA TCGAAAATCA AGAACACTTA GATTTAACCA ATCGTGAAGA TAGTTTCGAT
 TGGCATGTCA AAACAGCCTT TGGCAACGAA ACCAGTACTT GGACCCAAGC CAGCATGGTG
 GATGACATTA ATAAAGTGCT AGATATCATT GATGTGAAAG TCACCGACGA AAATGGTAAA
 GATGTTACAG CTAACGGCAC AGTAACACAA GAAAATAACA AAGTAACTTT TGAAATGAAC
 AAACAAGCAG ACAGCTATGA CTATTTAAGT GGTACATACGT ATACAATGAC TATCACCCT
 AAAATTAAAA CTGACGCAAC GGACGAAGAA TTAGCGCCTT ACATTGAACA AGGCGGGATT
 CCCAACCAAG CCGACTTAAA CTTTGGCAAT GAAGGTGACG TGTTACATTC CAACAAACCA
 ACCGTAACAC CACCGCCAGT TGATCCAAAT ATTGCTAAAG ACGTAGAAGG ACAAGAACAT
 TTAGATTTAA CCAACCGCGA TCAAGAATTT AAATGGAACG TCAAAACAGC TTTCGGTAAC
 GAAACAAGCA CTTGGACCCA AGCCAGCATG GTAGATGACA TTAATAAAGT GTTAGACATC
 ACTGATGTAA AAGTCACAGA TGAAAATGGT AAAGATGTTA CAGCTAACGG CAAAGTAACA
 CAAGAAAATA ACAAAGTAAC TTTTGAAATG AACAAACAAG CNGACAGCTA TGACTATTTA
 AGTGGTCATA CGTACACAAT GACCATTACT ACTAAAATCA AAGCTAGCGC AACGGACGAA
 GAATTATGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAACTTTGGC
 AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
 GAAGATCCAA CGATTACAAA AGATATCGAA GGCCAAGAAC ATTTAGATTT AACCAACCGT
 GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTCGGTA ACGAAAACAAG CACATGGACC
 CAAGCCAGCA TGGTGGATGA CATTAATAAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
 GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
 ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
 ATGACTATTA CCACTAAAAT TAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
 GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
 CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
 GAACCTAAAC AACCCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
 ACGAACCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCATTTACC AATGACTAAT
 ACAACAGTAA ATCCACTTTA CATGATCGCA GGTTTAATTG TCCTTATAGT GGCTATTAGC
 TTTGGCATAA CAAAAATAA AAAAAGAAAA AATTAG

EF128-2 (SEQ ID NO:478)

MF KKATKLLSTM VIVAGTVVGN FSPTLALAE AVKAGDTEGM TNTVKVKDDS
 LADCKRILEG QATFPVQAGE TEPVDLVVVE DASGSFSDNF PHVRQAIDEV VQGLSDQDRV
 MLASYRGGKQ FMFPDGKTKI NSADYDMNVR VNTQLTYDKS QFVSGFGDVR TYGGTPTAPG
 LKLALDTYNQ THGDLTNRKT YFLLVTDGVA NTRLDGYLHK TNTNDSINEY PDPRHPLQVS
 VEYSNDYQGA AAEVLALNQE ITNQGYEMIN AYWESVESLS SVNSYFDKYK TEVGPFVKQE
 LQQGSSTPED FITSQSIDDF TTQLKQIVKD RLAQSTPATA SLTIANQFDI QSATATDDAG
 NDVPVQINGQ TISATSTEGY VGNITIHIEV KENTAIDAAT LVSSGTMNQG TIAKEFPEAT
 IPKNDNAHAC DVPEDPTIT KDIENTEHLDT LNREDSFDW HVKTAFGNET STWTQASMVD
 DINKVLDIID VKVTDENGKD VTANGTVTQE NNKVTFEMNK QADSYDYLGS HTYTMTITTK
 IKTDATDEEL APYIEQGGIP NQADLNFGE GDVLHSNKPT VTPPPVDPNI AKDVEGQEH
 DLTNRDQEFK WNVKTAFGNE TSTWTQASMV DDINKVLDIT DVKVTDENGK DVTANGKVTQ
 ENNKVTFEMN XQADSVDYLS GHTYTMTITT KIKASATDEE LAPYIEQGGI PNQADLNFVN
 EGDVLHSNKP VTTPPAPTPE DPTITKDIEG QEHLDTNRD QEFKWNVKT FNETSTWTQ
 ASMVDDINKV LDITDVKVXX ENKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLPKPKP LTPTNHQAPT NPVNFGKSAS KGIHLPMNT TVNPLYMIAG LIVLIVAISF
 GITKNKKRKN

EF128-3 (SEQ ID NO:479)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

AGA TGAAAATGGT AAAGATGTGA CAGCTAACGG CAAAGTAACA
 CAAGAAAATA ACAAAGTAAC TTTTGAATG AACAAACAAG CNGACAGCTA TGACTATTTA
 AGTGGTCATA CGTACACAAT GACCATTACT ACTAAAATCA AAGCTAGCGC AACGGACGAA
 GAATTAGCAC CTTATATTGA ACAAGGTGGC ATTCCCAACC AAGCCGACTT GAAC'TTTGGC
 AACGAAGGTG ACGTGTGCA TTCCAACAAA CCAACCGTAA CACCACCTGC ACCAACGCCA
 GAAGATCCAA CGATTACAAA AGATATCGAA GGCCAAGAAC ATTTAGATTT AACCAACCGT
 GACCAAGAAT TTAAATGGAA CGTCAAAACA GCTTTCGGTA ACGAAACAAG CACATGGACC
 CAAGCCAGCA TGGTGGATGA CATTAATAAA GTGTTAGACA TCACAGACGT GAAAGTTNCT
 GANGAAAATG GCAAAGATGT TACAGATAAT GGCATAGTAA CACAAGAAAA TAACAAAGTA
 ACTTTTACTA TGAACAAAAA AGATGACAGC TACTCTTACT TAGCTGGTCA TACATACACA
 ATGACTATTA CCACTAAAAT TAAACTGAC GCAACGGATG AAGAATTAGC GCCTTATATT
 GAACAAGGCG GGATTCCCAA CCAAGCCGAC TTAAACTTTG GCAACGAAGG TGACGTGTTG
 CATTCCAACA AGCCAACCGT AACACCGCCT GCACCAACGC CAGAAGACCC AAAAAACCT
 GAACCTAAAC AACCGCTAAA ACCGAAAAAA CCGTTGACGC CTACAAATCA TCAAGCACCA
 ACGAACCAG TCAATTTTGG AAAATCAGCA AGTAAAGGAA TTCAT

EF128-4 (SEQ ID NO:480)

DENGK DVTANGKVTQ

ENNKVTFEMN XQADSYDYL S GHTYTMITT KIKASATDEE LAPYIEQGGI PNQADLNFGN
 EGDVLHSNKP TVTPPAPTPE DPTITKDIEG QEHLDLTNRD QEFKWNVKTA FGNETSTWTQ
 ASMVDDINKV LDITDVKVXX ENGKDVTDNG IVTQENNKVT FTMNKKDDSY SYLAGHTYTM
 TITTKIKTDA TDEELAPYIE QGGIPNQADL NFGNEGDVLH SNKPTVTPPA PTPEDPKKPE
 PKQPLPKPKP LPTPNHQAPT NPVNFGKSAS KGIH

EF129-1 (SEQ ID NO:481)

TGACAAGTGA AGAAACGTCT ATTTGCATCA GTATTACTAT GTTCATTAAC GCTATCAGCA
 ATTGCTACCC CAAGCATCGC TTTGGCGGAC AATGTTGATA AAAAAATTGA AGAAAAAAT
 CAAGAAATTT CATCATTTAA AGCAAAACAA GGGGATTTAG CTTCAACAAGT ATCTTCTTTA
 GAAGCAGAAG TATCTTCAGT ATTTGATGAA AGCATGGCTT TACGTGAACA AAAGCAAACA
 CTAAAAGCAA AATCAGAACA ATTACAACAA GAAATTACAA ACTTGAATCA ACGTATTGAA
 AAACGTAACG AAGCAATCAA AAATCAAGCA CGTGATGTTT AAGTTAATGG ACAAAGCACA
 ACAATGCTAG ATGCAGTTT AGATGCGGAC TCAGTTGCAG ATGCAATCAG CCGTGTTCAA
 GCTGTTTCAA CAATCGTAAG TGCCAACAAC GACTTAATGC AACAAACAAA AGAAGACAAA
 CAAGCCGTTG TTGATAAAAA AGCTGAAAAC GAGAAAAAAG TGAAACAAC TGAAGCAACA
 GAAGCTGAAT TAGAAACAAA ACGTCAAGAT TTACTTTCTA AACAACTCTGA ATTAACGTA
 ATGAAAGCTT CATTAGCATT AGAACAATCA TCAGCTGAAA GTTCTAAAGC TGGCTTAGAA
 AAACAAAAAG CAGCTGCTGA AGCAGAGCAA GCACGCTTAG CTGCTGAACA AAAAGCTGCA
 GCTGAAAAAG CCAAACAAGC TGCTGCAAAA CCAGCTAAAG CTGAAGTGAA AGCAGAAGCA
 CCAGTTGCCT CTTTCATCAAC AACAGAAGCA CAAGCACCAG CAAGCTCAAG CTCAGCAACT
 GAATCAAGCA CGTCAACAAAC AACTGAAACA ACTACACCAA GTACAGATAA TAGTGCAACA
 GAAAATACTG GCTCTTCTTC ATCAGAACAA CCAGTACAAC CTACAACACC AAGCGATAAT
 GGAAATAATG GTGGCCAAAC TGGTGGTGGG ACAGTTACAC CAACACCAGA ACCAACACCA
 GCGCCTTCTG CTGATCCAAC AATCAATGCA TTGAACGTTT TACGTCAATC ATTAGGTTTA
 CGTCCAGTAG TATGGGATGC AGGTTTGGCA GCTTCTGCAA CTGCTCGTGC AGCACAAGTT
 GAAGCAGGTG GCATTCCAAA TGATCACTGG TCTCGTGGAG ATGAAGTTAT CGCAATTATG
 TGGGCGCCAG GTAACTCAGT AATCATGGCG TGGTACAATG AAACAAACAT GGTAACAGCT
 TCAGGAAGCG GTCACCGTGA TTGGGAAATT AACCCAGGTA TTACGCGTGT CCGTTTTGGT
 TACTCAGGTA GCACAATCGT AGGACACTCA GCCTAA

EF129-2 (SEQ ID NO:482)

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

VKKRLFASV LLCSLTLSAI ATPSIALADN VDKKIEKNQ EISSLKAKQG DLASQVSSLE
 AEVSSVFDES MALREQKQTL KAKSEQLQQE ITNLNQRIEK RNEAIKNQAR DVQVNGQSTT
 MLDAVLDAVS VADAIQSRVQA VSTIVSANND LMQQQKEDKQ AVVDKKAENE KVKQLEATE
 AELETKRQDL LSKQSELNVM KASLALEQSS AESSKAGLEK QKAAAEAEQA RLAAEQKAAA
 EKAKQAAAKP AKAEVKAEAP VASSSTTEAQ APASSSSATE SSTQQTETT TPSTDNSATE
 NTGSSSSEQP VQPTTPSDNG NNGGQTGGGT VTPTPEPTPA PSADPTINAL NVLRQSLGLR
 PVVWDAGLAA SATARAAQVE AGGIPNDHWS RGDEVIAIMW APGNSVIMAW YNETNMVTAS
 GSGHRDWEIN PGITRVGFGY SGSTIVGHSA

EF129-3 (SEQ ID NO:483)

GGAC AATGTTGATA AAAAAATTGA AGAAAAAAT
 CAAGAAATTT CATCATTAAA AGCAAAACAA GGGGATTTAG CTTTACAAGT ATCTTCTTTA
 GAAGCAGAAG TATCTTCAGT ATTTGATGAA AGCATGGCTT TACGTGAACA AAAGCAAACA
 CTAAGAGCAA AATCAGAACA ATTACAACAA GAAATTACAA ACTTGAATCA ACGTATTGAA
 AAACGTAAACG AAGCAATCAA AAATCAAGCA CGTGATGTTT AAGTTAATGG ACAAAGCACA
 ACAATGCTAG ATGCAGTTTT AGATGCGGAC TCAGTTGCAG ATGCAATCAG CCGTGTTCAA
 GCTGTTTCAA CAATCGTAAG TGCCAACAAC GACTTAATGC AACAACAAAA AGAAGACAAA
 CAAGCCGTTG TTGATAAAAA AGCTGAAAAC GAGAAAAAAG TGAAACAAC TGAAGCAACA
 GAAGCTGAAT TAGAAACAAA ACGTCAAGAT TTACTTTCTA AACAATCTGA ATTAAACGTA
 ATGAAAGCTT CATTAGCATT AGAACAATCA TCAGCTGAAA GTTCTAAAGC TGGCTTAGAA
 AAACAAAAAG CAGCTGCTGA AGCAGAGCAA GCACGCTTAG CTGCTGAACA AAAAGCTGCA
 GCTGAAAAAG CCAAACAAGC TGCTGCAAAA CCAGCTAAAG CTGAAGTGAA AGCAGAAGCA
 CCAGTTGCCT CTTCATCAAC AACAGAAGCA CAAGCACCAG CAAGCTCAAG CTCAGCAACT
 GAATCAAGCA CGCAACAAAC AACTGAAACA ACTACACCAA GTACAGATAA TAGTGCAACA
 GAAAAACTG GCTCTTCTTC ATCAGAACAA CCAGTACAAC CTACAACACC AAGCGATAAT
 GGAAATAATG GTGGCCAAAC TGGTGGTGGA ACAGTTACAC CAACACCAGA ACCAACACCA
 GCGCCTTCTG CTGATCCAAC AATCAATGCA TTGAACGTTT TACGTCAATC ATTAGGTTTA
 CGTCCAGTAG TATGGGATGC AGGTTTGGCA GCTTCTGCAA CTGCTCGTGC AGCACAAGTT
 GAAGCAGGTG GCATTCCAAA TGATCACTGG TCTCGTGGAG ATGAAGTTAT CGCAATTATG
 TGGGCGCCAG GTAACCTAGT AATCATGGCG TGGTACAATG AAACAAACAT GGTAACAGCT
 TCAGGAAGCG GTCACCGTGA TTGGGAAATT AACCAGGTA TTACGCGTGT CCGTTTTGGT
 TACTCAGGTA GCACAATCGT AGGACACTCA GCC

EF129-4 (SEQ ID NO:484)

DN VDKKIEKNQ EISSLKAKQG DLASQVSSLE
 AEVSSVFDES MALREQKQTL KAKSEQLQQE ITNLNQRIEK RNEAIKNQAR DVQVNGQSTT
 MLDAVLDAVS VADAIQSRVQA VSTIVSANND LMQQQKEDKQ AVVDKKAENE KVKQLEATE
 AELETKRQDL LSKQSELNVM KASLALEQSS AESSKAGLEK QKAAAEAEQA RLAAEQKAAA
 EKAKQAAAKP AKAEVKAEAP VASSSTTEAQ APASSSSATE SSTQQTETT TPSTDNSATE
 NTGSSSSEQP VQPTTPSDNG NNGGQTGGGT VTPTPEPTPA PSADPTINAL NVLRQSLGLR
 PVVWDAGLAA SATARAAQVE AGGIPNDHWS RGDEVIAIMW APGNSVIMAW YNETNMVTAS
 GSGHRDWEIN PGITRVGFGY SGSTIVGHSA

EF130-1 (SEQ ID NO:485)

TGATACATTA AAAGGAGGGA AAATATGCGC CCAAAAGAGA AAAAAAGAGG AAAAAATTGG
 TTAATCAACA GTTTATTAGT TTTACTATTT ATCATTTGGT TAGCCTTAAT TTTTAACAAT
 CAGATACGTA GTTGGGTGGT TCAACAAAAT AGCCGCTCGT ACGCCGTTAG CAAGTTGAAA
 CCAGCTGATG TGAAGAAAAA TATGGCTCGT GAAACAACGT TTGACTTTGA TTCAGTTGAG
 TCCTTGAGCA CAGAAGCGGT GATGAAAGCC CAATTTGAAA ACAAACACTT ACCTGTGATT
 GGTGCCATTG CGATACCAAG TGTGAAATT AATTGCCCCA TTTTAAAGG ATTGTCCAAT
 GTCGCTTTAT TAACTGGTGC CGGGACCATG AAAGAAGATC AAGTCATGGG GAAAAACAAT

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

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TATGCCTTGG CTAGTCATCG AACGGAAGAT GCGGTTTCCT TATTTTCACC TTTAGAAAGA
ACCAAAAAAG ACGAACTCAT TTATATCACT GATTTATCTA CTGTTTATAC ATACAAAATA
ACTTCTGTAG AAAAAATCGA ACCAACCCGT GTTGAGTTAA TTGATGACGT TCCTGGTCAA
AATATGATTA CCTTAATTAC CTGTGGCGAT TTACAAGCAA CGACGCGAAT TGCTGTTCAA
GGAACATTAG CAGCAACGAC GCCTATTAAA GACGCCAACG ACGATATGTT GAAGGCTTTC
CAATTGGAGC AAAAAACTTT AGCCGATTGG GTGGCTTAA

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EF130-2 (SEQ ID NO:486)

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YIKRRENMRP KEKKRGKNWL INSLLVLLFI IGLALIFNNQ IRSWVQQNS RSYAVSKLKP
ADVKKNMARE TTFDFDSVES LSTEAVMKAQ FENKNLPVIG AIAIPSVEIN LPIFKGLSNV
ALLTGAGTMK EDQVMGKNNY ALASHRTEDG VSLFSPLEKT KKDELIYITD LSTVYTYKIT
SVEKIEPTRV ELIDDPGQN MITLITCGDL QATTRIAVQG TLAATTPIKD ANDDMLKAFQ
LEQKTLADWV A

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EF130-3 (SEQ ID NO:487)

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CGTTAG CAAGTTGAAA
CCAGCTGATG TGAAGAAAA TATGGCTCGT GAAACAACGT TTGACTTTGA TTCAGTTGAG
TCCTTGAGCA CAGAAGCGGT GATGAAAGCC CAATTTGAAA AAAAAACTT ACCTGTGATT
GGTGCCATTG CGATACCAAG TGTCGAAATT AATTTGCCCA TTTTAAAGG ATGTGCCAAT
GTCGCTTTAT TAACTGGTGC CGGGACCATG AAAGAAGATC AAGTCATGGG GAAAAACAAT
TATGCCTTGG CTAGTCATCG AACGGAAGAT GCGGTTTCCT TATTTTCACC TTTAGAAAGA
ACCAAAAAAG ACGAACTCAT TTATATCACT GATTTATCTA CTGTTTATAC ATACAAAATA
ACTTCTGTAG AAAAAATCGA ACCAACCCGT GTTGAGTTAA TTGATGACGT TCCTGGTCAA
AATATGATTA CCTTAATTAC CTGTGGCGAT TTACAAGCAA CGACGCGAAT TGCTGTTCAA
GGAACATTAG CAGCAACGAC GCCTATTAAA GACGCCAACG ACGATATGTT GAAGGCTTTC
CAATTGGAGC AAAAAACTTT AGCCGATTGG GTGGCT

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EF130-4 (SEQ ID NO:488)

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VSKLKP
ADVKKNMARE TTFDFDSVES LSTEAVMKAQ FENKNLPVIG AIAIPSVEIN LPIFKGLSNV
ALLTGAGTMK EDQVMGKNNY ALASHRTEDG VSLFSPLEKT KKDELIYITD LSTVYTYKIT
SVEKIEPTRV ELIDDPGQN MITLITCGDL QATTRIAVQG TLAATTPIKD ANDDMLKAFQ
LEQKTLADWV A

```

EF131-1 (SEQ ID NO:489)

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TAGGCGGAGG TAAGCGGTAT GCGTAAACGA CATGCAAAGA AAAGACATGG AGGAGTGAAT
TGGCTTTTTTA TAGTATGTTT GTTGGTGGTG ATTGGTGGTA GTGGTTATTT AATAAAAAACG
TTCTTTTTTCA CTAGAGATTC ACAAGTTAGT CAAGAATCGA AAGTGGTCTT GGAAGAAGAT
CGCCGAAGTG ATAATTATGC GAATTTAACG AAAGAAATAG TTGCACCAGA TAGTGGCGAA
CTTGATCAAA AAATTCAAGA AACAAATTAT ATTGGTTCGG CTTTGATCAT TAAAGATGAT
CAGGTTTTAG TAAATAAAGG ATATGGCTTT GCCAATTTTG AAAAGCAACA AGCCAACACG
CCAAACACAA GGTTTCAGAT TGGCTCAATT CAAAAATCTT TTACCACAAC CTGATCTTA
AAAGCAATTG AAGAAGGTAA ACTTACATTA GATACAAAAC TCGCTACGTT TTATCCGCAA
ATTCAAGGTG CTGAGGATAT TACGATTAGC GATATGTTGA ATATGACAAG TGGTTTAAAG
TTATCAGCAA TGCCTAATAA TATCGTTACC GATGAAGAAA TTATTCAATT TGTTAAACAA
AATACCATTG AAGTCAATAA AGGAAAATAC AATTATTCCC CAGTAAATTT TGTCTTTTA
GCAGGAATGT TAGAGAAAAT GTATCAACGT ACCTATCAAG AATTATTTAA TAATCTTTAT
CACAAAACGG CTGGTTTTAA GAATTTTGGC TTCTATGAAA CCTTATTGGA ACAGCCCAAT
AATTCAACAA GTTATAAATG GACAGAAGAT AATTCATATA ACCAAGTGCT CTCAATTCCCT

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TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCAGCTAGTT TTGCCCATGA ATTTGGGACT GGTAATGTGG ATATGACGAC AGGTGATTTG
TATTGGTACT TACATCAATT AACGAGTGGA CATTTAGTTT CCACCGCACT TTTGCAAAAA
TTATGGACGT CTTCTCAGCA AAGCTCTTAT CATGGCGGCA TCTATGTTCA TGATAATTAT
TTACGTTTAC ACGGCGTTGA AGCGGGTCAA CAAGCCCTGG TTTTATTTTC AAAAGATATG
AAGACAGGGG TCATATTGCT AACTAACTGT GTGAATCCAG CGAAATACAA AGAATTAATT
GGTTCGTTGT TCCATGATGT AACCAATTTA ACTGTAAAT TTAA

EF131-2 (SEQ ID NO:490)

MRKRH AKKRHGGVNW LFIVCLLVVI GSGYLIKTF FFTRDSQVSQ ESKVVLEEDR
RSDNYANLTK EIVAPDSGEL DQKIQETNYI GSALIIKDDQ VLVNKGYGFA NFEKQQANTP
NTRFQIGSIQ KSFTTTLILK AIEEGKLTLD TKLATFYPQI QGAEDITISD MLNMTSGLKL
SAMPNNIVTD EEIIQFVKQN TIQVNKGKYN YSPVNFVLLA GMLEKMYQRT YQELFNNLYH
KTAGLKNFGF YETLLEQPNN STSYKWTEEN SYNQVLSIPA ASFAHEFGTG NVDMTTGDL
WYLHQLTSGH LVSTALLQKL WTSSQQSSYH GGIYVHDNYL RLHGVEAGQQ ALVLFSDMK
TGVILLTNCV NPAKYKELIG SLFHDVTNLT VKF

EF131-3 (SEQ ID NO:491)

TTT AATAAAAACG
TTCTTTTCA CTAGAGATTC ACAAGTTAGT CAAGAATCGA AAGTGGTCTT GGAAGAAGAT
CGCCGAAGTG ATAATTATGC GAATTTAACG AAAGAAATAG TTGCACCAGA TAGTGGCGAA
CTTGATCAAA AAATTCAGA AACAAATTAT ATTGGTTCGG CTTTGATCAT TAAAGATGAT
CAGGTTTTAG TAAATAAAGG ATATGGCTTT GCCAATTTTG AAAAGCAACA AGCCAACACG
CCAAACACAA GGTTTCAGAT TGGCTCAATT CAAAATCTT TTACCACAAC CTTGATCTTA
AAAGCAATTG AAGAAGGTAA ACTTACATTA GATACAAAAC TCGCTACGTT TTATCCGCAA
ATTCAAGGTG CTGAGGATAT TACGATTAGC GATATGTTGA ATATGACAAG TGGTTTAAAG
TTATCAGCAA TGCCTAATAA TATCGTTACC GATGAAGAAA TTATTCAATT TGTTAAACAA
AATACCATTG AAGTCAATAA AGGAAAATAC AATTATTCCC CAGTAAATTT TGTCCTTTTA
GCAGGAATGT TAGAGAAAAT GTATCAACGT ACCTATCAAG AATTATTTAA TAATCTTTAT
CACAAAACGG CTGGTTTAA GAATTTTGGC TTCTATGAAA CCTTATTGGA ACAGCCCAAT
AATTCAACAA GTTATAAATG GACAGAAGAT AATTCATATA ACCAAGTGCT CTCAATTCCT
GCAGCTAGTT TTGCCCATGA ATTTGGGACT GGTAATGTGG ATATGACGAC AGGTGATTTG
TATTGGTACT TACATCAATT AACGAGTGGA CATTTAGTTT CCACCGCACT TTTGCAAAAA
TTATGGACGT CTTCTCAGCA AAGCTCTTAT CATGGCGGCA TCTATGTTCA TGATAATTAT
TTACGTTTAC ACGGCGTTGA AGCGGGTCAA CAAGCCCTGG TTTTATTTTC AAAAGATATG
AAGACAGGGG TCATATTGCT AACTAACTGT GTGAATCCAG CGAAATACAA AGAATTAATT
GGTTCGTTGT TCCATGATGT AACCAATTTA ACTGTAAAT TT

EF131-4 (SEQ ID NO:492)

LIKTF FFTRDSQVSQ ESKVVLEEDR
RSDNYANLTK EIVAPDSGEL DQKIQETNYI GSALIIKDDQ VLVNKGYGFA NFEKQQANTP
NTRFQIGSIQ KSFTTTLILK AIEEGKLTLD TKLATFYPQI QGAEDITISD MLNMTSGLKL
SAMPNNIVTD EEIIQFVKQN TIQVNKGKYN YSPVNFVLLA GMLEKMYQRT YQELFNNLYH
KTAGLKNFGF YETLLEQPNN STSYKWTEEN SYNQVLSIPA ASFAHEFGTG NVDMTTGDL
WYLHQLTSGH LVSTALLQKL WTSSQQSSYH GGIYVHDNYL RLHGVEAGQQ ALVLFSDMK
TGVILLTNCV NPAKYKELIG SLFHDVTNLT VKF

EF132-1 (SEQ ID NO:493)

TAGTTTTCTAATCTCACAAAACAAAAATTTTAAAGAAAGAAGGAGAGATCGTTATGATGAGAAAATGGAAGTAGTA
GTGGGAAGTCTGGGAATGTTGATTGCTCTTTTATATTTCGGGCATGTTCAACAAATAGTAAAGACAAAGATACAGTG

TABLE 1. Nucleotide and Amino Acid Sequences of *E. faecalis* Genes.

GCTTCGAACGAAAAATTAAAGGTAGTAGTTACTAATTCGATTTTAGCAGATATTACTGAAAAATATAGCAAAAGATAAA
 ATTGATTTACACAGTATCGTACCTATTGGGAAAGATCCCCACGAATATGAACCTTTGCCCTGAAGATGTTCAAAAAACT
 TCAAAAGCAGATTTGATTTTTTATAACGGTGTAACTTGGAmACTGGAGGAAATGCTTGGTTTACAAAATTAGTAAAA
 mATGCGAACAAAGAGGAAAAACAAAGACTATTTTGCAGCAAGTGATGGCATAGATGTTATTTACTTTAGAGGGTCAGAGT
 GAGAAAGGGAAGGAAGATCCCCATGCTTGGTTAAATTTAGAAAAACGGTATTATTTACGCTAAAAATATTGAAAAATGG
 TTAGCGGAAAAAGATCCTGATAATAAAAAATTCTATAAAAGAAAACTAGATAAGTATATTGAAAAGTTGGATTCTCTA
 GACAAAGAAGCTAAATCTAAATTTGCTTCAATTCGGAATGATAAAAAATGATTGTTACAAGTGAAGGATGCTTtAAA
 TATTTCTCGAAAGCGTATAATGTGCCTTCTGCTTACATTTGGGAAAtCAACACTGAAGAAGAAGGAACACCAGATCAA
 ATAAACACTTAGTTGAAAAATTACGCACAACAAAAGTTCCCTCCTTATTCGTAGAAAGTAGTGTGGACGATAGACCG
 ATGAAAACAGTATCAAAAGATACCAATATTCCTATCTATTCACGATTTTTTACTGATTCAATTGCAGAAAAAGGACAA
 GATGGTGATAGTTACTATGCGATGATGAAATGGAACCTGGATAAAATTGCTGAAGGCCTTTTCGAAATAA

EF132-2 (SEQ ID NO:494)

MMRKWKVVVGSGLMLIALFIFGACSTNSKDKDVTASNEKLKVVVTNSILADITENIAKDKIDLHSIVPIGKDPHEYEP
 LPEDVQKTSKADLIFYNGVNLXTGGNAWF TKLVKXANKEENKDYFAASDGIDVIYLEGQSEKGEDPHAWNLNLENGII
 YAKNIEKWLAEKDPDNKKFYKENLDKYIEKLDSL DKEAKSKFASIPNDKKMIVTSEGCFKYFSKAYNVPSAYIWEINT
 EEEGTPDQIKHLVEKLRTTKVPSLFVESSVDDRPMKTVSKDTNIPIYSTIFTDSIAEKGQDGDSYYAMMKWNLDKIAE
 GLSK.

EF132-3 (SEQ ID NO:495)

ATGTTCAACAAATAGTAAAGACAAAGATACAGTGGCTTCGAACGAAAAATTAAAGGTAGTAGTTACTAATTCGATTTT
 AGCAGATATTACTGAAAAATATAGCAAAAGATAAAATTGATTTACACAGTATCGTACCTATTGGGAAAGATCCCCACGA
 ATATGAACCTTTGCCCTGAAGATGTTCAAAAAACTTCAAAAGCAGATTTGATTTTTTATAACGGTGTAACTTGGAmAC
 TGGAGGAAATGCTTGGTTTACAAAATTAGTAAAAmATGCGAACAAAGAGGAAAAACAAAGACTATTTTGCAGCAAGTGA
 TGGCATAGATGTTATTTACTTTAGAGGGTCAGAGTGAGAAAGGAAGGAAGATCCCCATGCTTGGTTAAATTTAGAAAA
 CGGTATTATTTACGCTAAAAATATTGAAAAATGGTTAGCGGAAAAAGATCCTGATAATAAAAAATTTCTATAAAGAAAA
 TCTAGATAAGTATATTGAAAAGTTGGATTCTCTAGACAAAGAAGCTAAATCTAAATTTGCTTCAATTCGGAATGATAA
 AAAAATGATTGTTACAAGTGAAGGATGCTTtAAATATTTCTCGAAAGCGTATAATGTGCCTTCTGCTTACATTTGGGA
 AAtCAACACTGAAGAAGAAGGAACACCAGATCAAATAAAACACTTAGTTGAAAAATTACGCACAACAAAAGTTCCCTC
 CTTATTCGTAGAAAGTAGTGTGGACGATAGACCGATGAAAACAGTATCAAAAGATACCAATATTCCTATCTATTCAAC
 GATTTTTTACTGATTCAATTGCAGAAAAAGGACAAGATGGTGATAGTTACTATGCGATGATGAAATGGAACCTGGATAA
 AATTGCTGAAGGCCTTTTCGAAA

EF132-4 (SEQ ID NO:496)

CSTNSKDKDVTASNEKLKVVVTNSILADITENIAKDKIDLHSIVPIGKDPHEYEP LPEDVQKTSKADLIFYNGVNLXT
 GGNWFTKLVKXANKEENKDYFAASDGIDVIYLEGQSEKGEDPHAWNLNLENGIIYAKNIEKWLAEKDPDNKKFYKEN
 LDKYIEKLDSL DKEAKSKFASIPNDKKMIVTSEGCFKYFSKAYNVPSAYIWEINTEEGTPDQIKHLVEKLRTTKVPS
 LFVESSVDDRPMKTVSKDTNIPIYSTIFTDSIAEKGQDGDSYYAMMKWNLDKIAEGLSK

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

Query	GenBank Access. No.	GenBank Gene Description	BLAST Score	BLAST P-Value
EF002-2	gi 2338759	(AF018073) periplasmic sorbitol-binding protein; SmoE [Rhodobacter	113	3.60E-18
EF003-2	gi 1552773	hypothetical [Escherichia coli] >gnl PID d1012634 hypothetical 29.4	278	1.20E-53
EF003-2	gi 2196996	lipoprotein homolog [Treponema pallidum] >gi 2108234 29K protein	309	3.30E-44
EF003-2	gi 146649	lipoprotein-28 precursor [Escherichia coli] >gi 290510	263	9.20E-40
EF003-2	gi 148838	28 kDa membrane protein [Haemophilus influenzae]	197	2.10E-39
EF003-2	gi 1573614	28 kDa membrane protein (hlpA) [Haemophilus influenzae]	197	7.80E-39
EF003-2	gi 2314748	(AE000654) outer membrane protein [Helicobacter pylori]	263	4.60E-37
EF003-2	gi 349530	lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein	189	4.10E-29
EF003-2	gnl PID e118435	similar to hypothetical proteins [Bacillus subtilis]	158	2.70E-26
EF003-2	gi 349532	lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer	200	1.20E-25
EF003-2	gi 1336657	lipoprotein [Bacillus subtilis]	182	2.70E-25
EF003-2	gnl PID e233873	hypothetical protein [Bacillus subtilis] >gnl PID e1182900	186	1.30E-23
EF003-2	gi 294071	lipoprotein 3 [Pasteurella haemolytica]	199	6.60E-23
EF003-2	gi 349531	lipoprotein [Pasteurella haemolytica] >pir JN0752 JN0752 outer	198	1.30E-20
EF003-2	gi 294070	lipoprotein 2 [Pasteurella haemolytica]	198	1.80E-20
EF005-2	gi 537235	Kenn Rudd identifies as gpmB [Escherichia coli] >gi 1790856	127	6.20E-12
EF006-2	gi 1552773	hypothetical [Escherichia coli] >gnl PID d1012634 hypothetical 29.4	255	1.40E-60

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF006-2	gi 349532	lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer	221	6.40E-49
EF006-2	gi 2314748	(AE000654) outer membrane protein [Helicobacter pylori]	283	2.70E-48
EF006-2	gi 2196996	lipoprotein homolog [Treponema pallidum] >gi 2108234 29K protein	267	4.40E-47
EF006-2	gnl PID e118435	similar to hypothetical proteins [Bacillus subtilis]	359	1.80E-44
EF006-2	gi 349531	lipoprotein [Pasteurella haemolytica] >pir JN0752 JN0752 outer	218	3.80E-41
EF006-2	gi 294071	lipoprotein 3 [Pasteurella haemolytica]	220	2.30E-38
EF006-2	gi 146649	lipoprotein-28 precursor [Escherichia coli] >gi 290510	193	2.60E-38
EF006-2	gi 294070	lipoprotein 2 [Pasteurella haemolytica]	218	1.20E-36
EF006-2	gi 148838	28 kDa membrane protein [Haemophilus influenzae]	112	8.50E-34
EF006-2	gi 1573614	28 kDa membrane protein (hlpA) [Haemophilus influenzae]	112	1.50E-33
EF006-2	gi 349530	lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein	114	4.30E-29
EF006-2	gi 294069	lipoprotein 1 [Pasteurella haemolytica]	114	1.30E-27
EF006-2	gi 1336657	lipoprotein [Bacillus subtilis]	202	2.10E-26
EF006-2	gnl PID e233873	hypothetical protein [Bacillus subtilis] >gnl PID e1182900	200	6.50E-25
EF008-2	gi 493017	endocarditis specific antigen [Enterococcus faecalis]	1590	2.70E-211
EF008-2	gi 393269	adhesion protein [Streptococcus pneumoniae]	986	1.80E-129
EF008-2	gi 153834	adhesin specific for salivary pellicle of dental surfaces	973	1.00E-127
EF008-2	gi 1575030	surface adhesin A precursor [Streptococcus pneumoniae]	934	2.90E-126
EF008-2	gi 153826	adhesin B [Streptococcus sanguis] >pir A43583 A43583 adhesin B	916	3.90E-126
EF008-2	gi 1184932	ScbA [Streptococcus crista]	915	3.40E-125
EF008-2	gi 117994	surface antigen A variant precursor [Streptococcus pneumoniae]	917	5.60E-124

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF008-2	gi 310633	adhesin [Streptococcus gordonii]	891	6.00E-122
EF008-2	gnl PID e255529	lipoprotein [Staphylococcus epidermidis]	476	1.20E-99
EF008-2	gi 1573330	adhesin B precursor (fimA) [Haemophilus influenzae]	380	1.60E-68
EF008-2	gi 1245464	YfeA [Yersinia pestis] >gi 1245464 YfeA [Yersinia pestis]	355	1.20E-64
EF008-2	gi 755075	periplasmic-binding protein [Synechocystis sp.] >gnl PID d1018652 Mn	321	1.70E-62
EF008-2	gi 1335912	Ew1A [Erysipelothrix rhusiopathiae]	232	4.40E-42
EF008-2	gnl PID e118595	similar to ABC transporter (membrane protein) [Bacillus]	204	4.10E-38
EF008-2	gi 1777933	TroA [Treponema pallidum]	181	2.40E-35
EF009-2	gi 349531	lipoprotein [Pasteurella haemolytica] >pir JN0752 JN0752 outer	391	4.00E-64
EF009-2	gi 1552773	hypothetical [Escherichia coli] >gnl PID d1012634 hypothetical 29.4	359	1.90E-63
EF009-2	gi 294070	lipoprotein 2 [Pasteurella haemolytica]	391	6.40E-63
EF009-2	gi 349532	lipoprotein [Pasteurella haemolytica] >pir JN0753 JN0753 outer	386	1.10E-61
EF009-2	gi 148838	28 kDa membrane protein [Haemophilus influenzae]	286	5.60E-60
EF009-2	gi 1573614	28 kDa membrane protein (hlpA) [Haemophilus influenzae]	286	7.60E-60
EF009-2	gi 294069	lipoprotein 1 [Pasteurella haemolytica]	122	4.70E-59
EF009-2	gi 146649	lipoprotein-28 precursor [Escherichia coli] >gi 290510	326	2.20E-58
EF009-2	gi 349530	lipoprotein [Pasteurella haemolytica] >gi 150508 lipoprotein	239	7.80E-57
EF009-2	gi 294071	lipoprotein 3 [Pasteurella haemolytica]	344	4.90E-56
EF009-2	gi 2314748	(AE000654) outer membrane protein [Helicobacter pylori]	319	4.20E-53
EF009-2	gi 2196996	lipoprotein homolog [Treponema pallidum] >gi 2108234 29K protein	312	2.60E-41

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF009-2	gi 1336657	lipoprotein [Bacillus subtilis]	234	4.00E-32
EF009-2	gn PID e233873	hypothetical protein [Bacillus subtilis] > gn PID e1182900	242	1.40E-31
EF009-2	gn PID e118435	similar to hypothetical proteins [Bacillus subtilis]	102	6.80E-22
EF011-2	gn PID d10096 5	ferric anguibactin-binding protein precursor FatB of V.	579	3.10E-98
EF011-2	gn PID d10096 5	ferric anguibactin-binding protein precursor FatB of V.	579	3.10E-98
EF011-2	gn PID e185374	ceuE gene product [Campylobacter coli]	284	1.30E-89
EF011-2	gn PID e185374	ceuE gene product [Campylobacter coli]	284	1.30E-89
EF011-2	gi 150756	40 kDa protein [Plasmid pJM1] > pir A29928 A29928 membrane-associated	222	2.80E-52
EF011-2	gi 150756	40 kDa protein [Plasmid pJM1] > pir A29928 A29928 membrane-associated	222	2.80E-52
EF012-2	gi 309662	pheromone binding protein [Plasmid pCF10] > pir B53309 B53309	266	8.70E-116
EF012-2	gi 388269	traC [Plasmid pAD1] > pir A53310 A53310 pheromone cAD1 binding	252	1.10E-109
EF012-2	gn PID d10118 5	TRAC [Enterococcus faecalis]	281	3.60E-103
EF012-2	gn PID d10065 5	TraC [Enterococcus faecalis]	277	2.30E-102
EF012-2	gi 312940	threonine kinase [Streptococcus equisimilis] > pir S28153 S28153	227	1.90E-67
EF012-2	gi 48808	dciAE [Bacillus subtilis]	228	1.70E-46

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF012-2	pir S16651 S166	dciAE protein - <i>Bacillus subtilis</i>	228	1.00E-45
EF012-2	gnl PID e118149	(AJ002571) DppE [<i>Bacillus subtilis</i>] >gnl PID e1183316	228	3.80E-45
EF012-2	gi 40005	OppA gene product [<i>Bacillus subtilis</i>]	281	3.90E-44
EF012-2	gi 143603	sporulation protein [<i>Bacillus subtilis</i>] >gnl PID e1183163	281	7.70E-44
EF012-2	gnl PID d10156 3	Periplasmic oligopeptide-binding protein precursor.	152	2.20E-43
EF012-2	gi 1574679	oligopeptide binding protein (oppA) [<i>Haemophilus influenzae</i>]	178	2.20E-42
EF012-2	gi 47802	Opp A (AA1-542) [<i>Salmonella typhimurium</i>] >gi 47808 precursor	128	1.00E-37
EF012-2	gi 882550	ORF_f535 [<i>Escherichia coli</i>] >gi 1789397 (AE000384) f535; This 535 aa	228	5.30E-36
EF014-2	pir D70070 D70 0	transcriptional regulator homolog ywtF - <i>Bacillus subtilis</i>	101	1.40E-27
EF014-2	gnl PID e116988	capsular polysaccharide synthesis protein [<i>Streptococcus</i>	121	9.50E-27
EF014-2	gi 2804769	(AF030373) putative regulatory protein [<i>Streptococcus</i> pneumoniae]	121	9.50E-27
EF014-2	gnl PID e289126	unknown [<i>Streptococcus pneumoniae</i>]	121	1.00E-24
EF014-2	gi 2267239	ORF1 [<i>Staphylococcus epidermidis</i>]	234	1.50E-24
EF014-2	gi 485275	putative regulatory protein [<i>Streptococcus pneumoniae</i>]	121	3.90E-24
EF014-2	gi 2804735	(AF030367) putative regulatory protein [<i>Streptococcus</i> pneumoniae]	121	3.90E-24
EF014-2	gi 2804747	(AF030369) putative regulatory protein [<i>Streptococcus</i> pneumoniae]	121	3.90E-24

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF014-2	gi 1762327	putative transcriptional regulator [Bacillus subtilis]	185	2.80E-22
EF014-2	gi 143156	membrane bound protein [Bacillus subtilis] >gnl PID e1184471	116	1.10E-21
EF014-2	gnl PID d10189 5	membrane bound protein LytR [Synechocystis sp.]	113	6.20E-20
EF014-2	gi 1276874	EpsA [Streptococcus thermophilus]	103	4.00E-17
EF016-2	gnl PID e118566	similar to amino acid ABC transporter (binding protein)	194	3.70E-35
EF016-2	gi 40934	arginine binding protein [Escherichia coli] >gi 769794 artI	121	1.60E-31
EF016-2	gnl PID d10152 7	Arginine-binding periplasmic protein 2 precursor [Escherichia]	121	4.80E-31
EF016-2	gi 687652	FliY [Escherichia coli] >gnl PID d1016464 FliY protein precursor.	160	5.70E-31
EF016-2	gi 2650410	(AE001090) glutamine ABC transporter, periplasmic glutamine-binding	122	3.30E-29
EF016-2	gi 1649035	high-affinity periplasmic glutamine binding protein [Salmonella]	104	1.80E-27
EF016-2	gi 1574634	glutamine-binding periplasmic protein (glnH) [Haemophilus]	174	2.50E-27
EF016-2	gi 41569	GlnH precursor (AA -22 to 226) [Escherichia coli] >gnl PID d1015250	106	4.70E-27
EF016-2	gnl PID d10152 7	Arginine-binding periplasmic protein 1 precursor [Escherichia]	109	3.70E-26
EF016-2	gi 769791	artI [Escherichia coli] >gi 769791 artI [Escherichia coli]	127	2.30E-25
EF016-2	gnl PID d10089 2	homologous to Gln-binding periplasmic proteins [Bacillus]	117	8.50E-24
EF016-2	gi 154125	J protein [Salmonella typhimurium] >gi 47718 reading frame	118	2.10E-23

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	hisJ			
EF016-2	gnl PID d10168 8	HISTIDINE-BINDING PERIPLASMIC PROTEIN PRECURSOR (HBP).	117	4.50E-23
EF016-2	gi 1166636	histidine-binding periplasmic protein HisJ [Escherichia coli]	117	6.60E-23
EF017-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	421	4.50E-128
EF017-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	417	5.10E-124
EF017-2	gnl PID d10065 5	TraC [Enterococcus faecalis]	414	4.40E-123
EF017-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	415	2.40E-119
EF017-2	gi 40005	OppA gene product [Bacillus subtilis]	294	6.20E-82
EF017-2	gi 143603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	290	2.80E-79
EF017-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	241	2.40E-71
EF017-2	gi 48808	dciAE [Bacillus subtilis]	270	1.10E-61
EF017-2	gnl PID e118149	(AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316	270	1.50E-61
EF017-2	pir S16651 S166	dciAE protein - Bacillus subtilis	270	3.10E-60
EF017-2	gi 304925	periplasmic oligopeptide binding protein [Escherichia coli]	171	2.60E-57
EF017-2	gi 147014	oligopeptide binding protein precursor [Escherichia coli]	171	8.70E-56
EF017-2	gi 47802	Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	154	1.30E-52

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF017-2	gi 882550	ORF_f535 [Escherichia coli] >gi 1789397 (AE000384) f535; This 535 aa	135	5.50E-52
EF017-2	gi 1574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]	168	2.90E-43
EF019-2	gi 438458	likely N-terminal signal sequence; mature protein probably	104	2.30E-17
EF021-2	gnl PID e311492	unknown [Bacillus subtilis] >gnl PID e1184232 similar to ABC	317	2.50E-103
EF021-2	bbs 173803	CD4+ T cell-stimulating antigen [Listeria monocytogenes, 85EO-1167,	476	2.80E-81
EF021-2	gi 581809	tmbC gene product [Treponema pallidum] >pir A43595 A43595 membrane	152	3.20E-71
EF021-2	gi 2688280	(AE001143) basic membrane protein C (bmpC) [Borrelia burgdorferi]	101	5.50E-27
EF021-2	gnl PID e117283	membrane protein A [Borrelia garinii]	142	6.50E-22
EF021-2	gnl PID e117283	membrane protein A [Borrelia burgdorferi]	141	9.20E-22
EF021-2	gnl PID e117283	membrane protein A [Borrelia burgdorferi] >gi 516592 membrane	141	9.20E-22
EF021-2	gnl PID e117283	bmpA(p39,ORF1) [Borrelia burgdorferi]	141	1.70E-21
EF021-2	gi 508421	antigen P39 [Borrelia burgdorferi] >gi 2688281 (AE001143) basic	141	1.70E-21
EF021-2	gi 1753225	BmpA protein [Borrelia burgdorferi]	141	2.70E-20
EF021-2	gnl PID e117282	membrane protein A [Borrelia afzelii]	141	8.60E-20
EF021-2	gnl PID e117283	membrane protein A [Borrelia afzelii]	141	8.60E-20
EF021-2	gnl PID e117283	membrane protein A [Borrelia afzelii]	141	8.60E-20
EF021-2	gnl PID e117282	bmpA(p39,ORF1) [Borrelia burgdorferi]	141	1.50E-19

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF022-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	324	5.90E-66
EF022-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	307	5.60E-60
EF022-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	301	4.80E-59
EF022-2	gnl PID e118149	(AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316	170	5.10E-59
EF022-2	gi 48808	dciAE [Bacillus subtilis]	170	5.20E-59
EF022-2	gnl PID d10065 5	TraC [Enterococcus faecalis]	299	2.80E-58
EF022-2	pir S16651 S166	dciAE protein - Bacillus subtilis	170	1.60E-57
EF022-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	280	2.70E-53
EF022-2	gi 40005	OppA gene product [Bacillus subtilis]	154	7.30E-48
EF022-2	gi 143603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	154	3.10E-47
EF022-2	gi 2688227	(AE001139) oligopeptide ABC transporter, periplasmic	215	1.00E-36
EF022-2	gi 2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	215	1.00E-36
EF022-2	gi 304925	periplasmic oligopeptide binding protein [Escherichia coli]	131	1.30E-35
EF022-2	gi 147014	oligopeptide binding protein precursor [Escherichia coli]	131	1.80E-34
EF022-2	gi 47802	Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	138	4.90E-34
EF023-2	gi 309662	pheromone binding protein [Plasmid pCF10]	231	4.70E-66

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		>pir B53309 B53309		
EF023-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	223	4.80E-62
EF023-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	226	1.00E-58
EF023-2	gnl PID d10065 5	TraC [Enterococcus faecalis]	226	4.40E-58
EF023-2	gi 48808	dciaE [Bacillus subtilis]	157	1.20E-57
EF023-2	gnl PID e118149	(AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316	157	1.20E-57
EF023-2	pir S16651 S166	dciaE protein - Bacillus subtilis	157	3.80E-56
EF023-2	gi 40005	OppA gene product [Bacillus subtilis]	137	2.30E-53
EF023-2	gi 143603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	133	6.90E-53
EF023-2	gi 47802	Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	135	2.00E-41
EF023-2	gi 2688227	(AE001139) oligopeptide ABC transporter, periplasmic	187	9.40E-41
EF023-2	gi 2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	187	1.90E-40
EF023-2	gi 882550	ORF_f535 [Escherichia coli] >gi 1789397 (AE000384) f535; This 535 aa	155	1.30E-38
EF023-2	gi 304925	periplasmic oligopeptide binding protein [Escherichia coli]	130	9.00E-37
EF023-2	gi 147014	oligopeptide binding protein precursor [Escherichia coli]	130	3.70E-34
EF026-2	gi 2352482	(AF005097) unknown [Lactococcus lactis]	141	1.10E-23
EF027-2	gi 309662	pheromone binding protein [Plasmid pCF10]	198	6.20E-71

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		>pir B53309 B53309			
EF027-2	gnl PID d10065 5	TraC [Enterococcus faecalis]	202	1.50E-68	
EF027-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	202	1.50E-68	
EF027-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	213	8.30E-68	
EF027-2	gnl PID e118149	(AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316	222	3.70E-41	
EF027-2	gi 48808	dciAE [Bacillus subtilis]	222	4.90E-41	
EF027-2	pir S16651 S166	dciAE protein - Bacillus subtilis	222	1.10E-39	
EF027-2	gi 40005	OppA gene product [Bacillus subtilis]	251	4.10E-39	
EF027-2	gi 143603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	247	5.80E-39	
EF027-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	233	8.90E-33	
EF027-2	gi 2688227	(AE001139) oligopeptide ABC transporter, periplasmic	131	2.40E-24	
EF027-2	gi 2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	131	2.40E-24	
EF027-2	gi 2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gi 2689891 (AE000792)	117	3.00E-20	
EF027-2	gi 1574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]	130	3.50E-20	
EF028-2	gnl PID d10204 7	B. subtilis alkaline phosphatase IIIA; P19405 secretory	996	3.60E-131	
EF028-2	pir B39096 B39	alkaline phosphatase (EC 3.1.3.1) III precursor - Bacillus	982	2.90E-129	

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

	0			
EF028-2	gi 470383	alkaline phosphatase A [Bacillus subtilis] >gnl PID e1182942	803	4.80E-119
EF028-2	gi 143324	APase I [Bacillus licheniformis] >pir A44828 A44828 alkaline	184	3.00E-54
EF028-2	gi 147243	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	183	8.30E-54
EF028-2	gi 147237	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	178	4.40E-53
EF028-2	gi 147239	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	178	4.40E-53
EF028-2	gi 147241	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	178	4.40E-53
EF028-2	gi 1277127	phoA gene product [Cloning vector pFW_phoA1] >gi 1277130	174	4.90E-53
		phoA gene		
EF028-2	gi 147229	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	178	8.40E-53
EF028-2	gi 818851	alkaline phosphatase [synthetic construct]	174	1.10E-52
EF028-2	gi 147245	alkaline phosphatase (phoA) (EC 3.1.3.1) [Escherichia fergusonii]	177	1.20E-52
EF028-2	gi 147231	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	174	1.60E-52
EF028-2	gi 147235	alkaline phosphatase precursor (EC 3.1.3.1) [Escherichia coli]	174	1.60E-52
EF028-2	gi 1016010	alkaline phosphatase with N-terminal PelB-leader and C-terminal	174	1.60E-52
EF029-2	gi 1750126	YncB [Bacillus subtilis] >gnl PID e1183421 similar to micrococcal	257	3.50E-55
EF029-2	gnl PID e118360	similar to hypothetical proteins [Bacillus subtilis]	263	7.80E-53
EF029-2	gi 673492	nuclease [Staphylococcus aureus] >pir A00790 NCSAF micrococcal	320	2.20E-39
EF029-2	gi 532653	thermonuclease [Staphylococcus hyicus]	155	9.10E-39

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF029-2	gi 47146	thermonuclease [Staphylococcus intermedius] >pir S26079 S26079	145	4.90E-32
EF030-2	gi 48808	dciAE [Bacillus subtilis]	149	1.10E-66
EF030-2	gnl PID e118149	(AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316	149	1.50E-66
EF030-2	pir S16651 S166	dciAE protein - Bacillus subtilis	149	5.90E-66
EF030-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	227	7.40E-52
EF030-2	gnl PID d10118 5	TRAC [Enterococcus faecalis]	237	7.40E-52
EF030-2	gnl PID d10065 5	TraC [Enterococcus faecalis]	233	9.70E-51
EF030-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	229	3.00E-48
EF030-2	gi 312940	threonine kinase [Streptococcus equisimilis] >pir S28153 S28153	277	3.00E-45
EF030-2	gi 47802	Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	125	8.50E-34
EF030-2	gi 2688227	(AE001139) oligopeptide ABC transporter, periplasmic	211	4.80E-31
EF030-2	gi 2281458	(AF000366) oligopeptide permease homolog AII [Borrelia burgdorferi]	211	4.80E-31
EF030-2	gi 40005	OppA gene product [Bacillus subtilis]	148	1.20E-30
EF030-2	gi 143603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	144	4.80E-30
EF030-2	gi 2281468	(AF000948) OppAIV [Borrelia burgdorferi] >gi 2689891 (AE000792)	210	2.10E-29

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF030-2	gi 1574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]	148	6.00E-29
EF033-2	gn PID e118439	similar to iron-binding protein [Bacillus subtilis]	164	2.60E-14
EF033-2	pir S54437 S544	hemin binding protein - Yersinia enterocolitica	108	1.40E-11
EF033-2	gi 1619623	hemin binding protein [Yersinia enterocolitica]	108	2.00E-11
EF036-2	gn PID d10102 2	ORF108 [Bacillus subtilis] >gn PID e1185766 alternate gene	544	1.20E-96
EF036-2	gi 2622858	(AE000929) phosphate-binding protein PstS [Methanobacterium]	183	1.40E-45
EF036-2	gi 2622859	(AE000929) phosphate-binding protein PstS homolog [Methanobacterium]	158	2.40E-41
EF036-2	gi 2688115	(AE001132) phosphate ABC transporter, periplasmic phosphate-binding	117	1.10E-12
EF037-2	gi 2352482	(AF005097) unknown [Lactococcus lactis]	141	1.10E-23
EF040-2	gi 1657516	hypothetical protein [Escherichia coli] >gi 1786511 (AE000139)	208	1.90E-29
EF040-2	gi 293265	2-5A-dependent RNase [Mus musculus] >pir B45771 B45771	105	1.00E-17
EF040-2	gi 287865	G9a [Homo sapiens] >pir S30385 S30385 G9a protein - human	143	8.30E-14
EF040-2	gi 311817	erythroid ankyrin [Mus musculus] >pir S37771 S37771 ankyrin,	119	4.80E-13
EF040-2	gi 191940	ankyrin [Mus musculus] >pir 49502 49502 ankyrin - mouse	119	4.90E-13
EF040-2	gi 747710	alt. ankyrin (variant 2.2) [Homo sapiens]	120	1.50E-12
EF040-2	gi 178646	ankyrin [Homo sapiens]	120	1.80E-12
EF040-2	gi 1845265	ankyrin [Homo sapiens]	120	1.80E-12
EF040-2	pir A35049 A35 0	ankyrin 1, erythrocyte splice form 2 - human	120	1.80E-12

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF040-2	pir B35049 B350	ankyrin 1, erythrocyte splice form 3 - human	120	1.80E-12
EF040-2	gi 28702	ankyrin (variant 2.1) [Homo sapiens] >pir S08275 SJHUK ankyrin 1,	120	1.80E-12
EF041-2	gi 388269	traC [Plasmid pAD1] >pir A53310 A53310 pheromone cAD1 binding	670	1.40E-87
EF041-2	gnl PID d100655	TraC [Enterococcus faecalis]	662	1.50E-85
EF041-2	gnl PID d101185	TRAC [Enterococcus faecalis]	662	1.50E-85
EF041-2	gi 309662	pheromone binding protein [Plasmid pCF10] >pir B53309 B53309	648	1.20E-83
EF041-2	gi 48808	dcIAE [Bacillus subtilis]	218	1.20E-57
EF041-2	gnl PID e118149	(AJ002571) DppE [Bacillus subtilis] >gnl PID e1183316	218	1.40E-57
EF041-2	pir S16651 S166	dcIAE protein - Bacillus subtilis	218	2.10E-56
EF041-2	gi 882550	ORF_f535 [Escherichia coli] >gi 1789397 (AE000384) f535; This 535 aa	146	7.30E-40
EF041-2	gi 143603	sporulation protein [Bacillus subtilis] >gnl PID e1183163	278	1.00E-34
EF041-2	gi 40005	OppA gene product [Bacillus subtilis]	279	1.00E-34
EF041-2	gi 47802	Opp A (AA1-542) [Salmonella typhimurium] >gi 47808 precursor	141	6.60E-30
EF041-2	gi 304925	periplasmic oligopeptide binding protein [Escherichia coli]	160	1.90E-29
EF041-2	gi 1574679	oligopeptide binding protein (oppA) [Haemophilus influenzae]	163	1.00E-28

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF041-2	gi 147014	oligopeptide binding protein precursor [Escherichia coli]	160	1.50E-28
EF041-2	gi 2253286	(AF005657) plasminogen binding protein [Borrelia burgdorferi]	134	5.00E-27
EF045-2	gi 308854	oligopeptide binding protein [Lactococcus lactis] >pir E53290 E53290	437	3.20E-125
EF045-2	gi 495181	oligopeptide binding protein [Lactococcus lactis]	426	9.70E-124
EF045-2	gi 677945	AppA [Bacillus subtilis] >gnl PID e1183158 oligopeptide ABC	154	2.30E-31
EF045-2	gi 293014	peptide-binding protein [Lactococcus lactis] >pir B47098 B47098	158	2.40E-14
EF048-2	gi 1574060	hypothetical [Haemophilus influenzae] >pir I64164 I64164	250	2.30E-41
EF048-2	dbj AB001488_2	(AB001488) SIMILAR TO C4-DICARBOXYLATE-BINDING PERIPLASMIC	208	3.60E-34
EF048-2	gi 466717	No definition line found [Escherichia coli] >gi 1790004 (AE000435)	199	1.30E-30
EF048-2	gi 46006	periplasmic C4-dicarboxylate binding-protein [Rhodobacter capsulatus]	162	1.40E-25
EF048-2	gi 1573102	hypothetical [Haemophilus influenzae] >pir H64143 H64143	244	3.80E-25
EF048-2	gi 2182530	(AE000085) Y4mM [Rhizobium sp. NGR234]	114	5.60E-18
EF048-2	gi 1572999	hypothetical [Haemophilus influenzae] >pir E64141 E64141	116	5.90E-15
EF049-2	gi 149581	maturation protein [Lactobacillus paracasei] >pir A44858 A44858	241	2.40E-55
EF049-2	gi 47198	ORF (AA 1 to 299) [Lactococcus lactis cremoris] >pir S08083 S08083	239	1.00E-54
EF049-2	gi 432402	maturation protein [Lactococcus lactis] >gi 623055 proteinase	239	6.20E-54

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF049-2	gi 472835	ORF1 [<i>Lactococcus lactis cremoris</i>]	241	1.50E-53
EF049-2	gi 39782	33kDa lipoprotein [<i>Bacillus subtilis</i>] >gnl PID e325181 33kDa	128	8.90E-40
EF051-2	gnl PID d10114 2	molybdate-binding periplasmic protein [<i>Synechocystis</i> sp.]	173	3.20E-50
EF051-2	gnl PID e118602	alternate gene name: yvsD; similar to molybdate-binding	314	5.90E-50
EF051-2	gi 1574546	lsg locus hypothetical [<i>Haemophilus influenzae</i>] >pir A64175 A64175	161	2.20E-43
EF051-2	gi 504498	periplasmic molybdate-binding protein [<i>Escherichia coli</i>] >gi 1147817	148	1.40E-30
EF051-2	gi 148939	ORF 8 [<i>Haemophilus influenzae</i>] >pir S27583 S27583 hypothetical	150	8.10E-28
EF054-2	gi 150556	surface protein [Plasmid pCF10] >pir A41826 A41826 probable	1490	1.80E-192
EF054-2	gnl PID e236571	cell wall anchoring signal [<i>Enterococcus faecalis</i>]	515	8.10E-64
EF054-2	gi 45738	ORFC [<i>Enterococcus faecalis</i>] >pir JH0204 JH0204 hypothetical 30.5K	372	1.60E-58
EF054-2	gi 496520	orf iota [<i>Streptococcus pyogenes</i>] >pir S68125 S45091 hypothetical	362	1.30E-43
EF054-2	gi 160693	sporozoite surface protein [<i>Plasmodium yoelii</i>] >pir A45559 A45559	286	4.30E-33
EF054-2	gi 1813523	PbTRAP [<i>Plasmodium berghei</i>]	305	1.30E-32
EF054-2	gnl PID e225687	zinc finger protein [<i>Mus musculus</i>] >gnl PID e225688 zinc	246	3.60E-26
EF054-2	gi 2290394	IgG and IgE immunoreactive antigen recognized by sera from patients	242	1.40E-25

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF054-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from patients	237	7.80E-25
EF054-2	gi 46523	B antigen [Streptococcus agalactiae]	232	2.80E-23
EF054-2	pir S15330 FCS O	IgA Fc receptor precursor - Streptococcus agalactiae	228	1.00E-22
EF054-2	gi 1620100	Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B	210	3.10E-21
EF054-2	gi 63686	NF-M c-terminus [Gallus gallus]	222	6.90E-21
EF054-2	gi 63689	NF-M protein [Gallus gallus] >pir S15762 S15762 neurofilament triplet	222	8.50E-21
EF054-2	gi 757867	TATA-box like sequence (Us11) [Human herpesvirus 1] >gi 291493 18	194	4.10E-19
EF059-2	gn PID e236571	cell wall anchoring signal [Enterococcus faecalis]	418	5.60E-95
EF059-2	gi 150556	surface protein [Plasmid pCF10] >pir A41826 A41826 probable	606	3.70E-87
EF059-2	gi 45738	ORFC [Enterococcus faecalis] >pir JH0204 JH0204 hypothetical 30.5K	366	9.30E-50
EF059-2	gi 496520	orf iota [Streptococcus pyogenes] >pir S68125 S45091 hypothetical	367	5.90E-44
EF059-2	gi 160693	sporozoite surface protein [Plasmodium yoelii] >pir A45559 A45559	344	1.10E-38
EF059-2	gi 1813523	PbTRAP [Plasmodium berghei]	295	2.50E-32
EF059-2	gi 2290394	IgG and IgE immunoreactive antigen recognized by sera from patients	251	3.00E-29
EF059-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from patients	251	3.40E-29

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF059-2	gi 1620100	Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B	253	6.40E-27
EF059-2	gi 46521	Fc receptor [Streptococcus agalactiae] >pir A60234 A60234 IgA Fc	197	2.70E-26
EF059-2	gi 46523	B antigen [Streptococcus agalactiae]	232	9.30E-26
EF059-2	pir S15330 FCS O	IgA Fc receptor precursor - Streptococcus agalactiae	232	9.30E-26
EF059-2	gnl PID e225687	zinc finger protein [Mus musculus] >gnl PID e225688 zinc	234	1.40E-22
EF059-2	gi 425356	zona pellucida protein [Pseudopleuronectes americanus]	229	1.00E-21
EF059-2	gi 457769	Collagen [Bombyx mori] >pir S42886 S42886 collagen - silkworm	209	7.60E-19
EF061-2	gnl PID e236571	cell wall anchoring signal [Enterococcus faecalis]	925	8.10E-118
EF061-2	gi 150556	surface protein [Plasmid pCF10] >pir A41826 A41826 probable	350	1.50E-107
EF061-2	gi 496520	orf iota [Streptococcus pyogenes] >pir S68125 S45091 hypothetical	308	1.40E-58
EF061-2	gi 45738	ORFC [Enterococcus faecalis] >pir JH0204 JH0204 hypothetical 30.5K	322	6.40E-50
EF061-2	gi 1813523	PbTRAP [Plasmodium berghei]	263	1.00E-26
EF061-2	gi 160693	sporozoite surface protein [Plasmodium yoelii] >pir A45559 A45559	241	9.00E-25
EF061-2	gi 63686	NF-M c-terminus [Gallus gallus]	232	2.10E-22
EF061-2	gi 63689	NF-M protein [Gallus gallus] >pir S15762 S15762 neurofilament triplet	232	2.60E-22
EF061-2	gi 2290392	IgG and IgE immunoreactive antigen recognized by sera from	176	2.40E-21

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		patients		
EF061-2	gi 1620100	Pro- and Glu-rich, PENPEV (10x); similar to Streptococcus B	165	2.70E-20
EF061-2	gnl PIDe225687	zinc finger protein [Mus musculus] >gnl PIDe225688 zinc	197	7.80E-19
EF061-2	gi 160355	interspersed repeat antigen [Plasmodium falciparum]	199	8.20E-18
EF061-2	gi 410750	interspersed repeat antigen [Plasmodium falciparum]	199	8.90E-18
EF061-2	gi 2290388	IgG and IgE immunoreactive antigen recognized by sera from patients	182	1.40E-17
EF061-2	gi 2290394	IgG and IgE immunoreactive antigen recognized by sera from patients	180	2.80E-17
EF062-2	gi 47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis]	3716	0
EF062-2	gi 43324	aggregation substance (ASPI) [Enterococcus faecalis]	4003	0
EF062-2	gi 2109266	aggregation substance [Enterococcus faecium]	5523	0
EF062-2	gi 150555	aggregation substance [Plasmid pCF10] >pir H41662 H41662 150K mating	6338	0
EF062-2	gi 1100973	SspB precursor [Streptococcus gordonii]	110	9.90E-39
EF062-2	gi 47248	Pac protein precursor (AA -38 to 1527) [Streptococcus mutans]	107	1.70E-38
EF062-2	gnl PIDd10150 ₇	surface protein antigen precursor [Streptococcus sobrinus]	132	5.00E-36
EF062-2	gi 47267	cell surface antigen I/II [Streptococcus mutans] >pir S06839 S06839	107	6.50E-36
EF062-2	bbs 148453	SpaA=endocarditis immunodominant antigen [Streptococcus sobrinus,	132	1.20E-35

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF062-2	gi 47620	antigen I /II [Streptococcus sobrinus] >pir A60338 A60338 surface	132	2.90E-35
EF062-2	pir A35186 A351	salivary agglutinin receptor precursor - Streptococcus	109	2.10E-34
EF062-2	gi 1100971	SspA [Streptococcus gordonii]	110	3.80E-32
EF062-2	gi 1100975	SspA [Streptococcus gordonii]	110	2.30E-21
EF063-2	gi 47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis]	3716	0
EF063-2	gi 43324	aggregation substance (ASP1) [Enterococcus faecalis]	4003	0
EF063-2	gi 2109266	aggregation substance [Enterococcus faecium]	5523	0
EF063-2	gi 150555	aggregation substance [Plasmid pCF10] >pir H41662 H41662 150K mating	6338	0
EF063-2	gi 1100973	SspB precursor [Streptococcus gordonii]	110	9.90E-39
EF063-2	gi 47248	Pac protein precursor (AA -38 to 1527) [Streptococcus mutans]	107	1.70E-38
EF063-2	gn PID d101507	surface protein antigen precursor [Streptococcus sobrinus]	132	5.00E-36
EF063-2	gi 47267	cell surface antigen I/II [Streptococcus mutans] >pir S06839 S06839	107	6.50E-36
EF063-2	bbs 148453	SpaA=endocarditis immunodominant antigen [Streptococcus sobrinus]	132	1.20E-35
EF063-2	gi 47620	antigen I /II [Streptococcus sobrinus] >pir A60338 A60338 surface	132	2.90E-35
EF063-2	pir A35186 A351	salivary agglutinin receptor precursor - Streptococcus	109	2.10E-34

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF063-2	gi 1100971	SspA [Streptococcus gordonii]	110	3.80E-32
EF063-2	gi 1100975	SspA [Streptococcus gordonii]	110	2.30E-21
EF064-2	gi 47049	asa1 gene product (AA 1-1296) [Enterococcus faecalis]	3716	0
EF064-2	gi 43324	aggregation substance (ASPI) [Enterococcus faecalis]	4003	0
EF064-2	gi 2109266	aggregation substance [Enterococcus faecium]	5523	0
EF064-2	gi 150555	aggregation substance [Plasmid pCF10] >pir H41662 H41662 150K mating	6338	0
EF064-2	gi 1100973	SspB precursor [Streptococcus gordonii]	110	9.90E-39
EF064-2	gi 47248	PAC protein precursor (AA -38 to 1527) [Streptococcus mutans]	107	1.70E-38
EF064-2	gn PID d10150 7	surface protein antigen precursor [Streptococcus sobrinus]	132	5.00E-36
EF064-2	gi 47267	cell surface antigen I/II [Streptococcus mutans] >pir S06839 S06839	107	6.50E-36
EF064-2	bbs 148453	SpaA=endocarditis immunodominant antigen [Streptococcus sobrinus,	132	1.20E-35
EF064-2	gi 47620	antigen I /II [Streptococcus sobrinus] >pir A60338 A60338 surface	132	2.90E-35
EF064-2	pir A35186 A35 1	salivary agglutinin receptor precursor - Streptococcus	109	2.10E-34
EF064-2	gi 1100971	SspA [Streptococcus gordonii]	110	3.80E-32
EF064-2	gi 1100975	SspA [Streptococcus gordonii]	110	2.30E-21
EF068-2	gi 790398	T06D8.1 [Caenorhabditis elegans]	137	8.50E-17

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF068-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	210	5.80E-16
EF068-2	gi 2286204	(AF011339) unknown [Acinetobacter calcoaceticus]	121	8.40E-16
EF068-2	gi 330862	membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1	208	1.10E-15
EF068-2	gi 1707247	partial CDS [Caenorhabditis elegans]	131	3.70E-15
EF068-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	203	6.20E-15
EF068-2	gi 213392	antifreeze glycoprotein [Notothenia coriiceps] >pir A38420 A38420	102	4.60E-13
EF068-2	gnl PID e125464	(AL022022) PGRS-family protein [Mycobacterium tuberculosis]	145	1.50E-12
EF068-2	gi 951460	FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155 mucin	109	2.70E-12
EF069-2	gi 790398	T06D8.1 [Caenorhabditis elegans]	137	8.50E-17
EF069-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	210	5.80E-16
EF069-2	gi 2286204	(AF011339) unknown [Acinetobacter calcoaceticus]	121	8.40E-16
EF069-2	gi 330862	membrane glycoprotein [Equine herpesvirus 1] >pir H36802 VGBEX1	208	1.10E-15
EF069-2	gi 1707247	partial CDS [Caenorhabditis elegans]	131	3.70E-15
EF069-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	203	6.20E-15
EF069-2	gi 213392	antifreeze glycoprotein [Notothenia coriiceps]	102	4.60E-13

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		>pir A38420 A38420			
EF069-2	gnl PID e125464	(AL022022) PGRS-family protein [Mycobacterium tuberculosis]	145		1.50E-12
EF069-2	gi 951460	FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155	109		2.70E-12
		mucin			
EF070-2	gi 790398	T06D8.1 [Caenorhabditis elegans]	137		8.50E-17
EF070-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	210		5.80E-16
EF070-2	gi 2286204	(AF011339) unknown [Acinetobacter calcoaceticus]	121		8.40E-16
EF070-2	gi 330862	membrane glycoprotein [Equine herpesvirus 1]	208		1.10E-15
		>pir H36802 VGBEX1			
EF070-2	gi 1707247	partial CDS [Caenorhabditis elegans]	131		3.70E-15
EF070-2	gnl PID d10208 4	membrane glycoprotein [Equine herpesvirus 1]	203		6.20E-15
EF070-2	gi 213392	antifreeze glycoprotein [Notothenia coriiceps]	102		4.60E-13
		>pir A38420 A38420			
EF070-2	gnl PID e125464	(AL022022) PGRS-family protein [Mycobacterium tuberculosis]	145		1.50E-12
EF070-2	gi 951460	FIM-C.1 gene product [Xenopus laevis] >pir A45155 A45155	109		2.70E-12
		mucin			
EF071-2	gnl PID e306428	unnamed protein product [Bacteriophage r1t] >gi 1353566	127		2.00E-37
		Lysin			
EF071-2	gi 853751	N-acetylmutaromyl-L-alanine amidase [Bacteriophage A511]	273		2.60E-36
EF073-2	gi 143830	xpaC [Bacillus subtilis] >gnl PID d1005803 hydrolysis of	173		7.10E-16

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF074-2	gi 1256698	chitinase [Serratia marcescens] >gi 1256698 chitinase [Serratia	618	2.60E-104
EF074-2	gi 1763985	chitinase A [Vibrio harveyi]	526	2.80E-84
EF075-2	gi 143156	membrane bound protein [Bacillus subtilis] >gnl PID e1184471	593	1.70E-91
EF075-2	pir D70070 D70 0	transcriptional regulator homolog ywtF - Bacillus subtilis	118	1.90E-59
EF075-2	gi 1762327	putative transcriptional regulator [Bacillus subtilis]	148	9.60E-53
EF075-2	gi 1276874	EpsA [Streptococcus thermophilus]	239	2.20E-33
EF075-2	gnl PID e289126	unknown [Streptococcus pneumoniae]	150	1.20E-27
EF075-2	gi 485275	putative regulatory protein [Streptococcus pneumoniae]	150	2.50E-27
EF075-2	gi 2804735	(AF030367) putative regulatory protein [Streptococcus pneumoniae]	150	2.50E-27
EF075-2	gi 2804747	(AF030369) putative regulatory protein [Streptococcus pneumoniae]	150	2.50E-27
EF075-2	gnl PID e116988	capsular polysaccharide synthesis protein [Streptococcus	148	5.30E-27
EF075-2	gi 2804769	(AF030373) putative regulatory protein [Streptococcus pneumoniae]	148	5.30E-27
EF075-2	gi 1147744	PSR [Enterococcus hirae]	109	2.10E-23
EF075-2	gi 790435	PSR [Enterococcus faecium] >pir S54177 S54177 PSR protein -	102	4.40E-19
EF075-2	gi 2267239	ORF1 [Staphylococcus epidermidis]	109	8.50E-19
EF075-2	gnl PID d10189 5	membrane bound protein LytR [Synechocystis sp.]	121	2.80E-16
EF077-2	gnl PID d10113 5	cadmium-transporting ATPase [Synechocystis sp.]	396	2.30E-113

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF077-2	gi 150719	cadmium resistance protein [Plasmid pI258] >pir A32561 A32561	373	8.60E-112
EF077-2	gi 143753	cadmium-efflux ATPase [Bacillus firmus] >pir D42707 D42707 probable	361	8.10E-111
EF077-2	gi 152978	E1-E2 cadmium efflux adenosine triphosphatase [Staphylococcus]	381	4.30E-110
EF077-2	gnl PID e248808	unknown [Mycobacterium tuberculosis]	298	3.50E-107
EF077-2	gi 495646	ATPase [Transposon Tn5422]	361	2.10E-106
EF077-2	gnl PID e118497	similar to heavy metal-transporting ATPase [Bacillus]	286	3.50E-104
EF077-2	gi 1699049	cadmium resistance protein [Lactococcus lactis]	352	3.60E-100
EF077-2	gnl PID e118603	similar to heavy metal-transporting ATPase [Bacillus]	254	9.90E-100
EF077-2	gnl PID e306540	unknown [Mycobacterium tuberculosis]	352	5.20E-88
EF077-2	gnl PID e263525	P-type ATPase [Mycobacterium tuberculosis] >gnl PID e249413	199	5.50E-86
EF077-2	gnl PID e264090	unknown [Mycobacterium tuberculosis]	250	3.00E-84
EF077-2	gnl PID d10113 5	cadmium-transporting ATPase [Synecocystis sp.]	260	1.00E-81
EF077-2	gi 1773166	probable copper-transporting atpase [Escherichia coli] >gi 1786691	212	4.70E-80
EF077-2	gi 1354935	probable copper-transporting atpase [Escherichia coli]	212	8.50E-79
EF078-2	gi 143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	257	5.50E-58
EF078-2	gi 410142	ORFX18 [Bacillus subtilis] >gnl PID e1185580 two-component sensor	235	8.20E-51

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF078-2	gnl PID d10119 6	homologous to sp:PHOR_BACSU [Bacillus subtilis]	219	4.20E-44
EF078-2	gi 1575578	histidine protein kinase [Thermotoga maritima]	191	7.10E-44
EF078-2	gi 2182990	histidine kinase [Lactococcus lactis cremoris]	169	6.40E-40
EF078-2	gi 2182992	histidine kinase [Lactococcus lactis cremoris]	152	1.10E-39
EF078-2	gnl PID d10113 4	sensory transduction histidine kinase [Synechocystis sp.]	259	3.90E-38
EF078-2	gi 149296	phosphate regulatory protein phoR (gtg start codon) [Klebsiella	228	7.60E-33
EF078-2	gi 581188	phoR gene product (AA 1-431) [Escherichia coli] >gi 1657596	226	1.60E-32
EF078-2	gnl PID d10108 7	sensory transduction histidine kinase [Synechocystis sp.]	138	3.70E-32
EF078-2	gnl PID e266592	unknown [Mycobacterium tuberculosis]	232	1.10E-31
EF078-2	gi 2182996	histidine kinase [Lactococcus lactis cremoris]	206	1.30E-31
EF078-2	gnl PID d10113 5	sensory transduction histidine kinase [Synechocystis sp.]	256	1.30E-31
EF078-2	gi 294893	phosphate regulatory protein phoR (gtg start codon) [Shigella	225	1.60E-31
EF078-2	gi 288420	drug sensory protein A [Synechocystis PCC6803] >gnl PID d1017420	106	2.50E-31
EF079-2	gi 2098719	putative fimbrial-associated protein [Actinomyces naeslundii]	183	8.60E-26
EF081-2	gi 467806	penicillin-binding protein [Enterococcus faecalis]	1356	2.10E-178
EF081-2	gi 790429	low affinity penicillin-binding protein 5 (PBP5) [Enterococcus	607	1.00E-78
EF081-2	gnl PID e208365	penicillin-binding protein 5 [Enterococcus faecium]	604	1.10E-78
EF081-2	gi 790433	low affinity penicillin-binding protein 5 (PBP5) [Enterococcus	604	2.70E-78

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF081-2	gi 790437	low affinity penicillin-binding protein 5 (PBP5) [Enterococcus]	602	5.10E-78
EF081-2	gi 790431	low affinity penicillin-binding protein 5 (PBP5) [Enterococcus]	591	2.60E-77
EF081-2	gi 43342	D-alanyl-D-alanine carboxypeptidase [Enterococcus hirae]	587	9.30E-77
EF081-2	gi 49000	D-alanyl-D-alanine carboxypeptidase [Enterococcus hirae]	572	5.20E-74
EF081-2	gn PID d10079 4	penicillin-binding protein 2 [Bacillus subtilis]	149	7.40E-24
EF081-2	gn PID e315088	MecA1 [Staphylococcus sciuri]	111	4.40E-19
EF081-2	gn PID e286651	MecA protein [Staphylococcus sciuri]	106	2.90E-18
EF081-2	gn PID e316581	MecA protein [Staphylococcus sciuri]	111	2.90E-18
EF081-2	gn PID e316607	MecA2 protein [Staphylococcus sciuri]	101	3.70E-14
EF081-2	gn PID e316613	MecA protein [Staphylococcus sciuri] >gi 46613 mecA gene	101	3.70E-14
EF083-2	gi 496283	lysin [Bacteriophage Tuc2009]	436	6.20E-176
EF083-2	gi 530798	LysB [Bacteriophage phi-LC3]	421	3.00E-175
EF083-2	gi 166183	muramidase [Bacteriophage CP-7]	186	1.20E-21
EF083-2	gi 166188	muramidase [Bacteriophage CP-9] >pir JQ0438 MUBPC9	188	5.00E-21
EF083-2	gi 623084	muramidase; muramidase [Bacteriophage LL-H]	193	8.40E-20
EF083-2	gi 166175	muramidase [Bacteriophage CP-1]	175	3.40E-19
EF083-2	gn PID e221272	lysozyme [Bacteriophage CP-1] >pir A31086 MUBPCP	175	3.40E-19
EF083-2	pir JQ0437 MU BP	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) - phage	171	9.50E-19
EF083-2	gi 410502	LysA [Bacteriophage mv4] >pir S38477 S38477 lytic enzyme lysA -	187	8.90E-17
EF083-2	gi 793850	lysin [Lactobacillus bacteriophage phi adh] >gn PID e1217314	117	5.60E-15

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		lysine			
EF084-2	gi 2293312	(AF008220) YtP [Bacillus subtilis] >gnl PID e1185879 similar to	438		1.70E-140
EF084-2	gi 2367234	(AE000425) hypothetical 43.8 kD protein in rhsB-pit intergenic	167		2.20E-51
EF084-2	gi 912464	No definition line found [Escherichia coli]	167		6.00E-51
EF084-2	gnl PID d101127	hypothetical protein [Synecocystis sp.] >pir S76678 S76678	151		6.10E-42
EF084-2	gi 1573954	hypothetical [Haemophilus influenzae] >pir G64161 G64161	142		2.90E-40
EF085-2	gi 1209527	protein histidine kinase [Enterococcus faecalis]	2023		8.00E-279
EF085-2	gi 467057	phoR; B2168_C3_247 [Mycobacterium leprae] >pir S72905 S72905	226		8.80E-23
EF085-2	gnl PID e119229	SenX3 [Mycobacterium bovis BCG]	222		3.10E-22
EF085-2	gnl PID e255152	unknown [Mycobacterium tuberculosis] >gnl PID e321546	222		3.10E-22
EF085-2	gi 1778485	PcoS homolog [Escherichia coli] >gi 1786783 (AE000162) f480; This	111		3.80E-16
EF085-2	gi 149296	phosphate regulatory protein phoR (gig start codon) [Klebsiella	110		1.40E-14
EF085-2	gi 581188	phoR gene product (AA 1-431) [Escherichia coli] >gi 1657596	103		5.30E-14
EF085-2	gi 143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	118		4.90E-13
EF085-2	gi 537239	alternate gene name phoM; CG Site No. 395 [Escherichia coli]	126		9.50E-13
EF085-2	gi 147251	phoM [Escherichia coli] >gi 809670 phoM protein (1 is 3rd base in	126		9.50E-13
EF085-2	gi 2182992	histidine kinase [Lactococcus lactis cremoris]	109		5.90E-12

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF086-2	gi 437706	alternative truncated translation product from E.coli [Streptococcus]	221	3.00E-54
EF086-2	gi 437705	hyaluronidase [Streptococcus pneumoniae]	221	1.60E-53
EF086-2	gi 595847	hyaluronate lyase [Streptococcus agalactiae] >pir A55137 A55137	203	3.30E-44
EF086-2	gi 705406	hyaluronate lyase [Staphylococcus aureus]	191	3.40E-42
EF086-2	gi 562086	hyaluronidase [Propionibacterium acnes]	198	6.00E-27
EF087-2	gi 437706	alternative truncated translation product from E.coli [Streptococcus]	221	3.00E-54
EF087-2	gi 437705	hyaluronidase [Streptococcus pneumoniae]	221	1.60E-53
EF087-2	gi 595847	hyaluronate lyase [Streptococcus agalactiae] >pir A55137 A55137	203	3.30E-44
EF087-2	gi 705406	hyaluronate lyase [Staphylococcus aureus]	191	3.40E-42
EF087-2	gi 562086	hyaluronidase [Propionibacterium acnes]	198	6.00E-27
EF088-2	gi 437706	alternative truncated translation product from E.coli [Streptococcus]	221	3.00E-54
EF088-2	gi 437705	hyaluronidase [Streptococcus pneumoniae]	221	1.60E-53
EF088-2	gi 595847	hyaluronate lyase [Streptococcus agalactiae] >pir A55137 A55137	203	3.30E-44
EF088-2	gi 705406	hyaluronate lyase [Staphylococcus aureus]	191	3.40E-42
EF088-2	gi 562086	hyaluronidase [Propionibacterium acnes]	198	6.00E-27
EF091-2	gi 556016	similar to plant water stress proteins; ORF2 [Bacillus subtilis]	198	5.50E-21
EF091-2	gi 2353333	(AF016513) Ce-LEA [Caenorhabditis elegans]	189	2.40E-17

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF091-2	gnl PID e353216	seed maturation protein homolog [Arabidopsis thaliana]	146	3.60E-11
EF091-2	gi 1161171	late embryogenesis abundant protein [Picea glauca]	132	5.70E-11
EF091-2	pir S04909 S049	embryonic protein DC8 (clone 8/10) - carrot	127	6.50E-11
EF092-2	gi 2689898	(AE000792) PTS system, cellobiose-specific IIB component (celA)	145	4.00E-27
EF092-2	gnl PID d10204 8	B. subtilis, cellobiose phosphotransferase system, celA;	116	1.40E-26
EF096-2	gi 147329	transport protein [Escherichia coli] >gnl PID d1015409	532	2.10E-91
EF096-2	gi 1573475	spermidine/putrescine-binding periplasmic protein precursor (potD)	527	1.10E-79
EF096-2	gi 1574803	spermidine/putrescine-binding periplasmic protein precursor (potD)	468	1.60E-75
EF096-2	gi 1142681	Lpp38 [Pasteurella haemolytica]	446	4.40E-72
EF096-2	gnl PID d10152 6	Putrescine transport protein PotF [Escherichia coli]	216	1.50E-54
EF096-2	gi 147334	periplasmic putrescine binding protein [Escherichia coli]	216	2.10E-53
EF096-2	gi 2688565	(AE001165) spermidine/putrescine ABC transporter,	240	2.00E-48
EF096-2	gi 1881733	PotD [Salmonella typhimurium]	253	2.70E-28
EF096-2	gnl PID d10192 6	spermidine/putrescine-binding periplasmic protein	243	4.20E-26
EF096-2	gnl PID e152543	potF gene product [Clostridium perfringens]	204	3.30E-21
EF097-2	gi 622991	mannitol transport protein [Bacillus stearothermophilus]	547	4.90E-93
EF097-2	gi 42034	mannitol permease [Escherichia coli] >gi 466737 mannitol-	535	5.50E-85

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		specific		
EF097-2	gi 633650	enzyme II(mannitol) [Staphylococcus carnosus] >pir S68193 S22385	516	2.10E-82
EF097-2	gi 882462	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia	509	3.00E-76
EF097-2	gi 312763	protein-N(pi)-phosphohistidine-sugar phosphotransferase [Escherichia	357	7.50E-70
EF097-2	gnl PID d10096 6	homologue of mannitol transport protein of B.	492	3.10E-62
EF097-2	gnl PID d10079 2	mannitol-specific phosphotransferase enzyme II [Bacillus	484	5.20E-61
EF097-2	gi 1673855	(AE000020) Mycoplasma pneumoniae, PTS system mannitol- specific	232	3.50E-59
EF097-2	gnl PID d10065 1	phosphotransferase enzymell, mannitol-specific [Mycoplasma	158	8.20E-18
EF097-2	pir S77757 S777	phosphotransferase system enzyme II (EC 2.7.1.69),	103	2.00E-13
EF100-2	gi 2058546	ComYC [Streptococcus gordonii]	193	7.30E-27
EF100-2	gi 2058546	ComYC [Streptococcus gordonii]	193	7.30E-27
EF100-2	gi 142708	comG3 gene product [Bacillus subtilis] >gnl PID e1185739 comGC	150	2.90E-22
EF100-2	gi 142708	comG3 gene product [Bacillus subtilis] >gnl PID e1185739 comGC	150	2.90E-22
EF100-2	gi 148437	secretory component [Erwinia chrysanthemi] >pir E47021 E47021 pectic	134	4.40E-15

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF100-2	gi 148437	secretory component [Erwinia chrysanthemi] >pir E47021 E47021 pectic	134	4.40E-15
EF100-2	gi 606262	ORF_o145 [Escherichia coli] >gi 693706 HopG [Escherichia coli]	136	9.10E-13
EF100-2	gi 606262	ORF_o145 [Escherichia coli] >gi 693706 HopG [Escherichia coli]	136	9.10E-13
EF100-2	gi 38828	ExeG gene product [Aeromonas hydrophila] >pir S22910 I49905 protein	132	3.50E-12
EF100-2	gi 38828	ExeG gene product [Aeromonas hydrophila] >pir S22910 I49905 protein	132	3.50E-12
EF100-2	gnl PID e117259	etpG [Escherichia coli]	131	5.10E-12
EF100-2	gnl PID e117259	etpG [Escherichia coli]	131	5.10E-12
EF100-2	gi 42189	outG gene product [Erwinia carotovora] >pir S32861 S32861 outG	130	9.90E-12
EF100-2	gi 42189	outG gene product [Erwinia carotovora] >pir S32861 S32861 outG	130	9.90E-12
EF100-2	gi 609628	putative [Vibrio cholerae]	128	1.60E-11
EF100-2	gi 609628	putative [Vibrio cholerae]	128	1.60E-11
EF101-2	gnl PID d10257 3	bacG [Enterococcus faecalis]	106	3.60E-17
EF101-2	gnl PID e321943	hypothetical protein [Enterococcus faecalis] >gnl PID e321943	105	1.80E-16
EF101-2	gnl PID e118502	similar to hypothetical proteins from B. subtilis [Bacillus	113	1.80E-15
EF110-2	gi 43338	Staphylococcal serine proteinase homologue [Enterococcus faecalis]	1462	2.30E-195

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF110-2	gnl PID d10010 8	glutamic acid specific protease prepropeptide [Staphylococcus	106	3.70E-14
EF110-2	gi 46687	preproenzyme (AA -68 to 268) [Staphylococcus aureus]	106	6.70E-14
EF111-2	gi 606018	ORF_o783 [Escherichia coli] >gi 1789462 (AE000390) hypothetical 88.3	477	8.10E-80
EF121-2	gi 2626826	YfkN [Bacillus subtilis] >gnl PID e1182774 similar to	143	1.30E-96
EF121-2	gi 2313187	(AE000532) 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB)	413	2.60E-82
EF121-2	gi 48453	5'-nucleotidase [Vibrio parahaemolyticus] >gnl PID d1001218	279	8.50E-47
EF121-2	gi 757842	UDP-sugar hydrolase [Escherichia coli]	239	1.60E-44
EF121-2	gi 1773162	UDP-sugar hydrolase precursor [Escherichia coli] >gi 1786687	239	1.60E-44
EF121-2	gi 47950	precursor polypeptide (AA -25 to 525) [Salmonella typhimurium]	229	2.10E-41
EF121-2	gi 747913	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Yersinia	115	4.70E-36
EF121-2	gi 62772	5'-nucleotidase [Discopyge ommata] >pir S19564 S19564 5'- nucleotidase	137	5.80E-35
EF121-2	gi 1573573	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Haemophilus	114	8.90E-34
EF121-2	gi 537054	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Escherichia coli]	110	1.10E-31
EF121-2	bbs 135915	5'-nucleotidase=glycosylphosphatidylinositol-anchored protein {EC	128	7.70E-29
EF121-2	gi 1737443	5'-nucleotidase [Boophilus microplus]	104	1.60E-28
EF121-2	gi 202551	5'-nucleotidase precursor (EC 3.1.3.5) [Rattus norvegicus]	138	6.10E-28
EF121-2	gi 349783	ecto-5'-nucleotidase [Mus musculus] >pir JC2001 JC2001	136	1.10E-27

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF121-2	gi 23897	5'-nucleotidase [Homo sapiens] >pir S11032 S11032 5'-nucleotidase (EC)	133	1.60E-27
EF122-2	gi 2626826	YfkN [Bacillus subtilis] >gn PID e1182774 similar to	143	1.30E-96
EF122-2	gi 2313187	(AE000532) 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB)	413	2.60E-82
EF122-2	gi 48453	5'-nucleotidase [Vibrio parahaemolyticus] >gn PID d1001218	279	8.50E-47
EF122-2	gi 757842	UDP-sugar hydrolase [Escherichia coli]	239	1.60E-44
EF122-2	gi 1773162	UDP-sugar hydrolase precursor [Escherichia coli] >gi 1786687	239	1.60E-44
EF122-2	gi 47950	precursor polypeptide (AA -25 to 525) [Salmonella typhimurium]	229	2.10E-41
EF122-2	gi 747913	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Yersinia]	115	4.70E-36
EF122-2	gi 62772	5'-nucleotidase [Discopyge ommata] >pir S19564 S19564 5'-nucleotidase	137	5.80E-35
EF122-2	gi 1573573	2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB) [Haemophilus]	114	8.90E-34
EF122-2	gi 537054	2',3'-cyclic-nucleotide 2'-phosphodiesterase [Escherichia coli]	110	1.10E-31
EF122-2	bbs 135915	5'-nucleotidase=glycosylphosphatidylinositol-anchored protein {EC	128	7.70E-29
EF122-2	gi 1737443	5'-nucleotidase [Boophilus microplus]	104	1.60E-28
EF122-2	gi 202551	5'-nucleotidase precursor (EC 3.1.3.5) [Rattus norvegicus]	138	6.10E-28
EF122-2	gi 349783	ecto-5'-nucleotidase [Mus musculus] >pir JC2001 JC2001	136	1.10E-27
EF122-2	gi 23897	5'-nucleotidase [Homo sapiens] >pir S11032 S11032 5'-nucleotidase (EC	133	1.60E-27
EF129-2	gi 43334	P54 protein [Enterococcus faecium] >pir S05542 S05542	630	9.40E-79

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

		hypothetical		
EF129-2	gi 512521	usp 45 gene product [Lactococcus lactis] >pir JN0097 JN0097 secreted	374	1.30E-42
EF129-2	gi 149525	secreted protein [Lactococcus lactis]	371	3.60E-42
EF129-2	gnl PID e313022	hypothetical protein [Bacillus subtilis] >gnl PID e1186168	317	2.30E-33
EF130-2	gi 488339	alpha-amylase [unidentified cloning vector]	621	6.70E-81
EF130-2	gi 488336	ORF [unidentified cloning vector]	242	8.00E-27
EF130-2	bbs 112518	alpha-amylase {N-terminal region} [Artificial sequence, Peptide]	237	4.80E-26
EF130-2	gnl PID e289144	ywpE [Bacillus subtilis] >gnl PID e1184540 ywpE [Bacillus]	129	5.40E-11
EF131-2	gnl PID e118528	penicillin-binding protein [Bacillus subtilis]	277	7.40E-43
EF131-2	gi 488330	alpha-amylase [unidentified cloning vector]	280	1.30E-31
EF131-2	gi 509249	No definition line found [Lactobacillus plantarum]	274	1.10E-30
EF131-2	gnl PID d10249 I	(AB009635) Fmt [Staphylococcus aureus]	170	5.60E-20
EF131-2	gi 515050	DD-peptidase precursor [Streptomyces lividans] >pir S48220 S48220	131	2.30E-14
EF131-2	gi 153448	serine DD-peptidase [Streptomyces lividans]	131	1.20E-12
EF132-2	gi 153826	adhesin B [Streptococcus sanguis] >pir A43583 A43583 adhesin B	1257	2.30E-166
EF132-2	gi 1184932	ScbA [Streptococcus crista]	1248	3.70E-165
EF132-2	gi 310633	adhesin [Streptococcus gordonii]	1247	5.10E-165
EF132-2	gi 393269	adhesion protein [Streptococcus pneumoniae]	1204	3.40E-163
EF132-2	gi 1575030	surface adhesin A precursor [Streptococcus pneumoniae]	1220	2.40E-161

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF132-2	gi 153834	adhesin specific for salivary pellicle of dental surfaces	1203	4.80E-159
EF132-2	gi 1117994	surface antigen A variant precursor [Streptococcus pneumoniae]	1191	2.00E-157
EF132-2	gi 493017	endocarditis specific antigen [Enterococcus faecalis]	931	3.70E-122
EF132-2	gn PIDe255529	lipoprotein [Staphylococcus epidermidis]	453	3.20E-92
EF132-2	gi 1245464	YfeA [Yersinia pestis] >gi 1245464 YfeA [Yersinia pestis]	364	3.60E-64
EF132-2	gi 1573330	adhesin B precursor (fimA) [Haemophilus influenzae]	349	3.50E-63
EF132-2	gi 755075	periplasmic-binding protein [Synechocystis sp.]	326	6.80E-62
		>gn PID d1018652 Mn		
EF132-2	gn PIDe118595	similar to ABC transporter (membrane protein) [Bacillus]	174	3.10E-32
EF132-2	gi 1777933	TroA [Treponema pallidum]	171	3.40E-32
EF132-2	gi 790546	Tromp1 [Treponema pallidum]	171	5.10E-32
Query	Derwent Access. No.	Derwent Gene Description	BLAST Score	BLAST P-Value
EF003-2	W20909	H. pylori outer membrane protein 14ge10705orf5.	268	4.20E-39
EF003-2	W20166	Helicobacter pylori outer membrane protein, 16225006.aa.	241	3.00E-27
EF006-2	W20909	H. pylori outer membrane protein 14ge10705orf5.	283	1.20E-48
EF006-2	W20166	Helicobacter pylori outer membrane protein, 16225006.aa.	266	1.10E-30
EF008-2	R37495	Pneumococcal fimbrial protein A.	967	1.20E-127
EF008-2	W26367	Staphylococcus aureus saliva binding protein.	467	7.50E-100
EF008-2	R79722	ROM precursor TROMP1.	181	8.00E-36
EF008-2	W22134	Treponema pallidum rare outer membrane protein (TROMP-1).	181	8.00E-36
EF009-2	W20909	H. pylori outer membrane protein 14ge10705orf5.	319	1.40E-53

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF009-2	W20166	Helicobacter pylori outer membrane protein, 16225006.aa.	278	2.50E-32
EF012-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	227	3.20E-69
EF014-2	W14070	S.thermophilus exopolysaccharide biosynthesis protein EpsR.	103	5.90E-19
EF014-2	W22169	S.thermophilus exopolysaccharide synthesis operon epsA gene product.	103	7.30E-18
EF016-2	W15799	Adherence factor 104R of Lactobacillus fermentum.	157	9.60E-22
EF016-2	W15793	Adherence factor consensus sequence.	103	1.00E-11
EF017-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	241	8.90E-71
EF021-2	R31013	P39-alpha.	141	1.60E-19
EF021-2	R33280	P39-beta.	134	7.00E-14
EF022-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	324	2.20E-65
EF023-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	155	9.90E-33
EF023-2	R70152	Streptococcus pneumoniae strain SPRU98 P1pA.	125	5.90E-17
EF027-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	233	2.20E-34
EF028-2	W17830	Thermophilic alkaline phosphatase.	202	7.70E-59
EF028-2	W11568	E.coli alkaline phosphatase mutant D153H/Q329A.	182	7.90E-56
EF028-2	W11570	E.coli alkaline phosphatase mutant D153H/K328H/Q329A.	182	7.90E-56
EF028-2	W26300	E.coli alkaline phosphatase mutant D153H/K328H/Q329A/D330H.	182	1.10E-55
EF028-2	W11565	E.coli alkaline phosphatase mutant D153H/K328H/D330A.	182	3.10E-55
EF028-2	W11557	E.coli alkaline phosphatase mutant D153H/D330N.	182	4.30E-55
EF028-2	W11561	E.coli alkaline phosphatase mutant D153H/D330A.	182	4.30E-55
EF028-2	W11555	E.coli alkaline phosphatase mutant D153H/K328H/D330N.	182	4.70E-55

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF028-2	W11566	E.coli alkaline phosphatase mutant D153H/K328H/D330L.	182	1.20E-54
EF028-2	W11569	E.coli alkaline phosphatase mutant K328H/Q329A.	180	1.70E-54
EF028-2	W11562	E.coli alkaline phosphatase mutant D153H/D330L.	182	1.70E-54
EF028-2	R26980	Fv(FRP5)-phoA recombinant antibody.	174	1.90E-54
EF028-2	W11567	E.coli alkaline phosphatase mutant Q329A.	179	2.30E-54
EF028-2	W11558	E.coli alkaline phosphatase mutant K328H/D330N.	176	6.40E-54
EF028-2	W11563	E.coli alkaline phosphatase mutant K328H/D330A.	176	6.40E-54
EF029-2	R10044	Plasmid pOW360 encoded Human Growth Hormone (HGH) - nuclease A	320	3.50E-40
EF029-2	R10041	Plasmid pOW350 nuclease A product.	320	4.30E-40
EF029-2	R73997	Staphylococcus aureus (Foggi) nuclease signal and mature sequences.	320	5.60E-40
EF029-2	R10043	Plasmid pOW360 encoding Human Growth Hormone (HGH) - nuclease	320	2.90E-38
EF030-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	277	6.10E-47
EF040-2	R59077	2-5A-dependent RNA-ase.	105	1.90E-18
EF040-2	W12703	Mouse 2-5A-dependent RNase.	105	1.90E-18
EF040-2	R82661	Partial murine 2-5A-dependent RNase.	105	1.90E-18
EF041-2	R48035	Hyaluronic acid synthase of Streptococcus equisimilis.	225	6.30E-26
EF054-2	R26042	P. yoelii SSP2 antigen.	286	8.00E-34
EF054-2	R85782	Group B Streptococcal mutant beta antigen without IgA binding domain.	232	3.30E-24
EF054-2	R85781	Group B Streptococcal wild-type beta antigen.	232	5.20E-24

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF054-2	P91941	Sequence of preprospasmolysin.	204	3.10E-19
EF054-2	W32519	Collagen-like polypeptide SEQ ID NO:2.	180	7.50E-18
EF054-2	W12324	Silver halide emulsion protein monomeric repeat unit #2.	180	7.50E-18
EF054-2	W32522	Collagen-like polypeptide SEQ ID NO:5.	192	1.60E-17
EF054-2	W12327	Silver halide emulsion protein monomeric repeat unit #5.	192	1.60E-17
EF054-2	W32520	Collagen-like polypeptide SEQ ID NO:3.	189	2.40E-17
EF054-2	W32532	Collagen-like polypeptide SEQ ID NO:15.	189	2.40E-17
EF054-2	W12325	Silver halide emulsion protein monomeric repeat unit #3.	189	2.40E-17
EF054-2	W12337	Silver halide emulsion protein monomeric repeat unit #15.	189	2.40E-17
EF054-2	W12341	Silver halide emulsion FLAG(RTM)-tagged protein #2.	189	2.60E-17
EF054-2	W02098	S. mutans antigen I/II.	161	5.40E-15
EF054-2	W02096	S. mutans antigen I/II fragment (aa803-1114).	161	1.90E-13
EF059-2	R26042	P. yoelii SSP2 antigen.	344	1.90E-39
EF059-2	R85782	Group B Streptococcal mutant beta antigen without IgA binding domain.	232	1.10E-26
EF059-2	R85781	Group B Streptococcal wild-type beta antigen.	232	1.70E-26
EF059-2	P91941	Sequence of preprospasmolysin.	200	1.50E-18
EF059-2	P60570	Sequence of the Falciparum Interspersed Repeat Antigen	186	4.60E-18
EF059-2	W02096	S. mutans antigen I/II fragment (aa803-1114).	167	8.20E-16
EF059-2	W02098	S. mutans antigen I/II.	167	4.90E-15
EF059-2	R79625	Endocarditis specific antigen region.	147	4.40E-12
EF059-2	R26049	MSF precursor.	143	1.30E-11
EF059-2	R28150	Sugar beet chitinase 1.	148	1.70E-11

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EF059-2	R26842	Protease from <i>S. Aureus</i> ATCC12600.	147	2.10E-11
EF059-2	R79643	Immunodominant antigen of <i>Streptococcus sobrinus</i> .	151	2.10E-11
EF059-2	W07539	Collagen like protein (CLP).	146	3.00E-11
EF061-2	R26042	<i>P. yoelii</i> SSP2 antigen.	241	1.70E-25
EF061-2	P60570	Sequence of the <i>Falciparum</i> Interspersed Repeat Antigen	199	1.60E-18
EF061-2	R85782	Group B <i>Streptococcal</i> mutant beta antigen without IgA binding domain.	153	2.40E-14
EF061-2	R85781	Group B <i>Streptococcal</i> wild-type beta antigen.	153	3.60E-14
EF061-2	P91941	Sequence of preprospasmolysin.	163	9.70E-14
EF061-2	P83194	Sequence of a bioadhesive precursor protein encoded by cDNA clone	156	7.90E-13
EF061-2	R28150	Sugar beet chitinase 1.	156	9.10E-13
EF061-2	W02096	<i>S. mutans</i> antigen I/II fragment (aa803-1114).	148	1.20E-12
EF061-2	P82971	Bioadhesive precursor protein from cDNA 52.	148	9.70E-12
EF061-2	W02098	<i>S. mutans</i> antigen I/II.	148	1.50E-11
EF062-2	W02098	<i>S. mutans</i> antigen I/II.	107	1.20E-36
EF062-2	R79643	Immunodominant antigen of <i>Streptococcus sobrinus</i> .	132	3.00E-36
EF063-2	W02098	<i>S. mutans</i> antigen I/II.	107	1.20E-36
EF063-2	R79643	Immunodominant antigen of <i>Streptococcus sobrinus</i> .	132	3.00E-36
EF064-2	W02098	<i>S. mutans</i> antigen I/II.	107	1.20E-36
EF064-2	R79643	Immunodominant antigen of <i>Streptococcus sobrinus</i> .	132	3.00E-36
EF071-2	R85294	Phage R1-t LytR lysin.	127	3.70E-38
EF071-2	R91515	<i>Listeria</i> phage lysin PLY511.	273	4.70E-37

Table 2. Closest matching sequences between the polypeptides of the present invention and sequences in GenBank and Derwent databases.

EF075-2	W14070	<i>S. thermophilus</i> exopolysaccharide biosynthesis protein EpsR.	239	4.20E-36
EF075-2	W22169	<i>S. thermophilus</i> exopolysaccharide synthesis operon epsA gene product.	239	4.00E-34
EF077-2	R97280	<i>Helicobacter</i> -specific ATPase 439.	258	4.10E-74
EF077-2	R48036	<i>Mycobacterium</i> BCG immunogen.	192	2.20E-67
EF077-2	W06712	<i>Helicobacter</i> -specific ATPase 948 (ORF-4).	220	2.50E-67
EF077-2	R70419	Rat homologue of human Wilson disease gene ATP7B.	186	9.80E-54
EF077-2	R72343	Wilson disease protein ATP7B.	176	6.70E-40
EF077-2	R06376	Product of the sscI gene.	166	3.10E-28
EF077-2	R75396	Flea sodium pump alpha subunit.	146	2.40E-25
EF077-2	W20891	<i>H. pylori</i> transporter protein, 14ce20219orf1.	156	8.60E-14
EF078-2	R56667	<i>Bacteroides fragilis</i> RprX regulatory response protein.	148	8.30E-18
EF078-2	R74630	Tomato TGETR1 ethylene response protein.	130	7.80E-13
EF078-2	R69849	Ethylene response (ETR) gene product.	128	1.70E-11
EF078-2	R69850	Ethylene response (ETR) mutant protein etr1-1.	128	1.70E-11
EF078-2	R69851	Ethylene response (ETR) mutant protein etr1-2.	128	1.70E-11
EF078-2	R69852	Ethylene response (ETR) mutant protein etr1-3.	128	1.70E-11
EF078-2	R69853	Ethylene response (ETR) mutant protein etr1-4.	128	1.70E-11
EF078-2	R24296	Regulatory protein VanS involved in glycopeptide resistance.	142	2.70E-11
EF081-2	R27253	Penicillin binding protein PBP2A-epi.	101	4.70E-16
EF081-2	R27256	Penicillin binding protein PBP2A-27R.	101	6.00E-15
EF081-2	R27257	Penicillin binding protein derivative #1.	101	6.20E-15
EF081-2	R27258	Penicillin binding protein derivative #2.	101	6.20E-15

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EF081-2	R27259	Penicillin binding protein derivative #3.	101	6.20E-15
EF081-2	R27260	Penicillin binding protein derivative #4.	101	6.20E-15
EF081-2	R27261	Penicillin binding protein derivative #5.	101	6.20E-15
EF081-2	R27263	Penicillin binding protein derivative #7.	101	6.20E-15
EF081-2	R27264	Penicillin binding protein derivative #8.	101	6.20E-15
EF081-2	R27262	Penicillin binding protein derivative #6.	101	6.50E-15
EF081-2	R30845	Sequence encoded by the mec A gene.	101	6.90E-15
EF081-2	R27255	Penicillin binding protein PBP2A-27R.	101	6.90E-15
EF081-2	R31216	Penicillin binding protein PBP2A-27R.	101	7.00E-15
EF110-2	R91042	V8 mature protease (aa 1-213).	106	6.60E-16
EF110-2	R91043	V8 mature protease (aa 1-214).	106	7.20E-16
EF110-2	R91044	V8 mature protease (aa 1-215).	106	7.80E-16
EF110-2	R26842	Protease from <i>S. Aureus</i> ATCC12600.	106	6.70E-15
EF110-2	R29644	Protease from <i>S. Aureus</i> .	106	1.20E-14
EF110-2	W22218	Protein encoded by pV8RPT(-) construct.	106	7.60E-14
EF110-2	R91033	Beta-galactosidase-V8 protease fusion protein.	106	7.60E-14
EF110-2	R91034	Beta-galactosidase-V8 protease fusion protein.	106	1.70E-13
EF110-2	W22219	Protein encoded by pV8D construct.	106	7.60E-13
EF110-2	R91035	Recombinant V8 protease V8D fusion protein.	106	7.60E-13
EF110-2	W22220	Protein encoded by pV8F construct.	106	7.90E-13
EF129-2	R14530	Usp45 protein.	374	2.40E-43
EF129-2	R14150	MSP encoded by pUCRS (DSM 5803).	372	4.70E-43
EF131-2	R37495	Pneumococcal fimbrial protein A.	1185	6.80E-163

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EF131-2	W26367	Staphylococcus aureus saliva binding protein.	418	3.70E-85
EF131-2	R79722	ROM precursor TROMP1.	171	9.00E-31
EF131-2	W22134	Treponema pallidum rare outer membrane protein (TROMP-1).	171	9.00E-31

TABLE 3. Conservative Amino Acid Substitutions.

Aromatic	Phenylalanine Tryptophan Tyrosine
Hydrophobic	Leucine Isoleucine Valine
Polar	Glutamine Asparagine
Basic	Arginine Lysine Histidine
Acidic	Aspartic Acid Glutamic Acid
Small	Alanine Serine Threonine Methionine Glycine

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

EF001-2	from about Asp-150 to about Lys-152, from about Ser-256 to about Tyr-259, from about Lys-360 to about Lys-363, from about Asn-406 to about Asp-408.
EF002-2	from about Asp-80 to about Asp-83, from about Asp-281 to about Gly-283.
EF003-2	from about Asn-263 to about Gly-266.
EF004-2	from about Asn-23 to about Asn-26, from about Lys-83 to about Ser-87, from about Tyr-154 to about Asp-159.
EF005-2	from about Lys-249 to about Glu-252.
EF006-2	from about Gly-23 to about Asp-28.
EF008-2	from about Thr-92 to about Gly-94, from about Pro-161 to about Asp-165, from about Gly-287 to about Thr-289.
EF010-2	from about Pro-129 to about Asn-131.
EF012-2	from about Asp-77 to about Asp-79, from about Asp-94 to about Lys-98, from about Asp-256 to about Thr-258, from about Glu-461 to about Asn-468.
EF013-2	from about Thr-30 to about Asp-32, from about Glu-73 to about Ala-75, from about Gln-164 to about Asn-166, from about Lys-193 to about Gly-195.
EF014-2	from about Ser-203 to about Asp-206, from about Gln-314 to about Gly-316
EF015-2	from about Pro-66 to about Gly-69.
EF016-2	from about Lys-236 to about Asn-239.
EF017-2	from about Ser-90 to about Gly-93, from about Thr-197 to about Lys-199, from about Lys-230 to about Asn-233, from about Ser-428 to about Gly-431.
EF018-2	from about Lys-159 to about Tyr-161, from about Asn-165 to about Ser-167, from about Asn-250 to about Arg-256, from about Asn-392 to about Gly-395, from about Lys-416 to about Tyr-418, from about Asn-428 to

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

	about Arg-430.
EF019-2	from about Arg-209 to about Ser-211, from about Lys-287 to about Ser-290.
EF020-2	from about Lys-57 to about Asn-62.
EF021-2	from about Ser-33 to about Gly-35, from about Glu-77 to about Gly-81, from about Asp-139 to about Lys-141, from about Glu-255 to about Ser-258, from about Gln-271 to about Tyr-277.
EF023-2	from about Lys-232 to about Asp-234, from about Arg-304 to about Gly-306, from about Thr-453 to about Arg-456, from about Ser-478 to about Thr-480.
EF025-2	from about Arg-183 to about Asp-185.
EF026-2	from about Ser-25 to about Asp-30, from about Asp-90 to about Asp-94, from about Gln-107 to about Asn-110.
EF027-2	from about Gln-72 to about Lys-74, from about Lys-229 to about Asp-231.
EF028-2	from about Asp-186 to about Gln-188.
EF029-2	from about Asp-118 to about Lys-122, from about Asp-124 to about Tyr-126.
EF031-2	from about Glu-30 to about Gly-33.
EF034-2	from about Glu-25 to about Gly-27, from about Glu-75 to about Thr-77.
EF36-2	from about Gln-177 to about Ser-179.
EF037-2	from about Ser-25 to about Asp-30, from about Asp-90 to about Asp-94, from about Gln-107 to about Asn-110.
EF038-2	from about Asn-77 to about Lys-79, from about Tyr-88 to about Asn-92.
EF040-2	from about Lys-167 to about Gly-172, from about Lys-240 to about Asn-242.

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

EF044-2	from about Arg-192 to about Gly-194, from about Asn-200 to about Asn-203.
EF045-2	from about Asp-159 to about Asn-161, from about His-172 to about Gly-174, from about Tyr-261 to about Gly-264, from about Lys-305 to about Glu-308.
EF046-2	from about Ser-18 to about Gly-23, from about Gln-41 to about Ser-47, from about Thr-76 to about Asp-78.
EF047-2	from about Asn-28 to about Asp-30, from about Asp-273 to about Asn-277.
EF048-2	from about Asp-138 to about Lys-141, from about Asp-152 to about Gly-154.
EF051-2	from about Asp-73 to about Gly-76.
EF053-2	from about Ser-79 to about Gly-82.
EF055-2	from about Asp-26 to about Gly-28, from about Gln-67 to about Asp-69, from about Arg-71 to about Gly-74, from about Arg-87 to about Gly-89.
EF056-2	from about Arg-71 to about Gly-74, from about Arg-87 to about Gly-89.
EF058-2	from about Lys-129 to about Gly-133, from about Gln-571 to about Tyr-573, from about Pro-586 to about Gly-591.
EF065-2	from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642.
EF066-2	from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642.
EF067-2	from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642.

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

EF073-2	from about Met-98 to about Arg-100, from about Arg-110 to about Asp-112.
EF074-2	from about Ser-53 to about Tyr-59, from about Ser-86 to about Gly-88, from about Pro-97 to about Gln-100, from about Gln-230 to about Gly-232.
EF076-2	from about Asn-38 to about Tyr-40, from about Asp-48 to about Asn-53, from about Lys-79 to about Gly-81.
EF077-2	from about Arg-411 to about Gly-413.
EF078-2	from about Thr-294 to about Gly-296, from about Asp-366 to about Gln-368, from about Glu-524 to about Gly-526.
EF080-2	from about Glu-164 to about Gly-166, from about Ser-206 to about Tyr-208, from about Lys-239 to about Gly-243.
EF081-2	from about Asn-7 to about Ser-11, from about Lys-77 to about Tyr-80, from about Lys-112 to about Asn-114, from about Gly-162 to about Asp-164, from about Arg-181 to about Gly-183.
EF083-2	from about Gln-38 to about Arg-40.
EF084-2	from about Lys-140 to about Asp-142, from about Gly-164 to about Arg-166, from about Arg-262 to about Gly-264.
EF085-2	from about Asn-95 to about Asp-97, from about Arg-112 to about Asp-114, from about Asp-258 to about Ser-260, from about Arg-401 to about Ser-403.
EF086-2	from about Pro-112 to about Gly-115, from about Ser-222 to about Ser-224, from about Asn-296 to about Gly-299, from about Thr-346 to about Lys-348, from about Asp-428 to about Ser-432.
EF087-2	from about Pro-112 to about Gly-115, from about Ser-222 to about Ser-224, from about Asn-296 to about Gly-299, from about Thr-346 to about Lys-348, from about Asp-428 to about Ser-432.
EF088-2	from about Pro-112 to about Gly-115, from about Ser-222 to about Ser-224, from about Asn-296 to about Gly-299, from about Thr-346 to about Lys-348, from about Asp-428 to about Ser-432.

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

EF090-2	from about Arg-2 to about Arg-5.
EF091-2	from about Gln-40 to about Asp-43.
EF093-2	from about Lys-95 to about Gly-97.
EF094-2	from about Asp-314 to about Asp-316.
EF095-2	from about Ser-328 to about Thr-330, from about Asp-359 to about Asp-363, from about Glu-637 to about Gly-639, from about Asn-744 to about Gly-746.
EF096-2	from about Pro-128 to about Asn-130, from about Ser-193 to about Asp-196.
EF097-2	from about Val-357 to about Gly-359.
EF099-2	from about Glu-44 to about Asp-47, from about Lys-154 to about Gly-156, from about Asn-286 to about Asp-289.
EF101-2	from about Lys-40 to about Asp-42, from about Pro-255 to about Asn-258, from about Lys-288 to about Gly-290.
EF102-2	from about Asp-314 to about Asp-316.
EF103-2	from about Asn-46 to about Gly-48.
EF104-2	from about Pro-232 to about Lys-237, from about Ala-362 to about Asn-366, from about Ser-421 to about Gly-423, from about Lys-488 to about Ser-490, from about Asp-550 to about Asn-552, from about Pro-637 to about Lys-640, from about Asp-727 to about Gly-729, from about Asn-751 to about Ser-754, from about Lys-771 to about Asn-774, from about Ile-835 to about Asn-837, from about Pro-851 to about Gly-853.
EF105-2	from about Ser-40 to about Gly-43, from about Asn-94 to about Gln-97, from about Gln-220 to about Gly-222, from about Asn-263 to about Gly-265.
EF106-2	from about Asp-72 to about Gly-75, from about Thr-274 to about Asp-277, from about Asn-310 to about Arg-313.
EF107-2	from about Thr-155 to about Asn-157, from about Thr-189 to about Asp-

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

	191, from about Arg-270 to about Gly-272, from about Thr-330 to about Lys-335, from about Asp-365 to about Asp-368, from about Pro-451 to about Asp-453, from about Gly-485 to about Thr-488.
EF108-2	from about Lys-142 to about Trp-145, from about Thr-147 to about Tyr-150, from about Arg-212 to about Gly-214, from about Ser-248 to about Asp-251, from about Asp-384 to about Asp-387, from about Pro-481 to about Arg-483, from about Lys-491 to about Gly-494, from about Thr-619 to about Gly-624, from about Asp-656 to about Asp-659, from about Lys-717 to about Asn-721, from about Ser-822 to about Gly-824, from about Tyr-1137 to about Thr-1141.
EF110-2	from about Pro-123 to about Gly-127, from about Thr-223 to about Gly-225.
EF111-2	from about Lys-207 to about Asn-209, from about Asp-245 to about Asn-248, from about Lys-396 to about Asp-398, from about Glu-429 to about Ser-432, from about Thr-470 to about His-474.
EF119-2	from about Asp-90 to about Asn-92, from about Gln-142 to about Gly-144.
EF121-2	from about Asn-159 to about Asp-161, from about Asn-351 to about Lys-353, from about Pro-658 to about Gly-660, from about Lys-786 to about Ser-789.
EF122-2	from about Asn-159 to about Asp-161, from about Asn-351 to about Lys-353, from about Pro-658 to about Gly-660, from about Lys-786 to about Ser-789.
EF123-2	from about Asn-331 to about Arg-336, from about Asp-634 to about Gly-636, from about Glu-780 to about Ser-782, from about Tyr-909 to about Asn-911, from about Lys-939 to about Glu-942, from about Asp-1074 to about Gly-1076, from about Asp-1367 to about Gly-1369, from about Pro-1433 to about Lys-1435, from about Gly-1516 to about Asp-1518, from about Lys-1656 to about Asp-1660, from about Lys-1860 to about Gln-1863, from about Ser-1916 to about Gln-1919, from about Pro-1940 to about Gly-1942.
EF124-2	from about Asn-331 to about Arg-336, from about Asp-634 to about Gly-636, from about Glu-780 to about Ser-782, from about Tyr-909 to about Asn-911, from about Lys-939 to about Glu-942, from about Asp-1074 to about Gly-1076, from about Asp-1367 to about Gly-1369, from about Pro-1433 to about Lys-1435, from about Gly-1516 to about Asp-1518,

Table 4. Residues Comprising Antigenic Epitope-Bearing Portion.

	from about Lys-1656 to about Asp-1660, from about Lys-1860 to about Gln-1863, from about Ser-1916 to about Gln-1919, from about Pro-1940 to about Gly-1942.
EF125-2	from about Asn-331 to about Arg-336, from about Asp-634 to about Gly-636, from about Glu-780 to about Ser-782, from about Tyr-909 to about Asn-911, from about Lys-939 to about Glu-942, from about Asp-1074 to about Gly-1076, from about Asp-1367 to about Gly-1369, from about Pro-1433 to about Lys-1435, from about Gly-1516 to about Asp-1518, from about Lys-1656 to about Asp-1660, from about Lys-1860 to about Gln-1863, from about Ser-1916 to about Gln-1919, from about Pro-1940 to about Gly-1942.
EF126-2	from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642.
EF127-2	from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642.
EF128-2	from about Ser-236 to about Tyr-239, from about Asp-350 to about Gly-352, from about Lys-415 to about Asn-418, from about Arg-446 to about Asp-448, from about Asn-489 to about Lys-491, from about Ser-516 to about Asp-518, from about Glu-639 to about Lys-642.
EF129-2	from about Asn-300 to about Gly-302, from about Ser-316 to about Gly-319, from about Asn-385 to about His-387
EF131-2	from about Lys-201 to about Tyr-204, from about Glu-263 to about Ser-266.
EF132-2	from about Thr-26 to about Ser-28.

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>10</u> , line <u>12</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>May 2, 1997</u>	Accession Number <u>55969</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: right; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="text-align: center; margin-bottom: 10px;"></div> <div style="border-top: 1px solid black; margin-top: 10px;">Authorized officer</div>	<div style="text-align: right; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; margin-top: 10px;">Authorized officer</div>
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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence selected from the group consisting of:
 - (a) a nucleotide sequence encoding any one of the amino acid sequences of the polypeptides shown in Table 1; or
 - (b) a nucleotide sequence complementary to any one of the nucleotide sequences in (a).
 - (c) a nucleotide sequence at least 95% identical to any one of the nucleotide sequences shown in Table 1; or,
 - (d) a nucleotide sequence at least 95% identical to a nucleotide sequence complementary to any one of the nucleotide sequences shown in Table 1.
2. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which hybridizes under stringent hybridization conditions to a polynucleotide having a nucleotide sequence identical to a nucleotide sequence in (a) or (b) of claim 1.
3. An isolated nucleic acid molecule of claim 1 comprising a polynucleotide which encodes an epitope-bearing portion of a polypeptide in (a) of claim 1.
4. The isolated nucleic acid molecule of claim 3, wherein said epitope-bearing portion of a polypeptide comprises an amino acid sequence listed in Table 4.
5. A method for making a recombinant vector comprising inserting an isolated nucleic acid molecule of claim 1 into a vector.
6. A recombinant vector produced by the method of claim 5.
7. A host cell comprising the vector of claim 6.
8. A method of producing a polypeptide comprising:
 - (a) growing the host cell of claim 7 such that the protein is expressed by the cell; and
 - (b) recovering the expressed polypeptide.
9. An isolated polypeptide comprising a polypeptide selected from the group consisting of:
 - (a) a polypeptide consisting of one of the complete amino acid sequences of Table 1;
 - (b) a polypeptide consisting of one the complete amino acid sequences of Table 1 except the N-terminal residue;

- (c) a fragment of the polypeptide of (a) having biological activity; and
- (d) a fragment of the polypeptide of (a) which binds to an antibody specific for the polypeptide of (a).

10. An isolated antibody specific for the polypeptide of claim 9.

11. A polypeptide produced according to the method of claim 8.

12. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of an amino acid sequence of any one of the polypeptides in Table 1.

13. An isolated polypeptide antigen comprising an amino acid sequence of an *E. faecalis* epitope shown in Table 4.

14. An isolated nucleic acid molecule comprising a polynucleotide with a nucleotide sequence encoding a polypeptide of claim 9.

15. A hybridoma which produces an antibody of claim 10.

16. A vaccine, comprising:

(1) one or more *E. faecalis* polypeptides selected from the group consisting of a polypeptide of claim 9; and

(2) a pharmaceutically acceptable diluent, carrier, or excipient;

wherein said polypeptide is present, in an amount effective to elicit protective antibodies in an animal to a member of the *Enterococcus* genus.

17. A method of preventing or attenuating an infection caused by a member of the *Enterococcus* genus in an animal, comprising administering to said animal a polypeptide of claim 9, wherein said polypeptide is administered in an amount effective to prevent or attenuate said infection.

18. A method of detecting *Enterococcus* nucleic acids in a biological sample comprising:

(a) contacting the sample with one or more nucleic acids of claim 1, under conditions such that hybridization occurs, and

(b) detecting hybridization of said nucleic acids to the one or more *Enterococcus* nucleic acid sequences present in the biological sample.

19. A method of detecting *Enterococcus* nucleic acids in a biological sample obtained from an animal, comprising:

- (a) amplifying one or more *Enterococcus* nucleic acid sequences in said sample using polymerase chain reaction, and
- (b) detecting said amplified *Enterococcus* nucleic acid.

20. A kit for detecting *Enterococcus* antibodies in a biological sample obtained from an animal, comprising

- (a) a polypeptide of claim 9 attached to a solid support; and
- (b) detecting means.

21. A method of detecting *Enterococcus* antibodies in a biological sample obtained from an animal, comprising

- (a) contacting the sample with a polypeptide of claim 9; and
- (b) detecting antibody-antigen complexes.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/31, C07K 14/315, 16/12, C12Q 1/68, C12N 1/21, 5/12, G01N 33/569, 33/68, A61K 39/09		A3	(11) International Publication Number: WO 98/50554
			(43) International Publication Date: 12 November 1998 (12.11.98)
(21) International Application Number: PCT/US98/08959		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).	
(22) International Filing Date: 4 May 1998 (04.05.98)		Published <i>With international search report.</i>	
(30) Priority Data: 60/044,031 6 May 1997 (06.05.97) US 60/046,655 16 May 1997 (16.05.97) US 60/066,009 14 November 1997 (14.11.97) US			
(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).		(88) Date of publication of the international search report: 1 April 1999 (01.04.99)	
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(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).			
(54) Title: <i>ENTEROCOCCUS FAECALIS</i> POLYNUCLEOTIDES AND POLYPEPTIDES			
(57) Abstract			
<p>The present invention relates to novel genes from <i>Enterococcus faecalis</i> and the polypeptides they encode. Also provided are vectors, host cells, antibodies and methods for producing the same. The invention additionally relates to diagnostic methods for detecting <i>Enterococcus</i> nucleic acids, polypeptides and antibodies in a biological sample. The present invention further relates to novel vaccines for the prevention or attenuation of infection by <i>Enterococcus</i>.</p>			

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/08959

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 C07K14/315 C07K16/12 C12Q1/68 C12N1/21
C12N5/12 G01N33/569 G01N33/68 A61K39/09

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EVERS S & COURVALIN P: "Regulation of VanB-Type vancomycin resistance gene expression by the VanS(B)-VanR (B) two-component regulatory system in Enterococcus faecalis V583." JOURNAL OF BACTERIOLOGY, vol. 178, 1996, pages 1302-1309, XP002073904 see abstract --- -/--	1-21



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

2 September 1998

Date of mailing of the international search report

03.12.98

Name and mailing address of the ISA

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Authorized officer

Lejeune, R

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/08959

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	CLARK I M ET AL: "ISOLATION AND SEQUENCE DETERMINATION OF AN IMMUNODOMINANT ANTIGEN FROM ENTEROCOCCUS FAECALIS" SERODIAGNOSIS AND IMMUNOTHERAPY IN INFECTIOUS DISEASE, vol. 5, no. 2, July 1993, pages 85-92, XP002050866 see abstract see figure 3 ---	1-21
A	LOWE A M ET AL: "Cloning of an Enterococcus faecalis endocarditis antigen: homology with adhesins from some oral Streptococci." INFECTION AND IMMUNITY, vol. 63, no. 2, February 1995, pages 703-706, XP002073905 see abstract see figure 2 ---	1-21
A	BURNIE J P & CLARK I: "Diagnosing endocarditis with the cloned 112 kDa antigen of Enterococcus faecalis." JOURNAL OF IMMUNOLOGICAL METHODS, vol. 123, 1989, pages 217-225, XP002074342 see abstract see page 222, column 1, paragraph 2 ---	1-21
P,A	XU Y ET AL: "Enterococcus faecalis antigens in human infections." INFECTION AND IMMUNITY, vol. 65, no. 10, October 1997, pages 4207-4215, XP002073906 see abstract ---	1-21
X	EP 0 652 291 A (FUSO PHARMACEUTICAL IND ;OHNO TSUNEYA (JP)) 10 May 1995 see abstract see page 4, line 27 - line 31 see claim 5 -----	19

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/ 08959

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim(s) 17
is(are) directed to a method of treatment of the human/animal
body, the search has been carried out and based on the alleged
effects of the compound/composition.
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such
an extent that no meaningful International Search can be carried out, specifically:
Further defects(s) under article 17(2)(a):
The gene EF078 which is mentioned in Table 4, is not cited in Table 1
and is also absent from the sequence listing.
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all
searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment
of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report
covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is
restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

See extra sheet, Invention 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Inventions 7 to 41: Claims: (1-21) partially

Idem as invention 1, but concerning EF008 to EF0042

Inventions 42 to 74: Claims: (1-21) partially

Idem as invention 1, but concerning EF045 to EF077

Inventions 75 to 107: Claims: (1-21) partially

Idem as invention 1, but concerning EF079 to EF111

Inventions 108 to 123: Claims: (1-21) partially

Idem as invention 1, but concerning EF117 to EF132

Invention 124: Claim: 13 partially

An isolated polypeptide antigen comprising an amino acid sequence of an Enterococcus faecalis epitope of EF078 shown in Table 4.

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

Inform: on patent family members

International Application No

PCT/US 98/08959

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 0652291 A	10-05-95	AU 684250 B	11-12-97
		AU 4513593 A	31-01-94
		US 5807673 A	15-09-98
		WO 9401583 A	20-01-94
		JP 2798499 B	17-09-98
		US 5763188 A	09-06-98
		US 5770375 A	23-06-98
		US 5798211 A	25-08-98
